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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:10 ; Search time 117.948 Seconds
(without alignments)
119.206 Million cell updates/sec

Title: US-10-755-382-28
Perfect score: 160
Sequence: 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	159	99.4	32	2	AAR85155	Aar85155 Human ONS
2	159	99.4	32	2	AAR96288	Aar96288 Light cha
3	159	99.4	32	9	ADY31306	Ady31306 Human ant
4	159	99.4	32	9	ADY31297	Ady31297 Human ant
5	159	99.4	75	2	AAW62802	Aaw62802 Amino aci
6	159	99.4	75	2	AAW62818	Aaw62818 Amino aci
7	159	99.4	76	2	AAW80980	Aaw80980 Variable
8	159	99.4	76	6	ABO04825	Abo04825 Human epi
9	159	99.4	76	9	AEA17737	Aea17737 Hybridoma
10	159	99.4	80	8	ADU97910	Adu97910 Amino aci
11	159	99.4	80	9	AEB26568	Aeb26568 Human ant
12	159	99.4	85	2	AAR06351	Aar06351 M13 VKPCR
13	159	99.4	86	2	AAY39533	Aay39533 Humanised
14	159	99.4	86	5	ABB83945	Abb83945 Humanised
15	159	99.4	86	6	ABG75598	ABG75598 REI frame
16	159	99.4	90	3	AAY71451	Aay71451 Human mod
17	159	99.4	90	3	AAB19753	Aab19753 Human lig
18	159	99.4	90	4	ABB19441	Abb19441 Protein #
19	159	99.4	90	4	AAM67153	Aam67153 Human bon
20	159	99.4	90	4	AAM54766	Aam54766 Human bra
21	159	99.4	90	4	ABG48819	Abg48819 Human liv
22	159	99.4	90	4	AAM02744	Aam02744 Peptide #
23	159	99.4	90	5	ABG36817	Abg36817 Human pep
24	159	99.4	95	6	ABO27123	Abo27123 Human ger
25	159	99.4	95	6	ABO27124	Abo27124 Human ger
26	159	99.4	95	7	ADC99830	Adc99830 Germline
27	159	99.4	95	7	ADD05434	Add05434 Anti-MUC1
28	159	99.4	95	7	ADF10073	Adf10073 VEGF anti
29	159	99.4	95	7	ADF09968	Adf09968 Antibody
30	159	99.4	95	7	ADF10176	Adf10176 Antibody
31	159	99.4	95	7	ADF10074	Adf10074 VEGF anti
32	159	99.4	95	7	ADF09969	Adf09969 Antibody
33	159	99.4	95	7	ADF10175	Adf10175 Antibody
34	159	99.4	95	7	ADF09872	Adf09872 Anti-MUC1
35	159	99.4	95	7	ADJ80244	Adj80244 Vkappa ge
36	159	99.4	95	7	ADJ80243	Adj80243 Vkappa ge
37	159	99.4	95	8	ADO07313	Ado07313 Human ant
38	159	99.4	95	8	ADO07312	Ado07312 Human ant
39	159	99.4	95	8	ADU86533	Adu86533 Immunoglo
40	159	99.4	95	8	ADU86534	Adu86534 Immunoglo
41	159	99.4	95	9	ADY75418	Ady75418 Human ger
42	159	99.4	95	9	ADY75417	Ady75417 Human ger
43	159	99.4	95	9	ADZ47744	Adz47744 Human ger
44	159	99.4	95	9	AEB13628	Aeb13628 Human var
45	159	99.4	95	9	AEB13576	Aeb13576 Human var

ALIGNMENTS

RESULT 1
AAR85155
ID AAR85155 standard; protein; 32 AA.
XX
AC AAR85155;
XX
DT 18-JAN-1996 (first entry)
XX
DE Human ONS-M21 antibody light variable region FR 3.
XX
KW Human; ONS-M21 antibody; light variable region; chimeric protein;
KW framework region; FR 3; medulloblastoma; brain tumour; treatment;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO9514041-A1.
XX
PD 26-MAY-1995.
XX
PF 19-OCT-1994; 94WO-JP001763.
XX
PR 19-NOV-1993; 93JP-00291078.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Ohtomo T, Sato K, Tsuchiya M;
XX
DR WPI; 1995-200347/26.
XX
PT Reconstituted antibody against human medullo:blastoma cells - contains
PT high proportion of human antibody origin and has low antigenicity.
XX
PS Claim 9; Page 101; 120pp; Japanese.
XX
CC AAR85153-R85156 are human antibody ONS-M21 light variable region
CC framework regions (FRs). They were used in the construction of a
CC human/murine chimeric antibody, reactive with human medullo- blastoma (a
CC brain tumour) cells. The chimeric antibody can be used in the diagnosis
CC and treatment of this disease
XX
SQ Sequence 32 AA;

Query Match 99.4%; Score 159; DB 2; Length 32;
Best Local Similarity 93.8%; Pred. No. 3.4e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||||||||||||||||||||
Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32
```

RESULT 2
AAR96288
ID AAR96288 standard; peptide; 32 AA.
XX
AC AAR96288;
XX
DT 07-JAN-1997 (first entry)
XX
DE Light chain framework region 3 for human EGF-R antibody.
XX
KW Antibody; Ab; human; EGF-R; epidermal growth factor receptor; monoclonal;
KW humanised antibody; framework region; antigen binding site; light chain;
KW CDR; heavy chain; gamma-1 chain; kappa chain; immunoglobulin; epithelium;
KW malignant tumour; breast; bladder; ovary; colon; lung; brain; oesophagus;
KW therapy.
XX
OS Synthetic.
XX
PN EP712863-A1.
XX
PD 22-MAY-1996.
XX
PF 15-NOV-1995; 95EP-00203126.
XX
PR 18-NOV-1994; 94CU-00000128.
XX
PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX
PI Mateo Del Acosta Del Rio CM, Rodriquez RP, Frias EM;
XX
DR WPI; 1996-252836/26.
XX
PT Humanised and chimeric antibodies for EGF receptor - used in diagnosis
PT and therapy of tumours.
XX
PS Claim 6; Page 12; 24pp; English.
XX
CC AAR96286-R96293 represent framework regions (FR) for a humanised
CC monoclonal antibody (Ab) specific for the human epidermal growth factor
CC (EGF) receptor. This Ab binds to human EGF-R, and inhibits binding of EGF
CC to the EGF-R. The humanised Ab comprises antigen binding sites (CDR's) of
CC non-human origin, and FRs of the variable and constant regions of light
CC and heavy chains of human origin. The constant heavy chain region used
CC comprises the amino acid sequence of a gamma-1 chain. The constant light
CC chain region used comprises the kappa chain of a human immunoglobulin.
CC High levels of EGF-R have been detected in malignant tumours originating
CC in the epithelium. These include breast tumours, bladder tumours, ovarian
CC tumours, colonic tumours, lung tumours, brain tumours and tumours of the
CC oesophagus. The presence of EGF-R in tumour cells is an indicator of a
CC poor prognosis (particularly in human breast cancer). The Ab can
CC therefore be used for diagnostic localisation and assessment of tumour
CC growth. The Ab can also be used in the design of a drug targetted to the
CC tumour
XX
SQ Sequence 32 AA;

```
  Query Match             99.4%;  Score 159;  DB 2;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 3.4e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||||||||||||||||||||
Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32
```

RESULT 3
ADY31306
ID ADY31306 standard; peptide; 32 AA.
XX
AC ADY31306;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody kappa chain framework peptide - SEQ ID 138.
XX
KW DNA library; humanized antibody; antibody engineering;
KW kappa chain framework.
XX
OS Homo sapiens.
XX
PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
PF 20-AUG-2004; 2004US-00923068.
XX
PR 22-AUG-2003; 2003US-0497213P.
PR 13-OCT-2003; 2003US-0510741P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Wu H, Dall-Acqua W, Damschroder M;
XX
DR WPI; 2005-180802/19.
XX
PT New library of nucleic acid sequences comprises nucleotide sequences
PT encoding humanized heavy chain variable regions and humanized light chain
PT variable regions, useful for producing humanized antibodies.
XX
PS Disclosure; SEQ ID NO 138; 179pp; English.
XX
CC The invention comprises a library of nucleotide sequences encoding
CC humanized antibody heavy chain variable regions and humanized antibody
CC light chain variable regions. The library of the invention is useful for
CC producing humanized antibodies, or for re-engineering or reshaping an
CC antibody from a first species for use in a second species. The present
CC amino acid sequence represents a human germline kappa chain framework
CC peptide.
XX
SQ Sequence 32 AA;

```
  Query Match             99.4%;  Score 159;  DB 9;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 3.4e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||||||||||||||||||||
Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32
```

RESULT 4
ADY31297
ID ADY31297 standard; peptide; 32 AA.
XX
AC ADY31297;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody kappa chain framework peptide - SEQ ID 129.
XX
KW DNA library; humanized antibody; antibody engineering;
KW kappa chain framework.
XX
OS Homo sapiens.
XX
PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
PF 20-AUG-2004; 2004US-00923068.
XX

PR 22-AUG-2003; 2003US-0497213P.
PR 13-OCT-2003; 2003US-0510741P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Wu H, Dall-Acqua W, Damschroder M;
XX
DR WPI; 2005-180802/19.
XX
PT New library of nucleic acid sequences comprises nucleotide sequences
PT encoding humanized heavy chain variable regions and humanized light chain
PT variable regions, useful for producing humanized antibodies.
XX
PS Disclosure; SEQ ID NO 129; 179pp; English.
XX
CC The invention comprises a library of nucleotide sequences encoding
CC humanized antibody heavy chain variable regions and humanized antibody
CC light chain variable regions. The library of the invention is useful for
CC producing humanized antibodies, or for re-engineering or reshaping an
CC antibody from a first species for use in a second species. The present
CC amino acid sequence represents a human germline kappa chain framework
CC peptide.
XX
SQ Sequence 32 AA;

Query Match 99.4%; Score 159; DB 9; Length 32;
Best Local Similarity 93.8%; Pred. No. 3.4e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
||| ||||| |||||||||||||||||||||
Db 1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32

RESULT 5
AAW62802
ID AAW62802 standard; peptide; 75 AA.
XX
AC AAW62802;
XX
DT 23-SEP-1998 (first entry)
XX
DE Amino acid sequence of a human antibody fragment.
XX
KW Human; immunoglobulin; Ig; transgenic; non-human mammal;
KW inactivated endogenous Ig locus; B-cell development;
KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
KW production; antibody.
XX
OS Homo sapiens.
XX
PN WO9824893-A2.
XX
PD 11-JUN-1998.
XX
PF 03-DEC-1997; 97WO-US023091.
XX
PR 03-DEC-1996; 96US-00759620.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Jakobovits A, Kucherlapati R, Klapholz S, Mendez M, Green L;
XX
DR WPI; 1998-333314/29.
XX
PT New transgenic non-human mammals - having an inactivated immunoglobulin
PT locus and a near complete human immunoglobulin locus, used for production
PT of human antibodies.
XX
PS Disclosure; Page 76; 128pp; English.
XX
CC AAW62793-822 represent fragments of human antibodies produced by
CC transgenic Xenomice, created using the method of the invention. The
CC specification describes a transgenic non-human mammal which has genome
CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)
CC locus, so that the mammal does not display normal B-cell development. The
CC modified genome also has an inserted human heavy chain Ig locus in
CC germline configuration, the human heavy chain Ig locus comprising a human
CC micro constant region and regulatory and switch sequences, human J-H
CC genes, human D-H genes, and human V-H genes and an inserted human kappa
CC light chain Ig locus in germline configuration, the human kappa light
CC chain Ig locus comprising a human kappa constant region, J-kappa genes,
CC and V-kappa genes, where the number of V-H and V-kappa genes inserted are
CC selected to restore normal B-cell development in the mammal. The
CC transgenic animals have a near complete human Ig locus, including both a
CC human heavy chain locus and a human kappa light chain locus. They can be
CC used for the production of human antibodies when exposed to particular
CC antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha the mice
CC will produce antibodies to IL-8, EGFR or TNF- alpha respectively
XX
SQ Sequence 75 AA;

Query Match 99.4%; Score 159; DB 2; Length 75;
Best Local Similarity 93.8%; Pred. No. 7.9e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
||| ||||| |||||||||||||||||||||
Db 38 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 69

RESULT 6
AAW62818
ID AAW62818 standard; peptide; 75 AA.
XX
AC AAW62818;
XX
DT 23-SEP-1998 (first entry)
XX
DE Amino acid sequence of a human antibody fragment.
XX
KW Human; immunoglobulin; Ig; transgenic; non-human mammal;
KW inactivated endogenous Ig locus; B-cell development;
KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
KW production; antibody.
XX
OS Homo sapiens.
XX
PN WO9824893-A2.
XX
PD 11-JUN-1998.
XX
PF 03-DEC-1997; 97WO-US023091.
XX
PR 03-DEC-1996; 96US-00759620.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Jakobovits A, Kucherlapati R, Klapholz S, Mendez M, Green L;
XX
DR WPI; 1998-333314/29.
XX
PT New transgenic non-human mammals - having an inactivated immunoglobulin
PT locus and a near complete human immunoglobulin locus, used for production
PT of human antibodies.
XX
PS Disclosure; Page 84; 128pp; English.
XX
CC AAW62793-822 represent fragments of human antibodies produced by
CC transgenic Xenomice, created using the method of the invention. The
CC specification describes a transgenic non-human mammal which has genome
CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)
CC locus, so that the mammal does not display normal B-cell development. The
CC modified genome also has an inserted human heavy chain Ig locus in

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CC   germline configuration, the human heavy chain Ig locus comprising a human
CC   micro constant region and regulatory and switch sequences, human J-H
CC   genes, human D-H genes, and human V-H genes and an inserted human kappa
CC   light chain Ig locus in germline configuration, the human kappa light
CC   chain Ig locus comprising a human kappa constant region, J-kappa genes,
CC   and V-kappa genes, where the number of V-H and V-kappa genes inserted are
CC   selected to restore normal B-cell development in the mammal. The
CC   transgenic animals have a near complete human Ig locus, including both a
CC   human heavy chain locus and a human kappa light chain locus. They can be
CC   used for the production of human antibodies when exposed to particular
CC   antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha the mice
CC   will produce antibodies to IL-8, EGFR or TNF- alpha respectively
XX
SQ   Sequence 75 AA;

  Query Match             99.4%;  Score 159;  DB 2;  Length 75;
  Best Local Similarity   93.8%;  Pred. No. 7.9e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||||||||||||||||||||
Db         38 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 69


RESULT 7
AAW80980
ID   AAW80980 standard; protein; 76 AA.
XX
AC   AAW80980;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Variable kappa light region 018 encoded amino acid.
XX
KW   Human; epidermal growth factor receptor; tumour; EGF;
KW   transforming growth factor alpha; TGF-alpha.
XX
OS   Homo sapiens.
XX
PN   WO9850433-A2.
XX
PD   12-NOV-1998.
XX
PF   05-MAY-1998;   98WO-US009160.
XX
PR   05-MAY-1997;   97US-00851362.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Jakobovits A,  Yang X,  Gallo M,  Jia X;
XX
DR   WPI; 1999-034712/03.
XX
PT   Humanised antibodies against epidermal growth factor receptor, EGF-r -
PT   useful to treat solid tumours whilst inducing reduced immunogenic or
PT   allergic effects compared to mouse or mouse-derived antibodies.
XX
PS   Example 3; Page 104; 143pp; English.
XX
CC   The variable kappa light region 018 encoded amino acid was used in the
CC   production of anti-epidermal growth factor receptor (EGF-r)-antibodies.
CC   The antibodies can be administered therapeutically to patients (human or
CC   veterinary) to treat solid tumours. EGF-r is overexpressed on many human
CC   solid tumour types, and the fully human antibodies (i.e. comprising and
CC   inhibit both epidermal growth factor (EGF) and transforming growth factor
CC   alpha (TGF-alpha) binding to EGF-r (known to lead to cellular
CC   proliferation and tumour growth). They can prevent tumour cell growth
CC   and, in combination with an antineoplastic agent, may eradicate
CC   established tumours. The fully human antibodies can minimise the
CC   immunogenic and allergic responses intrinsic to previous mouse/rat or
CC   mouse/rat-derived antibodies
XX
SQ   Sequence 76 AA;

  Query Match             99.4%;  Score 159;  DB 2;  Length 76;
  Best Local Similarity   93.8%;  Pred. No. 8e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||||||||||||||||||||
Db         38 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 69


RESULT 8
ABO04825
ID   ABO04825 standard; protein; 76 AA.
XX
AC   ABO04825;
XX
DT   12-AUG-2003  (first entry)
XX
DE   Human epidermal growth factor receptor (EGF-r) antibody #34.
XX
KW   Human; epidermal growth factor receptor; EGF-r; antibody; cytostatic;
KW   antiinflammatory; immunosuppressive; tyrosine phosphorylation; EGF-2;
KW   EGF-r degradation; vascular endothelial cell growth factor; VEGF; tumour;
KW   endothelial cell; threonine phosphorylation; autoimmune disease; colon;
KW   inflammation; lung; cancer.
XX
OS   Homo sapiens.
XX
PN   US2002173629-A1.
XX
PD   21-NOV-2002.
XX
PF   05-NOV-1998;   98US-00187693.
XX
PR   05-MAY-1997;   97US-00851362.
PR   29-SEP-1998;   98US-00162280.
XX
PA   (JAKO/) JAKOBOVITS A.
PA   (YANG/) YANG X.
PA   (GALL/) GALLO M.
PA   (JIAX/) JIA X.
XX
PI   Jakobovits A,  Yang X,  Gallo M,  Jia X;
XX
DR   WPI; 2003-328430/31.
XX
PT   Fully human monoclonal antibodies that bind to epidermal growth factor
PT   receptors, useful in cancer therapy.
XX
PS   Example 3; Page 18; 100pp; English.
XX
CC   The invention relates to an antibody that binds to an epidermal growth
CC   factor receptor (FGF-r) and exhibits inhibition of tyrosine
CC   phosphorylation of EGF-2, the degradation of EGF-r, the EGF induced
CC   degradation of EGF-r, vascular endothelial cell growth factor (VEGF)
CC   production by tumour cells (by greater than 50%) and endothelial cells
CC   (by greater than 40%) and also protects threonine phosphorylation of EGF-
CC   r and a 63KD protein. The antibody is internalised with EGF-r. The
CC   antibody may be used for treating tumours such as lung tumours and colon
CC   tumours and for treating inflammation and autoimmune diseases. Sequences
CC   ABO04824-ABO04859 represent human EGF-r receptor antibodies of the
CC   invention
XX
SQ   Sequence 76 AA;

  Query Match             99.4%;  Score 159;  DB 6;  Length 76;
  Best Local Similarity   93.8%;  Pred. No. 8e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||||||||||||||||||||
Db         38 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 69
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RESULT 9
AEA17737
ID   AEA17737 standard; protein; 76 AA.
XX
AC   AEA17737;
XX
DT   14-JUL-2005  (first entry)
XX
DE   Hybridoma E1.1 immunoglobin Vkappa 018 amino acid sequence, seq id 36.
XX
KW   Cytostatic; gene therapy; epidermal growth factor receptor modulator;
KW   antibody therapy; tumor; immunoglobin.
XX
OS   Homo sapiens.
XX
PN   US2005100546-A1.
XX
PD   12-MAY-2005.
XX
PF   22-DEC-2004; 2004US-00021795.
XX
PR   05-MAY-1997;   97US-00851362.
PR   29-SEP-1998;   98US-00162280.
PR   05-NOV-1998;   98US-00187693.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Jakobovits A,  Yang X,  Gallo M,  Jia X;
XX
DR   WPI; 2005-345353/35.
XX
PT   New isolated human monoclonal antibody that binds to human epidermal
PT   growth factor receptor (EGF-r) and inhibits tyrosine phosphorylation or
PT   degradation of EGF-r, useful for treating tumors.
XX
PS   Example 3; SEQ ID NO 36; 128pp; English.
XX
CC   The invention relates to a novel isolated human antibody that binds to a
CC   human epidermal growth factor receptor. The antibody inhibits tyrosine
CC   phosphorylation of epidermal growth factor receptor (EGF-r), is
CC   internalized with EGF-r, inhibits the degradation of EGF-r, inhibits the
CC   EGF induced degradation of EGF-r, protects threonine phosphorylation of
CC   EGF-r, protects threonine phosphorylation of a 63 KD protein, inhibits
CC   vascular endothelial growth factor (VEGF) production by tumor cells by
CC   greater than 50%, and inhibits VEGF production by endothelial cells by
CC   greater than 40%. Further disclosed are nucleotide sequences encoding and
CC   amino acid sequences comprising heavy and light chain immunoglobulin
CC   molecules, particularly sequences corresponding to a contiguous heavy and
CC   light chain sequences from complementarity determining region (CDR)1-
CC   CDR3. Also disclosed are hybridomas expressing the immunoglobulin
CC   molecules and monoclonal antibodies. The antibody is useful for treating
CC   tumors or for inhibiting tyrosine phosphorylation or the degradation of
CC   EGF-r, for protecting threonine phosphorylation of EGF-r or 63 KD
CC   protein, or for inhibiting VEGF production by tumor cells. The current
CC   sequence represents the hybridoma E1.1 immunoglobin Vkappa 018 amino acid
CC   sequence.
XX
SQ   Sequence 76 AA;

  Query Match             99.4%;  Score 159;  DB 9;  Length 76;
  Best Local Similarity   93.8%;  Pred. No. 8e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||||
Db         38 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 69


RESULT 10
ADU97910
ID   ADU97910 standard; peptide; 80 AA.
XX
AC   ADU97910;
XX
DT   10-FEB-2005  (first entry)
XX
DE   Amino acid sequence of DPK1/JH6 region.
XX
KW   antiinflammatory; gastrointestinal-Gen; antiulcer; antibody; IP-10;
KW   inflammatory bowel disease; autoimmune disease; immunosuppressive;
KW   chemotaxis; T lymphocyte; Crohn's disease; ulcerative colitis.
XX
OS   Homo sapiens.
XX
PN   WO2004101511-A2.
XX
PD   25-NOV-2004.
XX
PF   07-MAY-2004; 2004WO-US014507.
XX
PR   09-MAY-2003; 2003US-0469299P.
PR   21-AUG-2003; 2003US-0497474P.
PR   04-DEC-2003; 2003US-0527882P.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Balasa B,  Tsurushita N,  Landolfi N;
XX
DR   WPI; 2004-821854/81.
XX
PT   New antibody or its antigen-binding fragment that binds to IP-10, useful
PT   for diagnosing, preventing and/or treating autoimmune diseases preferably
PT   inflammatory bowel disease including Crohn's disease and ulcerative
PT   colitis.
XX
PS   Example 5; SEQ ID NO 16; 80pp; English.
XX
CC   The specification describes an antibody that binds to IP-10, where the
CC   antibody is capable of preventing or reducing severity of at least one
CC   symptom of an inflammatory bowel disease. IP-10 (CXCL10) is a chemokine
CC   that is induced by interferon gamma and is the ligand for CXCR3. The
CC   antibody is useful for inhibiting chemotaxis or migration of lymphocytes
CC   such as T cells, and for diagnosing, preventing and treating autoimmune
CC   diseases, preferably inflammatory bowel diseases including Crohn's
CC   disease and ulcerative colitis. It is also useful for preventing or
CC   reducing severity of at least one symptom of an inflammatory bowel
CC   disease such as colon inflammatory lesions, body weight loss, diarrhea,
CC   and rectal prolapse. The antibody is also useful for evaluating the
CC   treatment efficacy of a therapeutic approach and as a detecting agent in
CC   in vitro assays for research purposes. It can be further used to identify
CC   or isolate novel receptors or other binding proteins for IP-10. The
CC   present sequence represents the DPK1/JH6 region which was used to produce
CC   humanized antibody HuAIP13, an antibody of the invention.
XX
SQ   Sequence 80 AA;

  Query Match             99.4%;  Score 159;  DB 8;  Length 80;
  Best Local Similarity   93.8%;  Pred. No. 8.4e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||||
Db         39 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 70


RESULT 11
AEB26568
ID   AEB26568 standard; protein; 80 AA.
XX
AC   AEB26568;
XX
DT   08-SEP-2005  (first entry)
XX
DE   Human anti-human IP-10 antibody related protein, SEQ ID NO: 16.
XX
```

```
KW   Antibody therapy; diagnosis; inflammatory bowel disease;
KW   antiinflammatory; gastrointestinal-gen.; gastrointestinal disease;
KW   inflammation; Crohns disease; immune disorder; ulcerative colitis;
KW   antiulcer; IP-10.
XX
OS   Homo sapiens.
XX
PN   WO2005060457-A2.
XX
PD   07-JUL-2005.
XX
PF   10-NOV-2004; 2004WO-US037600.
XX
PR   04-DEC-2003; 2003US-0527882P.
PR   07-MAY-2004; 2004WO-US014507.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Balasa B,  Tsurushita N,  Landolfi NF;
XX
DR   WPI; 2005-488564/49.
XX
PT   Novel high affinity anti-human IP-10 antibody or its fragment, useful for
PT   treating, preventing and diagnosing inflammatory bowel disease such as
PT   Crohns disease and ulcerative colitis.
XX
PS   Disclosure; SEQ ID NO 16; 78pp; English.
XX
CC   The invention relates to a high affinity anti-human IP-10 antibody or its
CC   fragment and a method of reducing the severity of symptoms of
CC   inflammatory bowel disease. The invention is useful for preventing,
CC   treating or reducing severity of at least one symptom of an inflammatory
CC   bowel disease (IBD) such as Crohn's disease (CD) or ulcerative colitis
CC   (UC). It is also useful in diagnostic and prognostic evaluation of
CC   diseases and disorders, preferably CD and UC, associated with IP-10
CC   expression. IP-10 antibody is useful for detecting IP-10. It is useful as
CC   detecting agents in in vitro assays for research purposes e.g. for
CC   identifying or isolating novel receptors or other binding proteins for IP
CC   -10. The present sequence is the human anti-human IP-10 antibody related
CC   protein.
XX
SQ   Sequence 80 AA;

  Query Match             99.4%;  Score 159;  DB 9;  Length 80;
  Best Local Similarity   93.8%;  Pred. No. 8.4e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||||
Db         39 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 70


RESULT 12
AAR06351
ID   AAR06351 standard; protein; 85 AA.
XX
AC   AAR06351;
XX
DT   09-SEP-2004  (revised)
DT   25-MAR-2003  (revised)
DT   24-SEP-1990  (first entry)
XX
DE   M13 VKPCR1 Ig light chain variable region (exon 2 encoded).
XX
KW   Immunoglobulin superfamily; single domain ligands; variable domain;
KW   light chain; cancer therapy; diagnosis; vaccines.
XX
OS   Mus musculus.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   Domain          28. .38
FT                   /note = hypervariable region, CDR1
FT   Domain          54. .60
FT                   /note = hypervariable region, CDR2
XX
PN   EP368684-A.
XX
PD   16-MAY-1990.
XX
PF   13-NOV-1989;   89EP-00311731.
XX
PR   11-NOV-1988;   88GB-00026444.
PR   16-MAR-1989;   89GB-00006034.
PR   22-APR-1989;   89GB-00009217.
PR   15-MAY-1989;   89GB-00011047.
PR   02-JUN-1989;   89GB-00012652.
PR   16-JUN-1989;   89GB-00013900.
PR   15-AUG-1989;   89GB-00018543.
XX
PA   (MEDI-) MEDICAL RES COUNCIL.
XX
PI   Winter GP,  Gussow D,  Ward ES;
XX
DR   WPI; 1990-149601/20.
DR   N-PSDB; AAQ04462.
XX
PT   Single domain ligands for therapy, diagnosis or catalysts - comprising at
PT   least part of variable domain from immunoglobulin super-family.
XX
PS   Disclosure; Page ?; 57pp; English.
XX
CC   The MBr1 light chain variable domain encoding sequence in M13-VKPCR1 was
CC   recloned into a pSV-hyg-HuCK vector with a hygromycin resistance marker
CC   and a human kappa constant region. When linearised with the pSV-gpt
CC   vector contg. M13-VHPCR1 and cotransfected into the non-secreting mouse
CC   myeloma line NSO, a chimeric antibody was found which binds to MCF-7
CC   cells but not the HT-29 cells, thus showing specificity. See also
CC   AAQ04461-Q04470. (Updated on 25-MAR-2003 to correct PR field.) (Updated
CC   on 25-MAR-2003 to correct PA field.)
CC
CC   Revised record issued on 09-SEP-2004 : Corrections to pages and features
XX
SQ   Sequence 85 AA;

  Query Match             99.4%;  Score 159;  DB 2;  Length 85;
  Best Local Similarity   93.8%;  Pred. No. 9e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||||
Db         34 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 65


RESULT 13
AAY39533
ID   AAY39533 standard; protein; 86 AA.
XX
AC   AAY39533;
XX
DT   22-NOV-1999  (first entry)
XX
DE   Humanised Murine COL1 VK chain (REIVK).
XX
KW   Antibody; human; carcinoembryonic antigen; CEA; cancer; tumour imaging;
KW   tumour identification; metastasis; diagnosis; mouse; VK chain.
XX
OS   Synthetic.
OS   Mus sp.
OS   Homo sapiens.
XX
PN   WO9943817-A1.
XX
PD   02-SEP-1999.
XX
PF   25-FEB-1998;   98WO-US003680.
```

XX
PR 25-FEB-1998; 98WO-US003680.
XX
PA (DOWC) DOW CHEM CO.
XX
PI Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
XX
DR WPI; 1999-550870/46.
XX
PT New antibody specific for treatment and diagnosis of cancer.
XX
PS Claim 2; Fig 2; 82pp; English.
XX
CC This sequence represents a humanised version of the murine COL1 VK chain,
CC designated REIVK, and was used to obtain the humanised antibody (Ab) of
CC the invention. The humanised Ab, or its fragment, specifically binds to
CC carcinoembryonic antigen (CEA). The Ab, optionally coupled to an effector
CC or label, is used to treat or prevent CEA-expressing cancers (e.g. of
CC breast, ovary, lung, stomach, or colon) and to detect CEA-expressing
CC cells, either in vitro (optionally on a solid support) or in vivo
CC (particularly by tumour imaging to identify tumours and metastases before
CC surgery), for diagnosis or prognosis. It is not significantly
CC immunogenic, i.e. the Ab does not induce a human anti-murine antibody or
CC allergic response, or non-specific cytotoxicity, so can be administered
CC repeatedly. It retains specificity for CEA, and has improved clearance
CC (allowing efficient targeting) and metabolic properties
XX
SQ Sequence 86 AA;

Query Match 99.4%; Score 159; DB 2; Length 86;
Best Local Similarity 93.8%; Pred. No. 9.1e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
||| ||||| ||||||||||||||||||||||
Db 47 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 78

RESULT 14
ABB83945
ID ABB83945 standard; protein; 86 AA.
XX
AC ABB83945;
XX
DT 30-OCT-2002 (first entry)
XX
DE Humanised monoclonal antibody chain REIVK.
XX
KW Mouse; COL1; humanised antibody; carcinoembryonic antigen; CEA; cancer;
KW cytostatic; antibody.
XX
OS Synthetic.
XX
PN US2002052479-A1.
XX
PD 02-MAY-2002.
XX
PF 18-FEB-1998; 98US-00025403.
XX
PR 31-OCT-1996; 96US-0029694P.
XX
PA (ANDE/) ANDERSON K W H.
PA (TEMP/) TEMPEST P.
PA (CARR/) CARR F J.
PA (HARR/) HARRIS W J.
PA (ARMO/) ARMOUR K.
XX
PI Anderson KWH, Tempest P, Carr FJ, Harris WJ, Armour K;
XX
DR WPI; 2002-415220/44.
XX
PT New humanized antibody or antibody fragment that is derived from murine
PT antibody, useful for treating and detecting carcinoembryonic antigen
PT expressing cancer in mammal.
XX
PS Claim 2; Fig 2; 34pp; English.
XX
CC The invention relates to a humanised antibody or humanised antibody
CC fragment (I) which specifically binds carcinoembryonic antigen (CEA) and
CC that is derived from a murine antibody that binds CEA. (I) is used for
CC treating (in vivo) and detecting a CEA-expressing cancer in a mammal. (I)
CC is used for in vitro or in vivo immunodetection of CEA-expressing cancer
CC cells. The present sequence is that of an antibody chain of the invention
XX
SQ Sequence 86 AA;

Query Match 99.4%; Score 159; DB 5; Length 86;
Best Local Similarity 93.8%; Pred. No. 9.1e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
||| ||||| ||||||||||||||||||||||
Db 47 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 78

RESULT 15
ABG75598
ID ABG75598 standard; protein; 86 AA.
XX
AC ABG75598;
XX
DT 25-APR-2003 (first entry)
XX
DE REI framework region (FR) variable light domain template.
XX
KW Human; humanised antibody; tumour antigen; carcinoembryonic antigen; CEA;
KW carcinoma; breast; lung; gastrointestinal; stomach cancer; colon cancer;
KW COL-1; cytostatic; variable light domain; VK; REI; framework region; FR;
KW complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
PN US2002165387-A1.
XX
PD 07-NOV-2002.
XX
PF 09-OCT-2001; 2001US-00974052.
XX
PR 31-OCT-1996; 96US-0029694P.
PR 30-OCT-1997; 97WO-US019642.
PR 18-FEB-1998; 98US-00025403.
PR 28-SEP-2000; 2000US-00672609.
XX
PA (ANDE/) KERR ANDERSON W H.
PA (TEMP/) TEMPEST P R.
PA (CARR/) CARR F J.
PA (HARR/) HARRIS W J.
PA (ARMO/) ARMOUR K.
XX
PI Kerr Anderson WH, Tempest PR, Carr FJ, Harris WJ, Armour K;
XX
DR WPI; 2003-247263/24.
XX
PT New humanized antibody or humanized antibody fragment that specifically
PT binds carcinoembryonic antigen CEA, useful for treating CEA-expressing
PT cancer.
XX
PS Claim 2; Fig 2; 34pp; English.
XX
CC The invention discloses a humanised antibody or humanised antibody
CC fragment that specifically binds the tumour antigen, carcinoembryonic
CC antigen (CEA). The antigen is expressed by various human carcinomas
CC including breast, lung and gastrointestinal carcinomas such as stomach
CC and colon cancers. The humanised antibody fragment is derived from a
CC murine antibody, COL-1, which has a high affinity for CEA. Also disclosed
CC is a nucleic acid sequence from which may be expressed the humanised

CC antibody or humanised antibody fragment and a composition for treating,
CC or detection of, cancer comprising the humanised antibody or humanised
CC antibody fragment. The humanised antibody or humanised antibody fragment
CC is useful for treating CEA-expressing cancer. The sequence presented is
CC the human REI framework region (FR) variable light domain template. The
CC FRs are regions of the antibody amino acid sequence interposed between
CC the complementarity determining regions (CDRs)
XX
SQ Sequence 86 AA;

Query Match 99.4%; Score 159; DB 6; Length 86;
Best Local Similarity 93.8%; Pred. No. 9.1e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||||||||||||||||||||
Db         47 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 78
```

Search completed: March 25, 2006, 09:02:17
Job time : 120.073 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:02:50 ; Search time 18.4293 Seconds
(without alignments)
167.067 Million cell updates/sec

Title: US-10-755-382-28
Perfect score: 160
Sequence: 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	159	99.4	87	2	I52592	Ig kappa chain V r
2	159	99.4	88	2	S34088	Ig kappa chain V r
3	159	99.4	108	1	K1HULY	Ig kappa chain V-I
4	159	99.4	110	2	S44118	Ig kappa chain V-J
5	159	99.4	117	2	S42263	Ig kappa chain V r
6	159	99.4	117	2	S43528	Ig kappa chain V r
7	156	97.5	108	1	K1HURE	Ig kappa chain V-I
8	156	97.5	108	1	K1HURY	Ig kappa chain V-I
9	155	96.9	88	2	S34087	Ig kappa chain V r
10	155	96.9	95	2	PH0864	Ig kappa chain V r
11	153	95.6	95	2	PH0862	Ig kappa chain V r
12	153	95.6	98	2	PH1067	Ig light chain V r
13	153	95.6	98	2	PH1066	Ig light chain V r
14	153	95.6	129	2	S52789	Ig kappa chain V r
15	152	95.0	88	2	S21525	Ig kappa chain V r
16	152	95.0	95	2	PH0863	Ig kappa chain V r
17	152	95.0	107	2	S47183	Ig kappa chain - h
18	152	95.0	107	2	S40366	Ig kappa chain V-J
19	152	95.0	108	2	I39154	Ig kappa chain (BR
20	152	95.0	117	2	S10227	Ig kappa chain pre
21	149	93.1	86	2	S34086	Ig kappa chain V r
22	149	93.1	86	2	S16840	Ig kappa chain V r
23	149	93.1	87	2	S34084	Ig kappa chain V r
24	149	93.1	87	2	S34083	Ig kappa chain V r
25	149	93.1	88	2	S21522	Ig kappa chain V r
26	149	93.1	88	2	S21528	Ig kappa chain V r
27	149	93.1	95	2	PH0867	Ig kappa chain V r
28	149	93.1	105	2	S36266	Ig lambda chain V
29	149	93.1	106	2	PC2397	anti-tetanus toxin
30	149	93.1	107	2	S36264	Ig lambda chain V
31	149	93.1	107	2	S36269	Ig lambda chain V
32	149	93.1	107	2	I69017	anti-HIV1 envelope
33	149	93.1	108	1	K1HUAG	Ig kappa chain V-I
34	149	93.1	108	1	K1HUHU	Ig kappa chain V-I
35	149	93.1	108	2	S47182	Ig kappa chain - h
36	149	93.1	108	2	B49047	Ig kappa chain V r
37	149	93.1	108	2	S31977	Ig kappa chain - h
38	149	93.1	109	2	S31998	Ig kappa chain - h
39	149	93.1	116	2	A27594	Ig kappa chain pre
40	149	93.1	117	1	K1HU11	Ig kappa chain pre
41	149	93.1	117	2	C21056	Ig kappa chain pre
42	149	93.1	117	2	S24206	Ig kappa chain V r
43	149	93.1	117	2	S42264	Ig kappa chain V r
44	149	93.1	117	2	S11700	Ig kappa chain pre
45	149	93.1	117	2	B21056	Ig kappa chain pre

ALIGNMENTS

RESULT 1
I52592
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I52592
R;Wagner, S.D.; Martinelli, V.; Luzzatto, L.
Blood 83, 3647-3653, 1994
A;Title: Similar patterns of V kappa gene usage but different degrees of somatic mutati
A;Reference number: I52592; MUID:94264318; PMID:8204889
A;Accession: I52592
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-87 <RES>
A;Cross-references: UNIPARC:UPI0000113F67; GB:S71057; NID:g547053; PIDN:AAB30971.1; PID
C;Genetics:
A;Gene: IgKV
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 99.4%; Score 159; DB 2; Length 87;
Best Local Similarity 93.8%; Pred. No. 9.2e-15;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
||| ||||| |||||||||||||||||||||||
Db 50 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 81

RESULT 2
S34088
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34088
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34088
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WAG>
A;Cross-references: UNIPARC:UPI0000176D9A; EMBL:X67172
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 99.4%; Score 159; DB 2; Length 88;
Best Local Similarity 93.8%; Pred. No. 9.3e-15;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db         50 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 81
```

RESULT 3
K1HULY
Ig kappa chain V-I region (Lay) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01871; F30609
R;Capra, J.D.; Klapper, D.G.
Scand. J. Immunol. 5, 677-684, 1976
A;Title: Complete amino acid sequence of the variable domains of two human IgM anti-gamm
A;Reference number: A01871; MUID:77038198; PMID:824717
A;Accession: A01871
A;Molecule type: protein
A;Residues: 1-108 <CAP>
A;Cross-references: UNIPROT:P01605; UNIPARC:UPI000012E148
A;Note: the second and third hypervariable regions of this chain are identical with thos
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc
J. Immunol. 142, 3158-3163, 1989
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoanti
A;Reference number: A30601; MUID:89215279; PMID:2496160
A;Accession: F30609
A;Molecule type: protein
A;Residues: 1-104 <GON>
A;Cross-references: UNIPARC:UPI0000173703
C;Comment: This chain was isolated from an IgM with anti-gamma globulin activity.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

```
  Query Match             99.4%;  Score 159;  DB 1;  Length 108;
  Best Local Similarity   93.8%;  Pred. No. 1.2e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db         57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88
```

RESULT 4
S44118
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44118
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
A;Accession: S44118
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 <HAW>
A;Cross-references: UNIPARC:UPI0000116635; EMBL:Z31395; NID:g472972; PIDN:CAA83270.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

```
  Query Match             99.4%;  Score 159;  DB 2;  Length 110;
  Best Local Similarity   93.8%;  Pred. No. 1.2e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db         57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88
```

RESULT 5
S42263
Ig kappa chain V region (08) - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42263
R;Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que
J. Immunol. 147, 4007-4013, 1991
A;Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus inf
A;Reference number: S42263; MUID:92043792; PMID:1940382
A;Accession: S42263
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <SCO>
A;Cross-references: UNIPARC:UPI0000113B51; EMBL:M64855; NID:g185963; PIDN:AAA58925.1; PI
C;Genetics:
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

```
  Query Match             99.4%;  Score 159;  DB 2;  Length 117;
  Best Local Similarity   93.8%;  Pred. No. 1.3e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db         79 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 110
```

RESULT 6
S43528
Ig kappa chain V region (018) - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: S43528
R;Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que
submitted to the EMBL Data Library, December 1991
A;Reference number: S43528
A;Accession: S43528
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <SCO>
A;Cross-references: UNIPARC:UPI0000113B52; EMBL:M64856
C;Genetics:
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;38-112/Domain: immunoglobulin homology <IMM>

```
  Query Match             99.4%;  Score 159;  DB 2;  Length 117;
  Best Local Similarity   93.8%;  Pred. No. 1.3e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db         79 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 110
```

RESULT 7
K1HURE
Ig kappa chain V-I region (Rei) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A91663; A01873
R;Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 167-191, 1975
A;Title: Die Primaerstruktur einer kristallinen monoklonalen Immunglobulin-L-Kette vom k
 vollstaendige Aminosaeuresequenz des Proteins.
A;Reference number: A91663; MUID:76023758; PMID:809329

A;Accession: A91663
A;Molecule type: protein
A;Residues: 1-108 <PAL>
A;Cross-references: UNIPROT:P01607; UNIPARC:UPI000002D0C9
A;Note: the C region of this chain has the Inv (1,2) marker
R;Epp, O.; Lattman, E.E.; Schiffer, M.; Huber, R.; Palm, W.
Biochemistry 14, 4943-4952, 1975
A;Title: The molecular structure of a dimer composed of the variable portions of the Ben
A;Reference number: A90392; MUID:76039968; PMID:1182131
A;Contents: annotation; X-ray crystallography, 2.0 angstroms
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status experimental

Query Match 97.5%; Score 156; DB 1; Length 108;
Best Local Similarity 90.6%; Pred. No. 3e-14;
Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
||| ||||| |||| :|||||||||||||||||||
Db 57 GVPSRFSGSGSGTDYTFTISSLQPEDIATYYC 88

RESULT 8
K1HURY
Ig kappa chain V-I region (Roy) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: A91638; B94417; A01874; S02575
R;Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 348, 1077-1080, 1967
A;Title: Die chemische Struktur von zwei Bence-Jones-Proteinen (Roy und Cum.) vom kappa-
A;Reference number: A91638; MUID:68362076; PMID:5595110
A;Accession: A91638
A;Molecule type: protein
A;Residues: 1-38,'GPK',42-108 <HIL>
A;Cross-references: UNIPROT:P01608; UNIPARC:UPI0000173704
A;Note: the sequence of the C region, which has the Inv (1,2) marker, is also given
R;Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne,
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74,
A;Reference number: A94417
A;Contents: revisions to residues 39 and 41
A;Accession: B94417
A;Molecule type: protein
A;Residues: 39;41 <HI2>
A;Cross-references: UNIPARC:UPI000011ECBE; UNIPARC:UPI000011ED5D
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 97.5%; Score 156; DB 1; Length 108;
Best Local Similarity 90.6%; Pred. No. 3e-14;
Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
||| |||| : |||||||||||||||||||||
Db 57 GVPSRFSGTGSGTDFTFTISSLQPEDIATYYC 88

RESULT 9
S34087
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34087
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribut
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34087
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WAG>
A;Cross-references: UNIPARC:UPI0000176D9B; EMBL:X67171
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

Query Match 96.9%; Score 155; DB 2; Length 88;
Best Local Similarity 90.6%; Pred. No. 3.3e-14;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
||| ||||| |||||||||||||||| |||||
Db 50 GVPSRFSGSGSGTDFTFTISSLQPEDFATYYC 81

RESULT 10
PH0864
Ig kappa chain V region (anti-DNA, IC4) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH0864
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0864
A;Molecule type: DNA
A;Residues: 1-95 <MAN>
A;Cross-references: UNIPARC:UPI0000176D9D
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3

Query Match 96.9%; Score 155; DB 2; Length 95;
Best Local Similarity 90.6%; Pred. No. 3.6e-14;
Matches 29; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
||| |||| ||||||||||||||||||||||
Db 57 GVPSRFSGGGSGTDFTFTISSLQPEDIATYYC 88

RESULT 11
PH0862
Ig kappa chain V region (anti-DNA, III-3R) - human (fragment)
C;Species: Homo sapiens (man)

```
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH0862
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0862
A;Molecule type: DNA
A;Residues: 1-95 <MAN>
A;Cross-references: UNIPARC:UPI0000176D9C
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3

  Query Match             95.6%;  Score 153;  DB 2;  Length 95;
  Best Local Similarity   90.6%;  Pred. No. 6.7e-14;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| | ||| ||||||||||||||||||||||
Db         57 GVPSRISGSGSGTDFTFTISSLQPEDIATYYC 88


RESULT 12
PH1067
Ig light chain V region (clone 163-c2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1067
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1067
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-98 <TIL>
A;Cross-references: UNIPARC:UPI0000176AB7
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             95.6%;  Score 153;  DB 2;  Length 98;
  Best Local Similarity   90.6%;  Pred. No. 6.9e-14;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||| ||||||||||||||||
Db         57 GVPSRFSGSGSGTDFTLTISSLQPEDIATYYC 88


RESULT 13
PH1066
Ig light chain V region (clone 165.14) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1066
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1066
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-98 <TIL>
A;Cross-references: UNIPARC:UPI0000176AB6
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             95.6%;  Score 153;  DB 2;  Length 98;
  Best Local Similarity   90.6%;  Pred. No. 6.9e-14;
  Matches   29;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||| ||||||||||||||||
Db         57 GVPSRFSGSGSGTDFTLTISSLQPEDIATYYC 88


RESULT 14
S52789
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52789
R;Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougenot, B.; Ronco, P.; Denoroy, L.; Deret,
submitted to the EMBL Data Library, March 1995
A;Description: Light chain V region gene usage restriction and peculiarities in myeloma-
A;Reference number: S52789
A;Accession: S52789
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-129 <ROC>
A;Cross-references: UNIPARC:UPI0000116220; EMBL:X85995; NID:g758588; PIDN:CAA59987.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

  Query Match             95.6%;  Score 153;  DB 2;  Length 129;
  Best Local Similarity   87.5%;  Pred. No. 9.2e-14;
  Matches   28;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||:||||||||||:|||||
Db         79 GVPSRFSGSGSGTDFSFTISSLQPEDLATYYC 110


RESULT 15
S21525
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jan-2000
C;Accession: S34081; S21525
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34081
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WA2>
A;Cross-references: UNIPARC:UPI000011604E; EMBL:X66041; NID:g33316; PIDN:CAA46840.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

  Query Match             95.0%;  Score 152;  DB 2;  Length 88;
  Best Local Similarity   87.5%;  Pred. No. 8.4e-14;
  Matches   28;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||| |||||||||:|||||
Db         50 GVPSRFSGSGSGTDFTLTISSLQPEDVATYYC 81


Search completed: March 25, 2006, 09:15:44
Job time : 18.4293 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:40 ; Search time 115.267 Seconds
(without alignments)
195.866 Million cell updates/sec

Title: US-10-755-382-28
Perfect score: 160
Sequence: 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	159	99.4	108	1	KV1M_HUMAN	P01605 homo sapien
2	159	99.4	108	1	KV1Y_HUMAN	P80362 homo sapien
3	156	97.5	108	1	KV1O_HUMAN	P01607 homo sapien
4	156	97.5	108	1	KV1P_HUMAN	P01608 homo sapien
5	152	95.0	108	2	Q9UL70_HUMAN	Q9ul70 homo sapien
6	149	93.1	107	2	Q96SA9_HUMAN	Q96sa9 homo sapien
7	149	93.1	108	1	KV1A_HUMAN	P01593 homo sapien
8	149	93.1	108	1	KV1H_HUMAN	P01600 homo sapien
9	149	93.1	108	2	Q9UL77_HUMAN	Q9ul77 homo sapien
10	149	93.1	117	1	KV1I_HUMAN	P01601 homo sapien
11	149	93.1	236	2	Q6GMX9_HUMAN	Q6gmx9 homo sapien
12	149	93.1	236	2	Q6GMX8_HUMAN	Q6gmx8 homo sapien
13	149	93.1	236	2	Q6GMW1_HUMAN	Q6gmw1 homo sapien
14	148	92.5	108	1	KV1N_HUMAN	P01606 homo sapien
15	145	90.6	236	2	Q6PIH7_HUMAN	Q6pih7 homo sapien
16	143	89.4	108	1	KV1B_HUMAN	P01594 homo sapien
17	142	88.8	108	1	KV1G_HUMAN	P01599 homo sapien
18	142	88.8	108	1	KV1R_HUMAN	P01610 homo sapien
19	142	88.8	109	1	KV1T_HUMAN	P01612 homo sapien
20	142	88.8	117	1	KV1J_HUMAN	P01602 homo sapien
21	142	88.8	236	2	Q6GMX0_HUMAN	Q6gmx0 homo sapien
22	142	88.8	236	2	Q502W4_HUMAN	Q502w4 homo sapien
23	142	88.8	244	2	Q65ZC8_HUMAN	Q65zc8 homo sapien
24	141	88.1	107	1	KV1D_HUMAN	P01596 homo sapien
25	141	88.1	108	1	KV1K_HUMAN	P01603 homo sapien
26	141	88.1	108	1	KV1Q_HUMAN	P01609 homo sapien
27	141	88.1	108	1	KV1S_HUMAN	P01611 homo sapien
28	140	87.5	115	1	KV3I_HUMAN	P04433 homo sapien
29	140	87.5	129	1	KV1X_HUMAN	P04432 homo sapien
30	139	86.9	108	1	KV1L_HUMAN	P01604 homo sapien
31	139	86.9	129	1	KV1W_HUMAN	P04431 homo sapien
32	138	86.2	108	1	KV1E_HUMAN	P01597 homo sapien
33	138	86.2	114	1	KV4A_HUMAN	P01625 homo sapien
34	138	86.2	121	1	KV4O_HUMAN	P06312 homo sapien
35	138	86.2	133	1	KV4B_HUMAN	P06313 homo sapien
36	138	86.2	134	1	KV4C_HUMAN	P06314 homo sapien
37	138	86.2	234	2	Q5EFE6_HUMAN	Q5efe6 homo sapien
38	138	86.2	236	2	Q6PIT5_HUMAN	Q6pit5 homo sapien
39	138	86.2	236	2	Q7Z3Y4_HUMAN	Q7z3y4 homo sapien
40	137	85.6	107	2	Q9UL81_HUMAN	Q9ul81 homo sapien
41	137	85.6	108	1	KV5J_MOUSE	P01643 mus musculu
42	137	85.6	116	1	KV3J_HUMAN	P04434 homo sapien
43	137	85.6	149	1	KV5A_MOUSE	P01633 mus musculu
44	136	85.0	108	1	KV1F_HUMAN	P01598 homo sapien
45	136	85.0	108	2	Q9UL79_HUMAN	Q9ul79 homo sapien

ALIGNMENTS

RESULT 1
KV1M_HUMAN
ID KV1M_HUMAN STANDARD; PRT; 108 AA.
AC P01605;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ig kappa chain V-I region Lay.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=77038198; PubMed=824717;
RA Capra J.D., Klapper D.G.;
RT "Complete amino acid sequence of the variable domains of two human IgM
RT anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
RL Scand. J. Immunol. 5:677-684(1976).
RN [2]
RP PROTEIN SEQUENCE OF 1-104.
RX MEDLINE=89215279; PubMed=2496160;
RA Goni F.R., Chen P.P., McGinnis D., Arjonilla M.L., Fernandez J.,
RA Carson D., Solomon A., Mendez E., Frangione B.;
RT "Structural and idiotypic characterization of the L chains of human
RT IgM autoantibodies with different specificities.";
RL J. Immunol. 142:3158-3163(1989).
RN [3]
RP ERRATUM.
RA Goni F.R., Chen P.P., McGinnis D., Arjonilla M.L., Fernandez J.,
RA Carson D., Solomon A., Mendez E., Frangione B.;
RL J. Immunol. 143:3864-3864(1989).
CC -!- MISCELLANEOUS: The second and third hypervariable regions of this
CC chain are identical with those of the human POM V-III kappa chain,
CC with which it shares certain idiotypic determinants.
CC -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC globulin activity.
CC ---
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ---
DR PIR; A01871; K1HULY.
DR HSSP; P01607; 1BWW.
DR SMR; P01605; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.

```
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11834 MW;  739993A95431434A CRC64;

 Query Match             99.4%;  Score 159;  DB 1;  Length 108;
 Best Local Similarity   93.8%;  Pred. No. 2.7e-15;
 Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db         57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88


RESULT 2
KV1Y_HUMAN
ID   KV1Y_HUMAN     STANDARD;      PRT;   108 AA.
AC   P80362;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region WAT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=95086080; PubMed=7993911;
RA   Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA   Solomon A., Stevens F.J., Schiffer M.;
RT   "Comparison of crystal structures of two homologous proteins:
RT   structural origin of altered domain interactions in immunoglobulin
RT   light-chain dimers.";
RL   Biochemistry 33:14848-14857(1994).
RN   [2]
RP   PROTEIN SEQUENCE OF 1-35.
RX   MEDLINE=81267384; PubMed=6167731;
RA   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA   Popp R.A., Solomon A.;
RT   "Characterization and preliminary crystallographic data on the VL-
RT   related fragment of the human kI Bence Jones protein Wat.";
RL   J. Mol. Biol. 147:185-193(1981).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PDB; 1WTL; X-ray; A/B=1-108.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin domain; Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   CONFLICT     30     31       TN -> SD (in Ref. 2).
FT   NON_TER     108    108
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       45     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       84     90
FT   STRAND       98     98
FT   STRAND      102    106
SQ   SEQUENCE   108 AA;  11737 MW;  D9D941B3F0FAE697 CRC64;

  Query Match             99.4%;  Score 159;  DB 1;  Length 108;
  Best Local Similarity   93.8%;  Pred. No. 2.7e-15;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db         57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88


RESULT 3
KV1O_HUMAN
ID   KV1O_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Rei.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC       marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ----------------------------------------------------------------------
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CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   PIR; A91663; K1HURE.
DR   PDB; 1AR2; X-ray; @=1-107.
DR   PDB; 1BWW; X-ray; A/B=1-107.
DR   PDB; 1REI; X-ray; A/B=1-107.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin domain; Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88
FT   NON_TER     108    108
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       45     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       84     90
FT   STRAND       97     98
FT   STRAND      102    106
SQ   SEQUENCE   108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;

  Query Match             97.5%;  Score 156;  DB 1;  Length 108;
  Best Local Similarity   90.6%;  Pred. No. 7.3e-15;
  Matches   29;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||:||||||||||||||||||
Db         57 GVPSRFSGSGSGTDYTFTISSLQPEDIATYYC 88


RESULT 4
KV1P_HUMAN
ID   KV1P_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01608;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Roy.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=68362076; PubMed=5595110;
RA   Hilschmann N.;
RT   "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT   Cum.).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN   [2]
RP   SEQUENCE REVISION TO 39 AND 41.
RA   Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA   Steinmetz-Kayne M., Suter L., Watanabe S.;
RL   (In) Franek F., Shugar D. (eds.);
RL   Gamma globulins: structure and function, pp.57-74, Academic Press, New
RL   York (1969).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC       marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   PIR; A91638; K1HURY.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01608; 1-108.
DR   Ensembl; ENSG00000173782; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11782 MW;  F5ACEDE5A313DF3A CRC64;

  Query Match             97.5%;  Score 156;  DB 1;  Length 108;
  Best Local Similarity   90.6%;  Pred. No. 7.3e-15;
  Matches   29;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||: ||||||||||||||||||||||
Db         57 GVPSRFSGTGSGTDFTFTISSLQPEDIATYYC 88


RESULT 5
Q9UL70_HUMAN
ID   Q9UL70_HUMAN PRELIMINARY;      PRT;   108 AA.
AC   Q9UL70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
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RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1660528;
RA   Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA   Diamond B.;
RT   "Molecular characteristics of antibodies bearing an anti-DNA-
RT   associated idiotype.";
RL   J. Exp. Med. 174:1639-1652(1991).
DR   EMBL; AF035044; AAD56280.1; -; mRNA.
DR   PIR; PH0863; PH0863.
DR   HSSP; P01607; 1BWW.
DR   SMR; Q9UL70; 1-108.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11633 MW;  B7BEDC3E41FCCA37 CRC64;

  Query Match             95.0%;  Score 152;  DB 2;  Length 108;
  Best Local Similarity   87.5%;  Pred. No. 2.8e-14;
  Matches   28;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||| |||||||||:|||||
Db         57 GVPSRFSGSGSGTDFTLTISSLQPEDVATYYC 88


RESULT 6
Q96SA9_HUMAN
ID   Q96SA9_HUMAN PRELIMINARY;      PRT;   107 AA.
AC   Q96SA9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE   variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98375893; PubMed=9712075;
RA   Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT   "Molecular analysis of polyreactive monoclonal antibodies from
RT   rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT   antibody V region genes.";
RL   J. Immunol. 161:2020-2031(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1516616;
RA   Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT   "Human monoclonal striational autoantibodies isolated from thymic B
RT   lymphocytes of patients with myasthenia gravis use VH and VL gene
RT   segments associated with the autoimmune repertoire.";
RL   Eur. J. Immunol. 22:2231-2236(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=8436174;
RA   Wagner S.D., Luzzatto L.;
RT   "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT   distributed over a large portion of the V kappa locus and do not show
RT   somatic mutation.";
RL   Eur. J. Immunol. 23:391-397(1993).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1660528;
RA   Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA   Diamond B.;
RT   "Molecular characteristics of antibodies bearing an anti-DNA-
RT   associated idiotype.";
RL   J. Exp. Med. 174:1639-1652(1991).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1903706;
RA   Blaison G., Kuntz J.L., Pasquali J.L.;
RT   "Molecular analysis of V kappa III variable regions of polyclonal
RT   rheumatoid factors during rheumatoid arthritis.";
RL   Eur. J. Immunol. 21:1221-1227(1991).
DR   EMBL; U96396; AAB68785.1; -; mRNA.
DR   PIR; B49047; B49047.
DR   PIR; PH0867; PH0867.
DR   PIR; S16840; S16840.
DR   PIR; S31977; S31977.
DR   PIR; S34083; S34083.
DR   PIR; S34086; S34086.
DR   HSSP; P01607; 1BWW.
DR   SMR; Q96SA9; 1-107.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11520 MW;  4BB43E9C5B577F16 CRC64;

  Query Match             93.1%;  Score 149;  DB 2;  Length 107;
  Best Local Similarity   87.5%;  Pred. No. 7.8e-14;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||| ||||||||| |||||
Db         57 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC 88


RESULT 7
KV1A_HUMAN
ID   KV1A_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01593;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region AG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=69234734; PubMed=4893682;
RA   Titani K., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT   complete sequence and the location of the disulfide bridges.";
RL   J. Biol. Chem. 244:3550-3560(1969).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01861; K1HUAG.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01593; 1-108.
DR   Ensembl; ENSG00000173782; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
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DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11992 MW;  E3B3B246C18F0C4F CRC64;

  Query Match             93.1%;  Score 149;  DB 1;  Length 108;
  Best Local Similarity   87.5%;  Pred. No. 7.9e-14;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| |||||  |||||||||| ||||||||||
Db         57 GVPSRFSGSGFGTDFTFTISGLQPEDIATYYC 88


RESULT 8
KV1H_HUMAN
ID   KV1H_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01600;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Hau.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=71032830; PubMed=4097974;
RA   Watanabe S., Hilschmann N.;
RT   "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT   chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT   subgroups.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A01868; K1HUHU.
DR   PDB; 1F6L; X-ray; L=1-108.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin domain; Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11671 MW;  08D3A6160D8D0618 CRC64;

  Query Match             93.1%;  Score 149;  DB 1;  Length 108;
  Best Local Similarity   87.5%;  Pred. No. 7.9e-14;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| |||||  |||||| |||||||||| |||||
Db         57 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC 88


RESULT 9
Q9UL77_HUMAN
ID   Q9UL77_HUMAN PRELIMINARY;      PRT;   108 AA.
AC   Q9UL77;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1516616;
RA   Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT   "Human monoclonal striational autoantibodies isolated from thymic B
RT   lymphocytes of patients with myasthenia gravis use VH and VL gene
RT   segments associated with the autoimmune repertoire.";
RL   Eur. J. Immunol. 22:2231-2236(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=8436174;
RA   Wagner S.D., Luzzatto L.;
RT   "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT   distributed over a large portion of the V kappa locus and do not show
RT   somatic mutation.";
RL   Eur. J. Immunol. 23:391-397(1993).
DR   EMBL; AF035037; AAD56273.1; -; mRNA.
DR   PIR; B49047; B49047.
DR   PIR; S34083; S34083.
DR   HSSP; P01607; 1BWW.
DR   SMR; Q9UL77; 1-108.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11738 MW;  C06681716C4D16F3 CRC64;

  Query Match             93.1%;  Score 149;  DB 2;  Length 108;
  Best Local Similarity   87.5%;  Pred. No. 7.9e-14;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
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                ||| ||||| |||||| ||||||||| |||||
Db         57 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC 88


RESULT 10
KV1I_HUMAN
ID   KV1I_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01601;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region HK101 precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=81098966; PubMed=6779204;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Human immunoglobulin variable region genes -- DNA sequences of two V
RT   kappa genes and a pseudogene.";
RL   Nature 288:730-733(1980).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=83129397; PubMed=6402305; DOI=10.1016/0092-8674(83)90508-1;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Evolution of immunoglobulin V genes: evidence indicating that
RT   recently duplicated human V kappa sequences have diverged by gene
RT   conversion.";
RL   Cell 32:181-189(1983).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; K01322; AAA58930.1; -; Genomic_DNA.
DR   EMBL; K01324; AAA58932.1; -; Genomic_DNA.
DR   EMBL; V00558; CAA23824.1; -; Genomic_DNA.
DR   PIR; A01881; K1HU11.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01601; 23-116.
DR   Ensembl; ENSG00000122156; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23   >117       Ig kappa chain V-I region HK101.
FT   REGION       23     45       Framework-1.
FT   REGION       46     56       Complementarity-determining-1.
FT   REGION       57     71       Framework-2.
FT   REGION       72     78       Complementarity-determining-2.
FT   REGION       79    110       Framework-3.
FT   REGION      111   >117       Complementarity-determining-3.
FT   DISULFID     45    110       By similarity.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12800 MW;  D7D0FF3718CEF587 CRC64;

  Query Match             93.1%;  Score 149;  DB 1;  Length 117;
  Best Local Similarity   87.5%;  Pred. No. 8.6e-14;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
                ||| ||||| |||||| ||||||||| |||||
Db         79 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC 110


RESULT 11
Q6GMX9_HUMAN
ID   Q6GMX9_HUMAN PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGKC protein.
GN   Name=IGKC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RG   NIH MGC Project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073763; AAH73763.1; -; mRNA.
DR   SMR; Q6GMX9; 23-236.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   236 AA;  25924 MW;  FDE2093DC560CFF7 CRC64;

  Query Match             93.1%;  Score 149;  DB 2;  Length 236;
  Best Local Similarity   87.5%;  Pred. No. 1.8e-13;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
                ||| ||||| |||||| ||||||||| |||||
Db         79 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC 110


RESULT 12
Q6GMX8_HUMAN
ID   Q6GMX8_HUMAN PRELIMINARY;      PRT;   236 AA.
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AC   Q6GMX8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGKC protein.
GN   Name=IGKC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RG   NIH MGC Project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073764; AAH73764.1; -; mRNA.
DR   SMR; Q6GMX8; 24-235.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   236 AA;  25707 MW;  4FC8E14B6559EFC9 CRC64;

  Query Match             93.1%;  Score 149;  DB 2;  Length 236;
  Best Local Similarity   87.5%;  Pred. No. 1.8e-13;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||| ||||||||| |||||
Db         79 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC 110


RESULT 13
Q6GMW1_HUMAN
ID   Q6GMW1_HUMAN PRELIMINARY;      PRT;   236 AA.
AC   Q6GMW1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGKC protein.
GN   Name=IGKC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RG   NIH MGC Project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073791; AAH73791.1; -; mRNA.
DR   SMR; Q6GMW1; 24-236.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   236 AA;  25751 MW;  5BFE6A087AFAC437 CRC64;

  Query Match             93.1%;  Score 149;  DB 2;  Length 236;
  Best Local Similarity   87.5%;  Pred. No. 1.8e-13;
  Matches   28;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||| ||||||||| |||||
Db         79 GVPSRFSGSGSGTDFTLTISSLQPEDFATYYC 110


RESULT 14
KV1N_HUMAN
ID   KV1N_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01606;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region OU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
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```
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=70201507; PubMed=5447531;
RA   Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT   "Macroglobulin structure: variable sequence of light and heavy
RT   chains.";
RL   Science 169:56-59(1970).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC       macroglobulin.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01872; K1HUOU.
DR   HSSP; P01607; 1BWW.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11779 MW;  8283D4A24105827E CRC64;

  Query Match             92.5%;  Score 148;  DB 1;  Length 108;
  Best Local Similarity   78.1%;  Pred. No. 1.1e-13;
  Matches   25;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||:||||||||:|:: |||||
Db         57 GVPSRFSGSGSGTBFTFTISSLZPZBFATYYC 88


RESULT 15
Q6PIH7_HUMAN
ID   Q6PIH7_HUMAN PRELIMINARY;      PRT;   236 AA.
AC   Q6PIH7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGKC protein.
GN   Name=IGKC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RG   NIH MGC Project;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034141; AAH34141.1; -; mRNA.
DR   HSSP; P01607; 1AR2.
DR   SMR; Q6PIH7; 23-236.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   236 AA;  25603 MW;  8BC561106861213F CRC64;

  Query Match             90.6%;  Score 145;  DB 2;  Length 236;
  Best Local Similarity   84.4%;  Pred. No. 7.1e-13;
  Matches   27;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

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Db         79 GVPSRFSGSGSGTEFTLTISSLQPEDFATYYC 110


Search completed: March 25, 2006, 09:13:48
Job time : 115.267 secs
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 25, 2006, 09:14:16 ; Search time 29.1518 Seconds
(without alignments)
90.753 Million cell updates/sec

Title: US-10-755-382-28
Perfect score: 160
Sequence: 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	159	99.4	32	1	US-08-137-117D-122	Sequence 122, App
2	159	99.4	32	1	US-08-137-117D-141	Sequence 141, App
3	159	99.4	32	1	US-08-436-717-122	Sequence 122, App
4	159	99.4	32	1	US-08-436-717-141	Sequence 141, App
5	159	99.4	32	1	US-08-553-501A-67	Sequence 67, Appl
6	159	99.4	32	1	US-08-560-558E-3	Sequence 3, Appli
7	159	99.4	32	1	US-08-765-783A-89	Sequence 89, Appl
8	159	99.4	32	2	US-09-205-231-67	Sequence 67, Appl
9	159	99.4	32	2	US-08-646-265A-123	Sequence 123, App
10	159	99.4	32	2	US-09-416-557-89	Sequence 89, Appl
11	159	99.4	32	2	US-09-217-268B-3	Sequence 3, Appli
12	159	99.4	76	2	US-08-851-362D-20	Sequence 20, Appl
13	159	99.4	80	1	US-08-553-501A-85	Sequence 85, Appl
14	159	99.4	80	1	US-08-765-783A-104	Sequence 104, App
15	159	99.4	80	2	US-09-205-231-85	Sequence 85, Appl
16	159	99.4	80	2	US-09-416-557-104	Sequence 104, App
17	159	99.4	80	2	US-09-269-921-131	Sequence 131, App
18	159	99.4	81	2	US-09-254-180C-160	Sequence 160, App
19	159	99.4	87	2	US-08-646-265A-112	Sequence 112, App
20	159	99.4	90	2	US-09-199-149-15	Sequence 15, Appl
21	159	99.4	95	2	US-10-194-975-56	Sequence 56, Appl
22	159	99.4	95	2	US-10-194-975-57	Sequence 57, Appl
23	159	99.4	95	2	US-10-330-613A-59	Sequence 59, Appl
24	159	99.4	106	1	US-08-553-501A-86	Sequence 86, Appl
25	159	99.4	106	1	US-08-318-157B-19	Sequence 19, Appl
26	159	99.4	106	2	US-09-205-231-86	Sequence 86, Appl
27	159	99.4	106	2	US-09-253-794-19	Sequence 19, Appl
28	159	99.4	107	1	US-07-634-278-34	Sequence 34, Appl
29	159	99.4	107	1	US-08-477-728-34	Sequence 34, Appl
30	159	99.4	107	1	US-08-459-310-14	Sequence 14, Appl
31	159	99.4	107	1	US-08-459-310-17	Sequence 17, Appl
32	159	99.4	107	1	US-08-276-852-108	Sequence 108, App
33	159	99.4	107	1	US-08-474-040-34	Sequence 34, Appl
34	159	99.4	107	1	US-08-487-200-34	Sequence 34, Appl
35	159	99.4	107	1	US-08-899-575-108	Sequence 108, App
36	159	99.4	107	1	US-08-491-845-12	Sequence 12, Appl
37	159	99.4	107	1	US-08-899-575-108	Sequence 108, App
38	159	99.4	107	1	US-08-318-157B-6	Sequence 6, Appli
39	159	99.4	107	2	US-08-484-537-34	Sequence 34, Appl
40	159	99.4	107	2	US-08-646-265A-130	Sequence 130, App
41	159	99.4	107	2	US-08-646-265A-131	Sequence 131, App
42	159	99.4	107	2	US-09-253-794-6	Sequence 6, Appli
43	159	99.4	107	4	PCT-US95-08743-108	Sequence 108, App
44	159	99.4	108	1	US-08-657-012-21	Sequence 21, Appl
45	159	99.4	108	2	US-09-013-872-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-137-117D-122
; Sequence 122, Application US/08137117D
; Patent No. 5795965
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: BENDIG, Mary
; APPLICANT: JONES, Steven
; APPLICANT: SALDANHA, Jose
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 RECEPTOR
; NUMBER OF SEQUENCES: 158
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,117D
; FILING DATE: 20-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP92/00544
; FILING DATE: 24-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-32084
; FILING DATE: 19-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 3-95476
; FILING DATE: 25-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/126/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid

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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-137-117D-122

  Query Match             99.4%;  Score 159;  DB 1;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 4e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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              ||| ||||| ||||||||||||||||||||||||
Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32


RESULT 2
US-08-137-117D-141
; Sequence 141, Application US/08137117D
; Patent No. 5795965
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  BENDIG, Mary
;    APPLICANT:  JONES, Steven
;    APPLICANT:  SALDANHA, Jose
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6 RECEPTOR
;    NUMBER OF SEQUENCES:  158
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,117D
;      FILING DATE:  20-DEC-1993
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP92/00544
;      FILING DATE:  24-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 4-32084
;      FILING DATE:  19-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 3-95476
;      FILING DATE:  25-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/126/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  141:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-137-117D-141

  Query Match             99.4%;  Score 159;  DB 1;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 4e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||||
Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32


RESULT 3
US-08-436-717-122
; Sequence 122, Application US/08436717
; Patent No. 5817790
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  BENDIG, Mary
;    APPLICANT:  JONES, Steven
;    APPLICANT:  SALDANHA, Jose
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6 RECEPTOR
;    NUMBER OF SEQUENCES:  158
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/436,717
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,117
;      FILING DATE:  20-DEC-1993
;      APPLICATION NUMBER:  WO PCT/JP92/00544
;      FILING DATE:  24-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 4-32084
;      FILING DATE:  19-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 3-95476
;      FILING DATE:  25-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/126/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  122:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-436-717-122

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  Best Local Similarity   93.8%;  Pred. No. 4e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
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Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32


RESULT 4
US-08-436-717-141
; Sequence 141, Application US/08436717
; Patent No. 5817790
;  GENERAL INFORMATION:
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;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  BENDIG, Mary
;    APPLICANT:  JONES, Steven
;    APPLICANT:  SALDANHA, Jose
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6 RECEPTOR
;    NUMBER OF SEQUENCES:  158
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,117
;      FILING DATE:  20-DEC-1993
;      APPLICATION NUMBER:  WO PCT/JP92/00544
;      FILING DATE:  24-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 4-32084
;      FILING DATE:  19-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 3-95476
;      FILING DATE:  25-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/126/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  141:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-436-717-141

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  Best Local Similarity   93.8%;  Pred. No. 4e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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RESULT 5
US-08-553-501A-67
; Sequence 67, Application US/08553501A
; Patent No. 5856135
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  HIRATA, Yuichi
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,501A
;      FILING DATE:  20-FEB-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/00859
;      FILING DATE:  30-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-129787
;      FILING DATE:  31-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/177/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  67:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-553-501A-67

  Query Match             99.4%;  Score 159;  DB 1;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 4e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||||
Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32


RESULT 6
US-08-560-558E-3
; Sequence 3, Application US/08560558E
; Patent No. 5891996
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Humanized and chimeric monoclonal
;    TITLE OF INVENTION:  antibodies that recognize epidermal growth factor receptor
;    TITLE OF INVENTION:  EGF-R); diagnostic and therapeutic use.
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Allen C. Turner, TRASK, BRITT & ROSSA
;      STREET:  P.O. Box 2250
;      CITY:  Salt Lake City
;      STATE:  Utah
;      COUNTRY:  United States of America
;      ZIP:  84110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  WINDOWS95
;      SOFTWARE:  WordPerfect 5.1/5.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/560,558E
;      FILING DATE:  No. 5891996ember 17, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Turner, Allen C.
;      REGISTRATION NUMBER:  33,041
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;       REFERENCE/DOCKET NUMBER:  2720US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (801) 532-1922
;       TELEFAX:  (801) 531-9168
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  32 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  unknown
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:  NO
US-08-560-558E-3

  Query Match             99.4%;  Score 159;  DB 1;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 4e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32


RESULT 7
US-08-765-783A-89
; Sequence 89, Application US/08765783A
; Patent No. 5994524
;  GENERAL INFORMATION:
;     APPLICANT:  Matsushima, Kouji
;     APPLICANT:  Matsumoto, Yoshihiro
;     APPLICANT:  Yamada, Yoshiki
;     APPLICANT:  Sato, Koh
;     APPLICANT:  Tsuchiya, Masayuki
;     APPLICANT:  Yamazaki, Tatsumi
;     TITLE OF INVENTION:  Reshaped Human Antibody to
;     TITLE OF INVENTION:  Interleukin-8
;     NUMBER OF SEQUENCES:  105
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  MORRISON & FOERSTER
;       STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20006-1888
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/765,783A
;       FILING DATE:  07-MAR-1997
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Murashige, Kate H
;       REGISTRATION NUMBER:  29,959
;       REFERENCE/DOCKET NUMBER:  35029-20001.20
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-887-1500
;       TELEFAX:  202-822-0168
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  89:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  32 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-765-783A-89

  Query Match             99.4%;  Score 159;  DB 1;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 4e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32


RESULT 8
US-09-205-231-67
; Sequence 67, Application US/09205231
; Patent No. 6121423
;  GENERAL INFORMATION:
;     APPLICANT:  TSUCHIYA, Masayuki
;     APPLICANT:  SATO, Koh
;     APPLICANT:  HIRATA, Yuichi
;     TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;     TITLE OF INVENTION:  INTERLEUKIN-6
;     NUMBER OF SEQUENCES:  91
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Foley & Lardner
;       STREET:  3000 K Street, N.W., Suite 500
;       CITY:  Washington
;       STATE:  D.C.
;       COUNTRY:  USA
;       ZIP:  20007-5109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/205,231
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/553,501
;       FILING DATE:  20-FEB-1996
;       APPLICATION NUMBER:  WO PCT/JP94/00859
;       FILING DATE:  30-MAY-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 5-129787
;       FILING DATE:  31-MAY-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WEGNER, Harold C.
;       REGISTRATION NUMBER:  25,258
;       REFERENCE/DOCKET NUMBER:  53466/177/AAOK
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)672-5300
;       TELEFAX:  (202)672-5399
;       TELEX:  904136
;   INFORMATION FOR SEQ ID NO:  67:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  32 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-09-205-231-67

  Query Match             99.4%;  Score 159;  DB 2;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 4e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32


RESULT 9
US-08-646-265A-123
; Sequence 123, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
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;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  123:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-123

  Query Match             99.4%;  Score 159;  DB 2;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 4e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
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Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32


RESULT 10
US-09-416-557-89
; Sequence 89, Application US/09416557
; Patent No. 6245894
;  GENERAL INFORMATION:
;    APPLICANT:  Matsushima, Kouji
;    APPLICANT:  Matsumoto, Yoshihiro
;    APPLICANT:  Yamada, Yoshiki
;    APPLICANT:  Sato, Koh
;    APPLICANT:  Tsuchiya, Masayuki
;    APPLICANT:  Yamazaki, Tatsumi
;    TITLE OF INVENTION:  Reshaped Human Antibody to
;    TITLE OF INVENTION:  Interleukin-8
;    NUMBER OF SEQUENCES:  105
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/416,557
;      FILING DATE:  12-October-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/765,783
;      FILING DATE:  7-March-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  35029-20001.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-822-0168
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  89:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-416-557-89

  Query Match             99.4%;  Score 159;  DB 2;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 4e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
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Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32


RESULT 11
US-09-217-268B-3
; Sequence 3, Application US/09217268B
; Patent No. 6506883
; GENERAL INFORMATION:
;  APPLICANT: Mateo de Acosta del Rio, Christina M
;  APPLICANT:  Rodriquez, Rolando P
;  APPLICANT:  Frias, Ernesto M
;  TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide
;  TITLE OF INVENTION:  Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use
;  FILE REFERENCE: 2720.1US
;  CURRENT APPLICATION NUMBER: US/09/217,268B
;  CURRENT FILING DATE:  1998-12-21
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 32
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-217-268B-3

  Query Match             99.4%;  Score 159;  DB 2;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 4e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32


RESULT 12
US-08-851-362D-20
; Sequence 20, Application US/08851362D
; Patent No. 6235883
; GENERAL INFORMATION:
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; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; TITLE OF INVENTION: Growth Factor Receptor
; FILE REFERENCE: Cell 4.20
; CURRENT APPLICATION NUMBER: US/08/851,362D
; CURRENT FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 76
; TYPE: PRT
; ORGANISM: human
US-08-851-362D-20

Query Match 99.4%; Score 159; DB 2; Length 76;
Best Local Similarity 93.8%; Pred. No. 1e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
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Db 38 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 69

RESULT 13
US-08-553-501A-85
; Sequence 85, Application US/08553501A
; Patent No. 5856135
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: HIRATA, Yuichi
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,501A
; FILING DATE: 20-FEB-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP94/00859
; FILING DATE: 30-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-129787
; FILING DATE: 31-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/177/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-553-501A-85

Query Match 99.4%; Score 159; DB 1; Length 80;
Best Local Similarity 93.8%; Pred. No. 1.1e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
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Db 39 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 70

RESULT 14
US-08-765-783A-104
; Sequence 104, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-765-783A-104

Query Match 99.4%; Score 159; DB 1; Length 80;
Best Local Similarity 93.8%; Pred. No. 1.1e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
||| ||||| ||||||||||||||||||||||
Db 39 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 70

RESULT 15
US-09-205-231-85
; Sequence 85, Application US/09205231
; Patent No. 6121423

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;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  HIRATA, Yuichi
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/205,231
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,501
;      FILING DATE:  20-FEB-1996
;      APPLICATION NUMBER:  WO PCT/JP94/00859
;      FILING DATE:  30-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-129787
;      FILING DATE:  31-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/177/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  85:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  80 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-205-231-85

  Query Match            99.4%;  Score 159;  DB 2;  Length 80;
  Best Local Similarity  93.8%;  Pred. No. 1.1e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db         39 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 70


Search completed: March 25, 2006, 09:18:45
Job time : 30.1518 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:55:36 ; Search time 95.4974 Seconds
(without alignments)
140.009 Million cell updates/sec

Title: US-10-755-382-28
Perfect score: 160
Sequence: 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32

Scoring table: BLOSUM62
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	159	99.4	32	3	US-09-217-268B-3	Sequence 3, Appli
2	159	99.4	32	3	US-09-730-857-89	Sequence 89, Appl
3	159	99.4	32	3	US-09-749-873-123	Sequence 123, App
4	159	99.4	32	5	US-10-923-068-129	Sequence 129, App
5	159	99.4	32	5	US-10-923-068-138	Sequence 138, App
6	159	99.4	75	4	US-10-078-958-25	Sequence 25, Appl
7	159	99.4	76	3	US-09-187-693-36	Sequence 36, Appl
8	159	99.4	76	6	US-11-021-795-36	Sequence 36, Appl
9	159	99.4	80	3	US-09-730-857-104	Sequence 104, App
10	159	99.4	80	3	US-09-269-921-131	Sequence 131, App
11	159	99.4	80	3	US-09-509-098-132	Sequence 132, App
12	159	99.4	80	4	US-10-218-253-131	Sequence 131, App
13	159	99.4	80	5	US-10-837-904-114	Sequence 114, App
14	159	99.4	80	5	US-10-837-904-123	Sequence 123, App
15	159	99.4	87	3	US-09-749-873-112	Sequence 112, App
16	159	99.4	90	3	US-09-864-761-34739	Sequence 34739, A
17	159	99.4	90	4	US-10-141-908-15	Sequence 15, Appl
18	159	99.4	95	4	US-10-194-975-56	Sequence 56, Appl
19	159	99.4	95	4	US-10-194-975-57	Sequence 57, Appl
20	159	99.4	95	4	US-10-308-817-3	Sequence 3, Appli
21	159	99.4	95	4	US-10-308-817-4	Sequence 4, Appli
22	159	99.4	95	4	US-10-453-698-3	Sequence 3, Appli
23	159	99.4	95	4	US-10-453-698-4	Sequence 4, Appli
24	159	99.4	95	4	US-10-379-392-73	Sequence 73, Appl
25	159	99.4	95	4	US-10-379-392-74	Sequence 74, Appl
26	159	99.4	103	4	US-10-379-392-99	Sequence 99, Appl
27	159	99.4	103	4	US-10-379-392-111	Sequence 111, App
28	159	99.4	106	3	US-09-253-794-19	Sequence 19, Appl
29	159	99.4	106	4	US-10-680-734-19	Sequence 19, Appl
30	159	99.4	106	5	US-10-727-155-130	Sequence 130, App
31	159	99.4	106	5	US-10-755-382-19	Sequence 19, Appl
32	159	99.4	107	3	US-09-253-794-6	Sequence 6, Appli
33	159	99.4	107	3	US-09-749-873-130	Sequence 130, App
34	159	99.4	107	3	US-09-749-873-131	Sequence 131, App
35	159	99.4	107	4	US-10-223-880-15	Sequence 15, Appl
36	159	99.4	107	4	US-10-016-986-108	Sequence 108, App
37	159	99.4	107	4	US-10-389-155-47	Sequence 47, Appl
38	159	99.4	107	4	US-10-389-417-47	Sequence 47, Appl
39	159	99.4	107	4	US-10-452-357-34	Sequence 34, Appl
40	159	99.4	107	4	US-10-680-734-6	Sequence 6, Appli
41	159	99.4	107	5	US-10-727-155-318	Sequence 318, App
42	159	99.4	107	5	US-10-755-382-6	Sequence 6, Appli
43	159	99.4	107	6	US-11-031-485-132	Sequence 132, App
44	159	99.4	108	3	US-09-155-106-24	Sequence 24, Appl
45	159	99.4	108	3	US-09-155-106-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-217-268B-3
; Sequence 3, Application US/09217268B
; Patent No. US20020065398A1
; GENERAL INFORMATION:
; APPLICANT: Mateo de Acosta del Rio, Christina M
; APPLICANT: Rodriquez, Rolando P
; APPLICANT: Frias, Ernesto M
; TITLE OF INVENTION: Humanized and Chimeric Monoclonal Antibodies That Recognize Epide
; TITLE OF INVENTION: Growth Factor Receptor (EGF-R); Diagnostic and Therapeutic Use
; FILE REFERENCE: 2720.1US
; CURRENT APPLICATION NUMBER: US/09/217,268B
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-217-268B-3

Query Match 99.4%; Score 159; DB 3; Length 32;
Best Local Similarity 93.8%; Pred. No. 1.9e-14;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
||| ||||| ||||||||||||||||||||||||
Db 1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32

RESULT 2
US-09-730-857-89
; Sequence 89, Application US/09730857
; Patent No. US20020082396A1
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; Matsumoto, Yoshihiro
; Yamada, Yoshiki
; Sato, Koh
; Tsuchiya, Masayuki
; Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA

```
;           ZIP: 20006-1888
;        COMPUTER READABLE FORM:
;           MEDIUM TYPE: Diskette
;           COMPUTER: IBM Compatible
;           OPERATING SYSTEM: DOS
;           SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/730,857
;           FILING DATE: 07-Dec-2000
;           CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 09/416,557
;           FILING DATE: 1999-10-12
;        ATTORNEY/AGENT INFORMATION:
;           NAME: Murashige, Kate H
;           REGISTRATION NUMBER: 29,959
;           REFERENCE/DOCKET NUMBER: 35029-20001.10
;        TELECOMMUNICATION INFORMATION:
;           TELEPHONE: 202-887-1500
;           TELEFAX: 202-822-0168
;           TELEX: <Unknown>
;     INFORMATION FOR SEQ ID NO: 89:
;        SEQUENCE CHARACTERISTICS:
;           LENGTH: 32 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 89:
US-09-730-857-89

  Query Match             99.4%;  Score 159;  DB 3;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 1.9e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||||||||||||||||||||
Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32


RESULT 3
US-09-749-873-123
; Sequence 123, Application US/09749873
; Publication No. US20030023045A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Foley & Lardner
;           STREET: 3000 K Street, N.W., Suite 500
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/749,873
;           FILING DATE: 29-Dec-2000
;           CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 08/646,265
;           FILING DATE: 1996-09-09
;           APPLICATION NUMBER: JP 5-291078
;           FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;           NAME: WEGNER, Harold C.
;           REGISTRATION NUMBER: 25,258
;           REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;     INFORMATION FOR SEQ ID NO: 123:
;        SEQUENCE CHARACTERISTICS:
;           LENGTH: 32 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-09-749-873-123

  Query Match             99.4%;  Score 159;  DB 3;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 1.9e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||||||||||||||||||||
Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32


RESULT 4
US-10-923-068-129
; Sequence 129, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 129
;   LENGTH: 32
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-129

  Query Match             99.4%;  Score 159;  DB 5;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 1.9e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||||||||||||||||||||
Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32


RESULT 5
US-10-923-068-138
; Sequence 138, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 138
;   LENGTH: 32
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-138
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  Query Match             99.4%;  Score 159;  DB 5;  Length 32;
  Best Local Similarity   93.8%;  Pred. No. 1.9e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db          1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32


RESULT 6
US-10-078-958-25
; Sequence 25, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
;  APPLICANT: JAKOBOVITS, AYA
;  APPLICANT:  KUCHERLAPATI, RAJU
;  APPLICANT:  KLAPHOLZ, SUSAN
;  APPLICANT:  MENDEZ, MICHAEL J.
;  APPLICANT:  GREEN, LARRY
;  TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
;  TITLE OF INVENTION:  PLURAL Vh AND Vk REGIONS AND ANTIBODIES PRODUCED
;  TITLE OF INVENTION:  THEREFROM
;  FILE REFERENCE: CELL 4.18 CON
;  CURRENT APPLICATION NUMBER: US/10/078,958
;  CURRENT FILING DATE:  2002-02-19
;  PRIOR APPLICATION NUMBER: 08/759,620
;  PRIOR FILING DATE: 1996-12-03
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 75
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-078-958-25

  Query Match             99.4%;  Score 159;  DB 4;  Length 75;
  Best Local Similarity   93.8%;  Pred. No. 4.9e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db         38 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 69


RESULT 7
US-09-187-693-36
; Sequence 36, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
;  APPLICANT: Jakobovits, Aya
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Gallo, Michael
;  APPLICANT:  Jia, Xiao-Chi
;  TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
;  TITLE OF INVENTION:  Growth Factor Receptor
;  FILE REFERENCE: Cell 4.20 CIP2
;  CURRENT APPLICATION NUMBER: US/09/187,693
;  CURRENT FILING DATE:  1998-11-05
;  PRIOR APPLICATION NUMBER: 09/162,280
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 08/851,362
;  PRIOR FILING DATE: 1997-05-05
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
;   LENGTH: 76
;   TYPE: PRT
;   ORGANISM: human
US-09-187-693-36

  Query Match             99.4%;  Score 159;  DB 3;  Length 76;
  Best Local Similarity   93.8%;  Pred. No. 4.9e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db         38 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 69


RESULT 8
US-11-021-795-36
; Sequence 36, Application US/11021795
; Publication No. US20050100546A1
; GENERAL INFORMATION:
;  APPLICANT: Jakobovits, Aya
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Gallo, Michael
;  APPLICANT:  Jia, Xiao-Chi
;  TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
;  TITLE OF INVENTION:  Growth Factor Receptor
;  FILE REFERENCE: Cell 4.20 CIP2
;  CURRENT APPLICATION NUMBER: US/11/021,795
;  CURRENT FILING DATE:  2004-12-22
;  PRIOR APPLICATION NUMBER: US/09/187,693
;  PRIOR FILING DATE: 1998-11-05
;  PRIOR APPLICATION NUMBER: 09/162,280
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 08/851,362
;  PRIOR FILING DATE: 1997-05-05
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
;   LENGTH: 76
;   TYPE: PRT
;   ORGANISM: human
US-11-021-795-36

  Query Match             99.4%;  Score 159;  DB 6;  Length 76;
  Best Local Similarity   93.8%;  Pred. No. 4.9e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db         38 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 69


RESULT 9
US-09-730-857-104
; Sequence 104, Application US/09730857
; Patent No. US20020082396A1
;   GENERAL INFORMATION:
;        APPLICANT: Matsushima, Kouji
;                   Matsumoto, Yoshihiro
;                   Yamada, Yoshiki
;                   Sato, Koh
;                   Tsuchiya, Masayuki
;                   Yamazaki, Tatsumi
;        TITLE OF INVENTION: Reshaped Human Antibody to
;                            Interleukin-8
;        NUMBER OF SEQUENCES: 105
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORRISON & FOERSTER
;             STREET: 2000 Pennsylvania Avenue, NW, suite 5500
;             CITY: Washington
;             STATE: DC
;             COUNTRY: USA
;             ZIP: 20006-1888
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/730,857
;             FILING DATE: 07-Dec-2000
;             CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/416,557
; FILING DATE: 1999-10-12
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-09-730-857-104

Query Match 99.4%; Score 159; DB 3; Length 80;
Best Local Similarity 93.8%; Pred. No. 5.2e-14;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
||| ||||| |||||||||||||||||||||||
Db 39 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 70

RESULT 10
US-09-269-921-131
; Sequence 131, Application US/09269921
; Publication No. US20030045691A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/09/269,921
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: PCT/JP97/03553
; EARLIER FILING DATE: 1997-10-03
; EARLIER APPLICATION NUMBER: JP 8-264756
; EARLIER FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: REI
; PUBLICATION INFORMATION:
; AUTHORS: Recchmann, L. et al.
; JOURNAL: NATURE
; VOLUME: 322
; PAGES: 21-25
; DATE: 1998
US-09-269-921-131

Query Match 99.4%; Score 159; DB 3; Length 80;
Best Local Similarity 93.8%; Pred. No. 5.2e-14;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
||| ||||| |||||||||||||||||||||||
Db 39 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 70

RESULT 11
US-09-509-098-132
; Sequence 132, Application US/09509098
; Publication No. US20030103970A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0274
; CURRENT APPLICATION NUMBER: US/09/509,098
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/JP98/04469
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: JP 9-271726
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of the L chain V region of REI
US-09-509-098-132

Query Match 99.4%; Score 159; DB 3; Length 80;
Best Local Similarity 93.8%; Pred. No. 5.2e-14;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
||| ||||| |||||||||||||||||||||||
Db 39 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 70

RESULT 12
US-10-218-253-131
; Sequence 131, Application US/10218253
; Publication No. US20030129185A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/10/218,253
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/269,921
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: PCT/JP97/03553
; PRIOR FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: JP 8-264756
; PRIOR FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: REI
; PUBLICATION INFORMATION:
; AUTHORS: Recchmann, L. et al.
; JOURNAL: NATURE
; VOLUME: 322
; PAGES: 21-25
; DATE: 1998
US-10-218-253-131

Query Match 99.4%; Score 159; DB 4; Length 80;
Best Local Similarity 93.8%; Pred. No. 5.2e-14;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||||
Db         39 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 70


RESULT 13
US-10-837-904-114
; Sequence 114, Application US/10837904
; Publication No. US20050142635A1
;   GENERAL INFORMATION:
;        APPLICANT: TSUCHIYA, Masayuki
;                   SATO, Koh
;                   BENDIG, Mary Margaret
;                   JONES, Steven Tarran
;                   SALDANHA, Jose William
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            INTERLEUKIN-6 RECEPTOR
;        NUMBER OF SEQUENCES: 134
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FOLEY & LARDNER
;             STREET: 3000 K Street, N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/837,904
;             FILING DATE: 04-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/114,285
;             FILING DATE: 13-Jul-1998
;             APPLICATION NUMBER: US 08/436,717
;             FILING DATE: 08-MAY-1995
;             APPLICATION NUMBER: US 08/137,117
;             FILING DATE: 20-DEC-1993
;             APPLICATION NUMBER: WO PCT/JP92/00544
;             FILING DATE: 24-APR-1992
;             APPLICATION NUMBER: JP 4-32084
;             FILING DATE: 19-FEB-1992
;             APPLICATION NUMBER: JP 3-95476
;             FILING DATE: 25-APR-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Wegner, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/234
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 672-5300
;             TELEFAX: (202) 672-5399
;   INFORMATION FOR SEQ ID NO: 114:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 80 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-837-904-114

  Query Match             99.4%;  Score 159;  DB 5;  Length 80;
  Best Local Similarity   93.8%;  Pred. No. 5.2e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||||
Db         39 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 70


RESULT 14
US-10-837-904-123
; Sequence 123, Application US/10837904
; Publication No. US20050142635A1
;   GENERAL INFORMATION:
;        APPLICANT: TSUCHIYA, Masayuki
;                   SATO, Koh
;                   BENDIG, Mary Margaret
;                   JONES, Steven Tarran
;                   SALDANHA, Jose William
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            INTERLEUKIN-6 RECEPTOR
;        NUMBER OF SEQUENCES: 134
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: FOLEY & LARDNER
;             STREET: 3000 K Street, N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: U.S.A.
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/837,904
;             FILING DATE: 04-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/114,285
;             FILING DATE: 13-Jul-1998
;             APPLICATION NUMBER: US 08/436,717
;             FILING DATE: 08-MAY-1995
;             APPLICATION NUMBER: US 08/137,117
;             FILING DATE: 20-DEC-1993
;             APPLICATION NUMBER: WO PCT/JP92/00544
;             FILING DATE: 24-APR-1992
;             APPLICATION NUMBER: JP 4-32084
;             FILING DATE: 19-FEB-1992
;             APPLICATION NUMBER: JP 3-95476
;             FILING DATE: 25-APR-1991
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Wegner, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/234
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202) 672-5300
;             TELEFAX: (202) 672-5399
;   INFORMATION FOR SEQ ID NO: 123:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 80 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-10-837-904-123

  Query Match             99.4%;  Score 159;  DB 5;  Length 80;
  Best Local Similarity   93.8%;  Pred. No. 5.2e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||||
Db         39 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 70


RESULT 15
US-09-749-873-112
; Sequence 112, Application US/09749873
; Publication No. US20030023045A1
;   GENERAL INFORMATION:
```

```
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/749,873
;             FILING DATE: 29-Dec-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/646,265
;             FILING DATE: 1996-09-09
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 112:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 87 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-09-749-873-112

  Query Match             99.4%;  Score 159;  DB 3;  Length 87;
  Best Local Similarity   93.8%;  Pred. No. 5.7e-14;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| |||||||||||||||||||||||
Db         46 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 77


Search completed: March 25, 2006, 10:08:03
Job time : 96.4974 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:58:56 ; Search time 11.5602 Seconds
(without alignments)
81.644 Million cell updates/sec

Title: US-10-755-382-28
Perfect score: 160
Sequence: 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	159	99.4	32	6	US-10-839-799-123	Sequence 123, App
2	159	99.4	80	7	US-11-226-325-132	Sequence 132, App
3	159	99.4	87	6	US-10-839-799-112	Sequence 112, App
4	159	99.4	90	7	US-11-173-071-23	Sequence 23, Appl
5	159	99.4	95	7	US-11-054-669-56	Sequence 56, Appl
6	159	99.4	95	7	US-11-054-669-57	Sequence 57, Appl
7	159	99.4	95	7	US-11-084-554-145	Sequence 145, App
8	159	99.4	95	7	US-11-084-554-148	Sequence 148, App
9	159	99.4	95	7	US-11-061-848-33	Sequence 33, Appl
10	159	99.4	95	7	US-11-061-848-62	Sequence 62, Appl
11	159	99.4	95	7	US-11-061-848-68	Sequence 68, Appl
12	159	99.4	95	7	US-11-004-590-68	Sequence 68, Appl
13	159	99.4	95	7	US-11-004-590-69	Sequence 69, Appl
14	159	99.4	95	7	US-11-136-250-145	Sequence 145, App
15	159	99.4	95	7	US-11-136-250-148	Sequence 148, App
16	159	99.4	107	6	US-10-839-799-130	Sequence 130, App
17	159	99.4	107	6	US-10-839-799-131	Sequence 131, App
18	159	99.4	108	7	US-11-061-848-10	Sequence 10, Appl
19	159	99.4	109	7	US-11-102-201-2	Sequence 2, Appli
20	159	99.4	126	6	US-10-839-799-43	Sequence 43, Appl
21	159	99.4	126	6	US-10-839-799-57	Sequence 57, Appl
22	159	99.4	126	6	US-10-839-799-77	Sequence 77, Appl
23	159	99.4	126	6	US-10-839-799-81	Sequence 81, Appl
24	159	99.4	126	6	US-10-839-799-85	Sequence 85, Appl
25	159	99.4	126	6	US-10-839-799-87	Sequence 87, Appl
26	159	99.4	126	6	US-10-839-799-91	Sequence 91, Appl
27	159	99.4	126	7	US-11-226-325-12	Sequence 12, Appl
28	159	99.4	128	7	US-11-096-074-20	Sequence 20, Appl
29	159	99.4	128	7	US-11-095-822-20	Sequence 20, Appl
30	159	99.4	213	7	US-11-158-505-34	Sequence 34, Appl
31	159	99.4	219	7	US-11-080-587-8	Sequence 8, Appli
32	159	99.4	269	6	US-10-839-799-109	Sequence 109, App
33	158	98.8	107	7	US-11-107-028-14	Sequence 14, Appl
34	158	98.8	107	7	US-11-004-590-289	Sequence 289, App
35	158	98.8	107	7	US-11-004-590-302	Sequence 302, App
36	158	98.8	108	7	US-11-173-071-18	Sequence 18, Appl
37	158	98.8	113	7	US-11-076-395-70	Sequence 70, Appl
38	156	97.5	93	7	US-11-240-195-66	Sequence 66, Appl
39	156	97.5	107	7	US-11-221-900-8	Sequence 8, Appli
40	156	97.5	107	7	US-11-221-900-9	Sequence 9, Appli
41	156	97.5	107	7	US-11-240-195-74	Sequence 74, Appl
42	156	97.5	108	7	US-11-221-900-7	Sequence 7, Appli
43	156	97.5	126	6	US-10-839-799-47	Sequence 47, Appl
44	156	97.5	126	7	US-11-226-325-14	Sequence 14, Appl
45	156	97.5	235	7	US-11-166-994-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-839-799-123
; Sequence 123, Application US/10839799
; Publication No. US20050249726A1
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; SATO, Koh
; TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/839,799
; FILING DATE: 06-May-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-10-839-799-123

Query Match 99.4%; Score 159; DB 6; Length 32;
Best Local Similarity 93.8%; Pred. No. 1.5e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
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Db 1 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 32

RESULT 2
US-11-226-325-132
; Sequence 132, Application US/11226325
; Publication No. US20060008456A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0274
; CURRENT APPLICATION NUMBER: US/11/226,325
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/509,098
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/JP98/04469
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: JP 9-271726
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of the L chain V region of REI
US-11-226-325-132

Query Match 99.4%; Score 159; DB 7; Length 80;
Best Local Similarity 93.8%; Pred. No. 3.5e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
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Db 39 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 70

RESULT 3
US-10-839-799-112
; Sequence 112, Application US/10839799
; Publication No. US20050249726A1
; GENERAL INFORMATION:
; APPLICANT: OHTOMO, Toshihiko
; SATO, Koh
; TSUCHIYA, Masayuki
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; MEDULLOBLASTOMA CELLS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/839,799
; FILING DATE: 06-May-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 87 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-839-799-112

Query Match 99.4%; Score 159; DB 6; Length 87;
Best Local Similarity 93.8%; Pred. No. 3.7e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
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Db 46 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 77

RESULT 4
US-11-173-071-23
; Sequence 23, Application US/11173071
; Publication No. US20050244409A1
; GENERAL INFORMATION:
; APPLICANT: ERICKSON-MILLER, CONNIE
; APPLICANT: HOLMES, STEPHEN D.
; APPLICANT: TAYLOR, ALEXANDER H.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR ANTIBODIES
; FILE REFERENCE: P50911
; CURRENT APPLICATION NUMBER: US/11/173,071
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/09/958,620
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: PCT/US00/10284
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,263
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derivative of human light chain REI, REI-con
US-11-173-071-23

Query Match 99.4%; Score 159; DB 7; Length 90;
Best Local Similarity 93.8%; Pred. No. 3.9e-13;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
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Db 57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88

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RESULT 5
US-11-054-669-56
; Sequence 56, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
;  FILE REFERENCE: 30219/US/3
;  CURRENT APPLICATION NUMBER: US/11/054,669
;  CURRENT FILING DATE:  2005-02-08
;  PRIOR APPLICATION NUMBER: US 10/194,975
;  PRIOR FILING DATE: 2002-07-12
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-669-56

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  Best Local Similarity   93.8%;  Pred. No. 4e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
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Db         57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88


RESULT 6
US-11-054-669-57
; Sequence 57, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
;  FILE REFERENCE: 30219/US/3
;  CURRENT APPLICATION NUMBER: US/11/054,669
;  CURRENT FILING DATE:  2005-02-08
;  PRIOR APPLICATION NUMBER: US 10/194,975
;  PRIOR FILING DATE: 2002-07-12
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-669-57

  Query Match             99.4%;  Score 159;  DB 7;  Length 95;
  Best Local Similarity   93.8%;  Pred. No. 4e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
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Db         57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88


RESULT 7
US-11-084-554-145
; Sequence 145, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-145

  Query Match             99.4%;  Score 159;  DB 7;  Length 95;
  Best Local Similarity   93.8%;  Pred. No. 4e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||||
Db         57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88


RESULT 8
US-11-084-554-148
; Sequence 148, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 148
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-148

  Query Match             99.4%;  Score 159;  DB 7;  Length 95;
  Best Local Similarity   93.8%;  Pred. No. 4e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||||
Db         57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88


RESULT 9
US-11-061-848-33
; Sequence 33, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
;  APPLICANT: Wilson, David S.
;  APPLICANT:  Nock, Steffen
;  APPLICANT:  Larrick, James W.
;  TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
;  FILE REFERENCE: 186280/US
;  CURRENT APPLICATION NUMBER: US/11/061,848
;  CURRENT FILING DATE:  2005-02-17
;  PRIOR APPLICATION NUMBER: US 60/545,011
;  PRIOR FILING DATE: 2004-02-17
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 33
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-061-848-33

  Query Match             99.4%;  Score 159;  DB 7;  Length 95;
  Best Local Similarity   93.8%;  Pred. No. 4e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db         57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88


RESULT 10
US-11-061-848-62
; Sequence 62, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
;  APPLICANT: Wilson, David S.
;  APPLICANT:  Nock, Steffen
;  APPLICANT:  Larrick, James W.
;  TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
;  FILE REFERENCE: 186280/US
;  CURRENT APPLICATION NUMBER: US/11/061,848
;  CURRENT FILING DATE:  2005-02-17
;  PRIOR APPLICATION NUMBER: US 60/545,011
;  PRIOR FILING DATE: 2004-02-17
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-061-848-62

  Query Match             99.4%;  Score 159;  DB 7;  Length 95;
  Best Local Similarity   93.8%;  Pred. No. 4e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
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Db         57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88


RESULT 11
US-11-061-848-68
; Sequence 68, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
;  APPLICANT: Wilson, David S.
;  APPLICANT:  Nock, Steffen
;  APPLICANT:  Larrick, James W.
;  TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
;  FILE REFERENCE: 186280/US
;  CURRENT APPLICATION NUMBER: US/11/061,848
;  CURRENT FILING DATE:  2005-02-17
;  PRIOR APPLICATION NUMBER: US 60/545,011
;  PRIOR FILING DATE: 2004-02-17
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-061-848-68

  Query Match             99.4%;  Score 159;  DB 7;  Length 95;
  Best Local Similarity   93.8%;  Pred. No. 4e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db         57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88


RESULT 12
US-11-004-590-68
; Sequence 68, Application US/11004590
; Publication No. US20060008883A1
; GENERAL INFORMATION:
;  APPLICANT: Lazar, Gregory Alan
;  APPLICANT:  Desjarlais, John R.
;  APPLICANT:  Hammond, Phillip W.
;  TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
;  TITLE OF INVENTION:  CONTENT AND COMPOSITIONS THEREOF
;  FILE REFERENCE: 185832/US/5
;  CURRENT APPLICATION NUMBER: US/11/004,590
;  CURRENT FILING DATE:  2004-12-03
;  PRIOR APPLICATION NUMBER: US 60/527,167
;  PRIOR FILING DATE: 2003-12-04
;  PRIOR APPLICATION NUMBER: US 60/581,613
;  PRIOR FILING DATE: 2004-06-21
;  PRIOR APPLICATION NUMBER: US 60/601,665
;  PRIOR FILING DATE: 2004-08-13
;  PRIOR APPLICATION NUMBER: US 60/619,483
;  PRIOR FILING DATE: 2004-10-14
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 68
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-004-590-68

  Query Match             99.4%;  Score 159;  DB 7;  Length 95;
  Best Local Similarity   93.8%;  Pred. No. 4e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||
Db         57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88


RESULT 13
US-11-004-590-69
; Sequence 69, Application US/11004590
; Publication No. US20060008883A1
; GENERAL INFORMATION:
;  APPLICANT: Lazar, Gregory Alan
;  APPLICANT:  Desjarlais, John R.
;  APPLICANT:  Hammond, Phillip W.
;  TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
;  TITLE OF INVENTION:  CONTENT AND COMPOSITIONS THEREOF
;  FILE REFERENCE: 185832/US/5
;  CURRENT APPLICATION NUMBER: US/11/004,590
;  CURRENT FILING DATE:  2004-12-03
;  PRIOR APPLICATION NUMBER: US 60/527,167
;  PRIOR FILING DATE: 2003-12-04
;  PRIOR APPLICATION NUMBER: US 60/581,613
;  PRIOR FILING DATE: 2004-06-21
;  PRIOR APPLICATION NUMBER: US 60/601,665
;  PRIOR FILING DATE: 2004-08-13
;  PRIOR APPLICATION NUMBER: US 60/619,483
;  PRIOR FILING DATE: 2004-10-14
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-004-590-69

  Query Match             99.4%;  Score 159;  DB 7;  Length 95;
  Best Local Similarity   93.8%;  Pred. No. 4e-13;
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  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||||
Db         57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88


RESULT 14
US-11-136-250-145
; Sequence 145, Application US/11136250
; Publication No. US20060021074A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A2
;  CURRENT APPLICATION NUMBER: US/11/136,250
;  CURRENT FILING DATE:  2005-05-23
;  PRIOR APPLICATION NUMBER: 11/084,554
;  PRIOR FILING DATE: 2005-03-17
;  PRIOR APPLICATION NUMBER: PCT/US2005/009306
;  PRIOR FILING DATE: 2005-03-17
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-136-250-145

  Query Match             99.4%;  Score 159;  DB 7;  Length 95;
  Best Local Similarity   93.8%;  Pred. No. 4e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||||
Db         57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88


RESULT 15
US-11-136-250-148
; Sequence 148, Application US/11136250
; Publication No. US20060021074A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A2
;  CURRENT APPLICATION NUMBER: US/11/136,250
;  CURRENT FILING DATE:  2005-05-23
;  PRIOR APPLICATION NUMBER: 11/084,554
;  PRIOR FILING DATE: 2005-03-17
;  PRIOR APPLICATION NUMBER: PCT/US2005/009306
;  PRIOR FILING DATE: 2005-03-17
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 148
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-136-250-148

  Query Match             99.4%;  Score 159;  DB 7;  Length 95;
  Best Local Similarity   93.8%;  Pred. No. 4e-13;
  Matches   30;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GVPXRFSGSXSGTDFTFTISSLQPEDIATYYC 32
              ||| ||||| ||||||||||||||||||||||||
Db         57 GVPSRFSGSGSGTDFTFTISSLQPEDIATYYC 88


Search completed: March 25, 2006, 10:09:18
Job time : 11.5602 secs
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:10 ; Search time 36.8586 Seconds
(without alignments)
119.206 Million cell updates/sec

Title: US-10-755-382-29
Perfect score: 51
Sequence: 1 FGQGTKVEIK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	10	2	AAR27044	Aar27044 Human lig
2	51	100.0	10	2	AAR85156	Aar85156 Human ONS
3	51	100.0	10	3	AAB11827	Aab11827 Human Ig
4	51	100.0	10	5	AAU70397	Aau70397 Human lig
5	51	100.0	10	5	AAU70401	Aau70401 Human lig
6	51	100.0	10	5	AAU70409	Aau70409 Human lig
7	51	100.0	10	5	AAU70405	Aau70405 Human lig
8	51	100.0	10	7	ADG75672	Adg75672 Peptide o
9	51	100.0	10	8	ADL93541	Adl93541 Human CD4
10	51	100.0	10	8	ADQ92392	Adq92392 Human hu1
11	51	100.0	10	8	ADQ80581	Adq80581 Human lig
12	51	100.0	10	9	AEA21490	Aea21490 Human ant
13	51	100.0	10	9	AEA21454	Aea21454 Human ant
14	51	100.0	10	9	AEA21472	Aea21472 Human ant
15	51	100.0	10	9	AEA45326	Aea45326 Apolipopr
16	51	100.0	11	2	AAR87044	Aar87044 Human gro
17	51	100.0	11	2	AAW70795	Aaw70795 J peptide
18	51	100.0	11	5	AAE19674	Aae19674 Human gro
19	51	100.0	11	7	ABW02162	Abw02162 Human gp1
20	51	100.0	11	7	ABG75306	Abg75306 Human JK1
21	51	100.0	11	8	ABM79518	Abm79518 Human JK1
22	51	100.0	11	8	ADO60482	Ado60482 Humanised
23	51	100.0	11	8	ADR38860	Adr38860 Mouse lig
24	51	100.0	11	8	ADR38848	Adr38848 Mouse lig
25	51	100.0	11	8	ADR38857	Adr38857 Mouse lig
26	51	100.0	11	8	ADR38851	Adr38851 Mouse lig
27	51	100.0	11	8	ADR38854	Adr38854 Mouse lig
28	51	100.0	11	9	ADW96733	Adw96733 Anti-EGFR
29	51	100.0	11	9	ADW80305	Adw80305 Human ant
30	51	100.0	11	9	ADX27020	Adx27020 Human gro
31	51	100.0	11	9	AEB24634	Aeb24634 Humanized
32	51	100.0	12	5	AAU90895	Aau90895 Insulin/i
33	51	100.0	12	7	ADJ80385	Adj80385 Jk gene l
34	51	100.0	12	8	ADH17977	Adh17977 Human mod
35	51	100.0	12	8	ADH18001	Adh18001 Human mod
36	51	100.0	12	8	ADH17985	Adh17985 Human mod
37	51	100.0	12	8	ADH17952	Adh17952 Human 15H
38	51	100.0	12	8	ADH17944	Adh17944 Human 15H
39	51	100.0	12	8	ADH17993	Adh17993 Human mod
40	51	100.0	12	8	ADL15703	Adl15703 Human imm
41	51	100.0	12	9	ADY31307	Ady31307 Human ant
42	51	100.0	12	9	ADY75486	Ady75486 Human ger
43	51	100.0	12	9	AEA21546	Aea21546 Human ant
44	51	100.0	12	9	AEA53905	Aea53905 Novel hum
45	51	100.0	12	9	AEA53986	Aea53986 Novel hum

ALIGNMENTS

RESULT 1
AAR27044
ID AAR27044 standard; peptide; 10 AA.
XX
AC AAR27044;
XX
DT 25-MAR-2003 (revised)
DT 01-MAR-1993 (first entry)
XX
DE Human light chain framework 4 used in humanised MAb.
XX
KW Monoclonal antibody; complementarity determining region; CDR; antigens;
KW tumour; melanoma; carcinoma; glioma.
XX
OS Homo sapiens.
XX
PN WO9215683-A1.
XX
PD 17-SEP-1992.
XX
PF 04-MAR-1992; 92WO-EP000480.
XX
PR 06-MAR-1991; 91EP-00103389.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Bendig MM, Kettleborough CA, Saldanha J;
XX
DR WPI; 1992-331729/40.
XX
PT Human monoclonal antibodies binding to human receptors - for treatment
PT and diagnosis of tumours, e.g. melanoma and carcinoma.
XX
PS Claim 5; Page 63; 89pp; English.
XX
CC The human framework sequence FR4 was used in the prodn. of humanised
CC monoclonal antibodies comprising antigen binding sites (CDRs) of non
CC human origen based on consensus sequence of CDRs. The sequence is a light
CC chain framework region. The humanised antibodies or their chimeric
CC variants may be used as therapeutic or diagnostic agents in order to
CC combat e.g. glioma, melanoma or carcinoma. See also AAR27299-300 and
CC AAR27037-51. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;

```
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 2
AAR85156
ID   AAR85156 standard; protein; 10 AA.
XX
AC   AAR85156;
XX
DT   18-JAN-1996  (first entry)
XX
DE   Human ONS-M21 antibody light variable region FR 4.
XX
KW   Human; ONS-M21 antibody; light variable region; chimeric protein;
KW   framework region; FR 4; medulloblastoma; brain tumour; treatment;
KW   diagnosis.
XX
OS   Homo sapiens.
XX
PN   WO9514041-A1.
XX
PD   26-MAY-1995.
XX
PF   19-OCT-1994;   94WO-JP001763.
XX
PR   19-NOV-1993;   93JP-00291078.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Ohtomo T,  Sato K,  Tsuchiya M;
XX
DR   WPI; 1995-200347/26.
XX
PT   Reconstituted antibody against human medullo:blastoma cells - contains
PT   high proportion of human antibody origin and has low antigenicity.
XX
PS   Claim 9; Page 101; 120pp; Japanese.
XX
CC   AAR85153-R85156 are human antibody ONS-M21 light variable region
CC   framework regions (FRs). They were used in the construction of a
CC   human/murine chimeric antibody, reactive with human medullo- blastoma (a
CC   brain tumour) cells. The chimeric antibody can be used in the diagnosis
CC   and treatment of this disease
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.021;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 3
AAB11827
ID   AAB11827 standard; peptide; 10 AA.
XX
AC   AAB11827;
XX
DT   16-NOV-2000  (first entry)
XX
DE   Human Ig light chain-like protein polymorphic peptide, SEQ ID NO:1271.
XX
KW   Human; polymorphic peptide; SNP; single nucleotide polymorphism;
KW   detection; identification; gene therapy; antibody.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 7. .10
FT                   /note= "This sequence is replaced by SGDQ in a
FT                   polymorphic variant"
XX
PN   WO200029623-A2.
XX
PD   25-MAY-2000.
XX
PF   17-NOV-1999;   99WO-US027293.
XX
PR   17-NOV-1998;   98US-0109024P.
PR   16-NOV-1999;   99US-00443199.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Shimkets RA,  Leach MD;
XX
DR   WPI; 2000-387826/33.
DR   N-PSDB; AAA77508.
XX
PT   Human nucleic acids containing single nucleotide polymorphisms, useful
PT   for treating a subject suffering, or at risk from a pathology due to the
PT   presence of a sequence polymorphism.
XX
PS   Disclosure; Page 543; 543pp; English.
XX
CC   Sequences AAB11749-B11828 represent 80 polymorphic peptide sequences
CC   encoded by human nucleic acid sequences (sequences 1113 to 1192; AAA77430
CC   - AAA77509) which contain single nucleotide polymorphisms (SNPs).
CC   Sequences 1193 to 1208 (AAB11749-B11764) are consecutive pairs of
CC   peptides exhibiting conservative amino acid changes, while sequences 1209
CC   to 1266 (AAB11765- AAB11822) exhibit non-conservative changes. Sequences
CC   1267 to 1272 (AAB11823- AAB11828) result from frameshift mutations. The
CC   invention also relates to antibodies raised against the peptides, to a
CC   method of detecting polymorphic proteins/ peptides using the antibodies,
CC   and to human nucleic acids which contain silent SNPs (AAA76318-A77429).
CC   It also encompasses a method of detecting a polymorphic site in a nucleic
CC   acid and a method of determining the relatedness of two nucleic acids.
CC   The nucleic acids containing SNPs, and antibodies raised against the
CC   peptides are useful for treatment of an individual having, suspected of
CC   having, or at risk of developing a pathological condition due to the
CC   presence of a sequence polymorphism
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.021;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 4
AAU70397
ID   AAU70397 standard; peptide; 10 AA.
XX
AC   AAU70397;
XX
DT   14-FEB-2002  (first entry)
XX
DE   Human light chain immunoglobulin framework region 4 #1.
XX
KW   Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW   complementarity determining region; framework region; IgBP;
KW   transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
KW   IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
XX
OS   Homo sapiens.
XX
```

PN WO200183806-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014349.
XX
PR 02-MAY-2000; 2000US-00563222.
XX
PA (EPIC-) EPICYTE PHARM INC.
XX
PI Hiatt AC, Hein MB;
XX
DR WPI; 2002-055482/07.
XX
PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
PS Disclosure; Fig 1A; 129pp; English.
XX
CC The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IgBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 1 FGQGTKVEIK 10

RESULT 5
AAU70401
ID AAU70401 standard; peptide; 10 AA.
XX
AC AAU70401;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human light chain immunoglobulin framework region 4 #2.
XX
KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IgBP;
KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
XX
OS Homo sapiens.
XX
PN WO200183806-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014349.
XX
PR 02-MAY-2000; 2000US-00563222.
XX
PA (EPIC-) EPICYTE PHARM INC.
XX
PI Hiatt AC, Hein MB;
XX
DR WPI; 2002-055482/07.
XX
PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
PS Disclosure; Fig 1A; 129pp; English.
XX
CC The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IgBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 1 FGQGTKVEIK 10

RESULT 6
AAU70409
ID AAU70409 standard; peptide; 10 AA.
XX
AC AAU70409;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human light chain immunoglobulin framework region 4 #4.
XX
KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IgBP;
KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
XX
OS Homo sapiens.
XX
PN WO200183806-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014349.
XX
PR 02-MAY-2000; 2000US-00563222.
XX
PA (EPIC-) EPICYTE PHARM INC.
XX
PI Hiatt AC, Hein MB;
XX
DR WPI; 2002-055482/07.
XX

PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
PS Disclosure; Fig 1A; 129pp; English.
XX
CC The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IgBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 1 FGQGTKVEIK 10

RESULT 7
AAU70405
ID AAU70405 standard; peptide; 10 AA.
XX
AC AAU70405;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human light chain immunoglobulin framework region 4 #3.
XX
KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IgBP;
KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
XX
OS Homo sapiens.
XX
PN WO200183806-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014349.
XX
PR 02-MAY-2000; 2000US-00563222.
XX
PA (EPIC-) EPICYTE PHARM INC.
XX
PI Hiatt AC, Hein MB;
XX
DR WPI; 2002-055482/07.
XX
PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
PS Disclosure; Fig 1A; 129pp; English.
XX
CC The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IgBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 1 FGQGTKVEIK 10

RESULT 8
ADG75672
ID ADG75672 standard; peptide; 10 AA.
XX
AC ADG75672;
XX
DT 11-MAR-2004 (first entry)
XX
DE Peptide of the human light chain framework region 4 SeqID136.
XX
KW interleukin-9; IL-9; anti-IL-9; antibody; MH9A3; MH9D1; MH9L1;
KW bronchial hyperresponsiveness; asthma; atopic allergy;
KW mucin overproduction; chronic obstructive pulmonary disorder;
KW cystic fibrosis; chronic obstructive pulmonary disorder; antiallergic;
KW antiasthmatic; cytostatic; human.
XX
OS Homo sapiens.
XX
PN WO2003086458-A1.
XX
PD 23-OCT-2003.
XX
PF 11-APR-2003; 2003WO-US011113.
XX
PR 12-APR-2002; 2002US-0371683P.
PR 12-APR-2002; 2002US-0371728P.
XX
PA (MEDI-) MEDIMMUNE INC.
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Reed JL, Dall'acqua W, Van Snick J, Renauld J, Cormont F;
PI Uyttenhove C;
XX
DR WPI; 2003-845267/78.
XX
PT New antibody or antibody fragment that specifically binds to IL-9, useful
PT for preparing a composition for preventing or treating e.g., atopic
PT allergy, asthma, mucin overproduction, chronic obstructive pulmonary
PT disorder or cystic fibrosis.
XX
PS Disclosure; SEQ ID NO 136; 206pp; English.
XX
CC This invention relates to novel humanised and chimeric antibody
CC molecules, and functional fragments thereof, which have specificity for
CC human interleukin-9 (IL-9). Specifically, it refers to recombinant

CC antibodies derived from several mouse anti-IL-9 monoclonal antibodies,
CC namely MH9A3, MH9D1 and MH9L1. The present invention describes using the
CC humanised and chimeric antibody molecules to treat, prevent and/ or
CC ameliorate disorders including bronchial hyperresponsiveness, asthma,
CC atopic allergy, mucin overproduction, chronic obstructive pulmonary
CC disorder, cystic fibrosis, chronic obstructive pulmonary disorder,
CC excessive T cell or neutrophil activity. Accordingly, these IL-9
CC antagonists exhibit antiallergic, antiasthmatic and cytostatic
CC activities. This peptide sequence is a peptide from the human light chain
CC framework region 4, used in an exemplification of the invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 1 FGQGTKVEIK 10

RESULT 9
ADL93541
ID ADL93541 standard; peptide; 10 AA.
XX
AC ADL93541;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human CD44-binding antibody H1 VLC FR4 SEQ ID NO:36.
XX
KW human; CD44; light chain immunoglobulin variable domain;
KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;
KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;
KW dermatological; vasotropic; neuroprotective; antibody therapy;
KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
KW graft versus host response; multiple sclerosis; neoplastic disorder;
KW cancer; antibody.
XX
OS Homo sapiens.
XX
PN WO2004024750-A2.
XX
PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US029318.
XX
PR 13-SEP-2002; 2002US-0410758P.
PR 09-MAY-2003; 2003US-0469123P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Rondon IJ, Edge A, Baribault Kent R;
XX
DR WPI; 2004-270003/25.
XX
PT New protein comprising a light chain (LC) immunoglobulin variable domain
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
PT useful for preparing a composition for treating inflammatory or
PT neoplastic disorders.
XX
PS Disclosure; SEQ ID NO 36; 128pp; English.
XX
CC The invention relates to a novel isolated protein comprising a light
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
CC immunoglobulin variable domain sequence that form an antigen binding site
CC with binding affinity for the human CD44 extracellular domain and where
CC CDR3 of the LC variable domain sequence. A protein of the invention has
CC cytostatic, antiinflammatory, immunosuppressive, antiarthritic,
CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,
CC and may have a use in antibody therapy. The protein is useful for
CC preparing a composition for treating inflammatory disorders, e.g.,
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
CC multiple sclerosis or neoplastic disorder, which is a malignant or
CC metastatic cancer. The present sequence represents a framework (FR)
CC region of a human CD44-binding antibody.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 1 FGQGTKVEIK 10

RESULT 10
ADQ92392
ID ADQ92392 standard; peptide; 10 AA.
XX
AC ADQ92392;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human hu1 FRL4 peptide.
XX
KW Tumour necrosis factor alpha; TNF-alpha; TNF-alpha mediated disease;
KW sepsis; autoimmune disease; rheumatoid arthritis; inflammatory disease;
KW neurodegenerative disease; malignancy; TNF-secreting tumour;
KW alcohol-induced hepatitis; psoriasis; psoriatic arthritis;
KW Wegener's granulomatosis; ankylosing spondylitis; heart failure;
KW reperfusion injury; chronic obstructive pulmonary disease;
KW pulmonary fibrosis; hepatitis C infection; Kawasaki's pathology;
KW Refsum's disease; ataxia; telangiectasia; Alzheimer's disease;
KW Down's syndrome; Parkinson's disease; leukaemia; myelodyspastic syndrome;
KW lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma; Burkitt's syndrome;
KW hypokinetic movement disorder; drug-induced movement disorder;
KW crohn's disease; ulcerative colitis; amyotrophic lateral sclerosis;
KW multiple sclerosis; Grave's disease; diabetes mellitus; atherosclerosis;
KW Shy-drager syndrome; cachexia; infectious disease; antibody therapy;
KW human; light chain variable region; VL; FR; framework region.
XX
OS Homo sapiens.
XX
PN US2004131613-A1.
XX
PD 08-JUL-2004.
XX
PF 08-JAN-2003; 2003US-00338627.
XX
PR 08-JAN-2003; 2003US-00338627.
XX
PA (WATK/) WATKINS J D.
PA (VASS/) VASSEROT A P.
PA (MARQ/) MARQUIS D.
PA (HUSE/) HUSE W D.
XX
PI Watkins JD, Vasserot AP, Marquis D, Huse WD;
XX
DR WPI; 2004-524894/50.
DR N-PSDB; ADQ92396.
XX
PT New composition comprising a tumor necrosis factor alpha (TNF-alpha)
PT binding molecule, useful for treating a TNF-alpha mediated disease such
PT as sepsis, an autoimmune disease, rheumatoid arthritis, and
PT neurodegenerative diseases.
XX
PS Disclosure; SEQ ID NO 60; 60pp; English.
XX
CC The present invention relates to tumour necrosis factor alpha (TNF-alpha)
CC binding polypeptides and their encoding polynucleotides. The invention is
CC useful for treating TNF-alpha mediated disease such as sepsis, an
CC autoimmune disease, rheumatoid arthritis, inflammatory diseases,

CC neurodegenerative diseases, malignant pathologies involving TNF-secreting
CC tumours, alcohol-induced hepatitis, psoriasis, psoriatic arthritis,
CC Wegener's granulomatosis, ankylosing spondylitis, heart failure,
CC reperfusion injury, chronic obstructive pulmonary disease, pulmonary
CC fibrosis, hepatitis C infection, Kawasaki's pathology, Refsum's disease,
CC ataxia, telangiectasia, Alzheimer's disease, Down's syndrome, Parkinson's
CC disease, leukaemias (acute, chronic myelocytic, chronic lymphocytic
CC and/or myelodyspastic syndrome), lymphomas (Hodgkin's, non-Hodgkin's and
CC Burkitt's syndrome), hypokinetic movement disorders, drug-induced
CC movement disorders, crohn's disease, ulcerative colitis, amyotrophic
CC lateral sclerosis, multiple sclerosis, Grave's disease, diabetes
CC mellitus, atherosclerosis, Shy-drager syndrome, cachexia and infectious
CC diseases. The invention is also useful in antibody therapy. The present
CC sequence is human hu1 framework sub-region of light chain variable (VL)
CC region (FRL) peptide. This sequence is used in the invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 1 FGQGTKVEIK 10

RESULT 11
ADQ80581
ID ADQ80581 standard; peptide; 10 AA.
XX
AC ADQ80581;
XX
DT 23-SEP-2004 (first entry)
XX
DE Human light chain framework region FR4.
XX
KW TNF-alpha binding; complementarity determining region; CDR; TNF-alpha;
KW immunoassay; CDRL-3; CDRH-3; sepsis; autoimmune disease;
KW rheumatoid arthritis; allergy; multiple sclerosis;
KW systemic lupus erythematosus; scleroderma; diabetes mellitus; cachexia;
KW parasitic disease; infectious disease; sarcoidosis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW disseminated intravascular coagulation; Parkinson's disease;
KW Alzheimer's disease; Down's syndrome; psoriasis; ankylosing spondylitis;
KW Wegener's granulomatosis; idiopathic pulmonary fibrosis; asthma;
KW graft-versus-host disease; leukemia; human.
XX
OS Homo sapiens.
XX
PN US2004131612-A1.
XX
PD 08-JUL-2004.
XX
PF 08-JAN-2003; 2003US-00338552.
XX
PR 08-JAN-2003; 2003US-00338552.
XX
PA (WATK/) WATKINS J D.
PA (VASS/) VASSEROT A P.
PA (MARQ/) MARQUIS D.
PA (HUSE/) HUSE W D.
XX
PI Watkins JD, Vasserot AP, Marquis D, Huse WD;
XX
DR WPI; 2004-516978/49.
DR N-PSDB; ADQ80585.
XX
PT Composition useful for treating diseases such as leukemia, asthma,
PT rheumatoid arthritis, Alzheimer's disease, psoriasis or multiple
PT sclerosis, comprises TNF-alpha binding molecule.
XX
PS Disclosure; SEQ ID NO 60; 60pp; English.
XX
CC The invention relates to a composition which comprises a TNF-alpha
CC binding molecule having sequence of complementarity determining region
CC (CDR) in light chain variable region (CDRL)-3 and sequence of CDR in
CC heavy chain variable region (CDRH)-3. The composition is useful in the
CC treatment of TNF-alpha mediated diseases. TNF-alpha binding molecule is
CC useful for treating sepsis, autoimmune disease, rheumatoid arthritis,
CC allergy, multiple sclerosis, systemic lupus erythematosus, scleroderma,
CC diabetes mellitus, cachexia, acute and chronic parasitic and/or
CC infectious diseases, sarcoidosis, inflammatory bowel disease, ulcerative
CC colitis, Crohn's disease, disseminated intravascular coagulation,
CC Parkinson's disease, Alzheimer's disease, Down's syndrome, psoriasis,
CC ankylosing spondylitis, Wegener's granulomatosis, idiopathic pulmonary
CC fibrosis, asthma, graft-versus-host disease, or leukemia. TNF-alpha
CC binding molecule is useful in diagnostic methods for detecting TNF-alpha
CC in patients known to be or suspected of having TNF-alpha-mediated
CC disease. TNF-alpha binding molecule is useful in immunoassays for
CC detecting or quantifying TNF-alpha in a sample. The present sequence
CC represents the amino acid sequence of a human light chain framework
CC region.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 1 FGQGTKVEIK 10

RESULT 12
AEA21490
ID AEA21490 standard; peptide; 10 AA.
XX
AC AEA21490;
XX
DT 28-JUL-2005 (first entry)
XX
DE Human anti-SLPI antibody-related peptide SeqID54.
XX
KW antibody; cytostatic; immunotherapy; cancer.
XX
OS Homo sapiens.
XX
PN WO2005047328-A2.
XX
PD 26-MAY-2005.
XX
PF 08-NOV-2004; 2004WO-US038634.
XX
PR 07-NOV-2003; 2003US-0518275P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Gulshan A, Chui D, Larochelle WJ, Gallo ML, Zhong H;
XX
DR WPI; 2005-367001/37.
XX
PT New isolated human antibody that specifically binds to secretory
PT leukocyte protease inhibitor (SLPI), useful for treating and preventing
PT cancer.
XX
PS Example 8; SEQ ID NO 54; 97pp; English.
XX
CC This invention relates to a novel isolated human antibody that
CC specifically binds to secretory leukocyte protease inhibitor (SLPI). The
CC invention may be useful for the development of compounds with a
CC cytostatic activity or for immunotherapy. The antibody, composition and
CC methods are useful for treating and preventing cancer. The antibodies are
CC useful for detecting the presence of SLPI in biological samples. The
CC present sequence is that of a peptide which was used during the

```
CC   development of the novel antibody of the invention.
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 51;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.021;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 13
AEA21454
ID   AEA21454 standard; peptide; 10 AA.
XX
AC   AEA21454;
XX
DT   28-JUL-2005  (first entry)
XX
DE   Human anti-SLPI antibody-related peptide SeqID18.
XX
KW   antibody; cytostatic; immunotherapy; cancer.
XX
OS   Homo sapiens.
XX
PN   WO2005047328-A2.
XX
PD   26-MAY-2005.
XX
PF   08-NOV-2004; 2004WO-US038634.
XX
PR   07-NOV-2003; 2003US-0518275P.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Gulshan A,  Chui D,  Larochelle WJ,  Gallo ML,  Zhong H;
XX
DR   WPI; 2005-367001/37.
XX
PT   New isolated human antibody that specifically binds to secretory
PT   leukocyte protease inhibitor (SLPI), useful for treating and preventing
PT   cancer.
XX
PS   Example 8; SEQ ID NO 18; 97pp; English.
XX
CC   This invention relates to a novel isolated human antibody that
CC   specifically binds to secretory leukocyte protease inhibitor (SLPI). The
CC   invention may be useful for the development of compounds with a
CC   cytostatic activity or for immunotherapy. The antibody, composition and
CC   methods are useful for treating and preventing cancer. The antibodies are
CC   useful for detecting the presence of SLPI in biological samples. The
CC   present sequence is that of a peptide which was used during the
CC   development of the novel antibody of the invention.
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 51;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.021;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 14
AEA21472
ID   AEA21472 standard; peptide; 10 AA.
XX
AC   AEA21472;
XX
DT   28-JUL-2005  (first entry)
XX
DE   Human anti-SLPI antibody-related peptide SeqID36.
XX
KW   antibody; cytostatic; immunotherapy; cancer.
XX
OS   Homo sapiens.
XX
PN   WO2005047328-A2.
XX
PD   26-MAY-2005.
XX
PF   08-NOV-2004; 2004WO-US038634.
XX
PR   07-NOV-2003; 2003US-0518275P.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Gulshan A,  Chui D,  Larochelle WJ,  Gallo ML,  Zhong H;
XX
DR   WPI; 2005-367001/37.
XX
PT   New isolated human antibody that specifically binds to secretory
PT   leukocyte protease inhibitor (SLPI), useful for treating and preventing
PT   cancer.
XX
PS   Example 8; SEQ ID NO 36; 97pp; English.
XX
CC   This invention relates to a novel isolated human antibody that
CC   specifically binds to secretory leukocyte protease inhibitor (SLPI). The
CC   invention may be useful for the development of compounds with a
CC   cytostatic activity or for immunotherapy. The antibody, composition and
CC   methods are useful for treating and preventing cancer. The antibodies are
CC   useful for detecting the presence of SLPI in biological samples. The
CC   present sequence is that of a peptide which was used during the
CC   development of the novel antibody of the invention.
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 51;  DB 9;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.021;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 15
AEA45326
ID   AEA45326 standard; peptide; 10 AA.
XX
AC   AEA45326;
XX
DT   11-AUG-2005  (first entry)
XX
DE   Apolipoprotein E C-terminal domain related sequence, SEQ ID 524.
XX
KW   Neuroprotective; Nootropic; Antidiabetic; Endocrine-Gen.; Nephrotropic;
KW   Antiparkinsonian; Anticonvulsant; Respiratory-Gen; Apolipoprotein E;
KW   Alzheimers disease; amyloidosis; Parkinsons disease; Huntingtons chorea;
KW   Kuru; Dementia; non-insulin dependent diabetes; Down syndrome;
KW   Spongiform encephalopathy; Creutzfeldt Jakob disease;
KW   motor neurone disease; chronic obstructive pulmonary disease.
XX
OS   Homo sapiens.
XX
PN   GB2408508-A.
XX
PD   01-JUN-2005.
XX
PF   26-NOV-2004; 2004GB-00026043.
XX
```

PR 28-NOV-2003; 2003US-0525174P.
XX
PA (ASTR) ASTRAZENECA AB.
PA (DYAX-) DYAX CORP.
XX
PI Nordstedt C, Goldschmidt T, Henderikx M, Hoet R, Hoogenboom H;
PI Hufton S, Andersson CV, Lindquist J, Sunnemark D, Leonov S;
XX
DR WPI; 2005-408785/42.
XX
PT New human antibody or antibody fragment which binds to a sequence of the
PT C-terminal domain of Apolipoprotein E (ApoE-CTD), useful for
PT manufacturing a medicament for treating or preventing an amyloid disorder
PT e.g. Alzheimers disease.
XX
PS Example 8; SEQ ID NO 524; 392pp; English.
XX
CC The present invention relates to a human antibody or antibody fragment,
CC which binds to the C-terminal domain of Apolipoprotein E (ApoE-CTD;
CC AEA44803) and also to human plaques. The antibody or its fragment is
CC useful for manufacturing a medicament for treating or preventing an
CC amyloid disorder such as Alzheimers disease, primary systemic
CC amyloidosis, secondary systemic amyloidosis, senile systemic amyloidosis,
CC familial amyloid polyneuropathy I, familial amyloid polyneuropathy III,
CC familial non-neuropathic amyloidosis, hereditary cerebral amyloid
CC angiopathy, Familial British Dementia, Hemodialysis-related amyloidosis,
CC Familial amyloidosis (Finnish type), Familial subepithelial corneal
CC amyloid, type II diabetes, Hereditary renal amyloidosis, Pituitary-gland
CC amyloidosis, injection localized amyloidosis, Medullary carcinoma of the
CC thyroid, Atrial amyloidosis, Familial Danish dementia (FDD), Downs
CC syndrome, Spongiform encephalopathies, Sporadic Creutzfeldt-Jakob
CC disease, Gerstmann-Straussler-Scheinker Disease (GSS), Kuru, Parkinsons
CC disease, Huntingtons disease, Familial amyotrophic lateral sclerosis, and
CC chronic obstructive pulmonary disease. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10
```

Search completed: March 25, 2006, 09:02:19
Job time : 38.9836 secs

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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:02:50 ; Search time 5.75916 Seconds
(without alignments)
167.067 Million cell updates/sec

Title: US-10-755-382-29
Perfect score: 51
Sequence: 1 FGQGTKVEIK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	13	2	S23638	Ig kappa chain J s
2	51	100.0	91	2	S37520	Ig kappa chain V r
3	51	100.0	91	2	S37515	Ig kappa chain V r
4	51	100.0	91	2	S37527	Ig kappa chain V r
5	51	100.0	92	2	S37514	Ig kappa chain V r
6	51	100.0	92	2	S37533	Ig kappa chain V r
7	51	100.0	92	2	S37519	Ig kappa chain V r
8	51	100.0	93	2	S37526	Ig kappa chain V r
9	51	100.0	93	2	S37501	Ig kappa chain V r
10	51	100.0	107	2	S34005	Ig kappa chain V r
11	51	100.0	107	2	S36268	Ig lambda chain V
12	51	100.0	107	2	S36275	Ig lambda chain V
13	51	100.0	107	2	PH0965	Ig kappa chain V r
14	51	100.0	108	1	K1HUAU	Ig kappa chain V-I
15	51	100.0	108	1	K1HUGL	Ig kappa chain V-I
16	51	100.0	108	2	S44122	Ig kappa chain V r
17	51	100.0	108	2	I39154	Ig kappa chain (BR
18	51	100.0	109	1	K3HUGO	Ig kappa chain V-I
19	51	100.0	109	1	K3HUWL	Ig kappa chain V-I
20	51	100.0	109	2	C30601	Ig kappa chain V-I
21	51	100.0	109	2	B30601	Ig kappa chain V-I
22	51	100.0	109	2	PH0963	Ig kappa chain V r
23	51	100.0	109	2	D30601	Ig kappa chain V-I
24	51	100.0	109	2	F30607	Ig kappa chain V-I
25	51	100.0	110	2	E30607	Ig kappa chain V-I
26	51	100.0	110	2	S44120	Ig kappa chain V-J
27	51	100.0	110	2	S20635	Ig kappa chain V r
28	51	100.0	111	2	S23628	Ig kappa chain V r
29	51	100.0	112	2	S58207	Ig light chain V r
30	51	100.0	113	2	S34002	Ig kappa chain V r
31	51	100.0	117	1	K2HUGM	Ig kappa chain pre
32	51	100.0	120	2	S51147	antibody light cha
33	51	100.0	122	2	S40351	Ig kappa chain V-J
34	51	100.0	122	2	S40314	Ig kappa chain - h
35	51	100.0	122	2	S40370	Ig kappa chain - h
36	51	100.0	123	2	S40331	Ig kappa chain - h
37	51	100.0	123	2	S40313	Ig kappa chain V-J
38	51	100.0	124	2	S40336	Ig kappa chain V-J
39	51	100.0	125	2	S40333	Ig kappa chain V-J
40	51	100.0	126	2	S40339	Ig kappa chain - h
41	51	100.0	127	2	S40367	Ig kappa chain V-J
42	51	100.0	128	2	S46372	IG light chain var
43	51	100.0	128	2	S20636	Ig kappa chain V r
44	51	100.0	128	2	A56701	Ig kappa chain V r
45	51	100.0	128	2	S40379	Ig kappa chain V-J

ALIGNMENTS

RESULT 1
S23638
Ig kappa chain J segment (J-kappa-1) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S23638
R;Huber, C.; Klobeck, H.G.; Zachau, H.G.
Eur. J. Immunol. 22, 1561-1565, 1992
A;Title: Ongoing V(kappa)-J(kappa) recombination after formation of a productive V(kappa
A;Reference number: S23637; MUID:92289816; PMID:1601042
A;Accession: S23638
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-13 <HUB>
A;Cross-references: UNIPROT:Q8NEK0; UNIPROT:Q9UL80; UNIPROT:Q9UL79; UNIPARC:UPI000017C25
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 51; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          3 FGQGTKVEIK 12
```

RESULT 2
S37520
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37520
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37520
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <KLE>
A;Cross-references: UNIPARC:UPI000011657C; EMBL:Z26612; NID:g405682; PIDN:CAA81365.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 51; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 FGQGTKVEIK 10
              ||||||||||
Db         81 FGQGTKVEIK 90
```

RESULT 3
S37515
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37515
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37515
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <KLE>
A;Cross-references: UNIPARC:UPI000011656D; EMBL:Z26596; NID:g405672; PIDN:CAA81350.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 51; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 81 FGQGTKVEIK 90

RESULT 4
S37527
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37527
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37527
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-91 <KLE>
A;Cross-references: UNIPARC:UPI0000116581; EMBL:Z26617; NID:g405696; PIDN:CAA81370.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 51; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 81 FGQGTKVEIK 90

RESULT 5
S37514
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37514
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37514
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: UNIPARC:UPI000011656E; EMBL:Z26597; NID:g405670; PIDN:CAA81351.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 51; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 82 FGQGTKVEIK 91

RESULT 6
S37533
Ig kappa chain V region (V-kappa 4) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37533
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37533
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: UNIPARC:UPI000011658B; EMBL:Z26627; NID:g405708; PIDN:CAA81380.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 51; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 82 FGQGTKVEIK 91

RESULT 7
S37519
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37519
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral bloo
A;Reference number: S37501
A;Accession: S37519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-92 <KLE>
A;Cross-references: UNIPARC:UPI000011657D; EMBL:Z26613; NID:g405680; PIDN:CAA81366.1; P
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 51; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 82 FGQGTKVEIK 91

RESULT 8
S37526
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C;Accession: S37526
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blo

A;Reference number: S37501
A;Accession: S37526
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-93 <KLE>
A;Cross-references: UNIPARC:UPI0000116582; EMBL:Z26618; NID:g405694; PIDN:CAA81371.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 51; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 83 FGQGTKVEIK 92

RESULT 9
S37501
Ig kappa chain V region (V-kappa 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37501
R;Klein, U.; Kueppers, R.; Rajewsky, K.
submitted to the EMBL Data Library, September 1993
A;Description: Human IgM(+)IgD(+) cells, the major B cell subset in the peripheral blood
A;Reference number: S37501
A;Accession: S37501
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-93 <KLE>
A;Cross-references: UNIPARC:UPI000011657B; EMBL:Z26611; NID:g405643; PIDN:CAA81364.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 51; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 83 FGQGTKVEIK 92

RESULT 10
S34005
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S34005; S30524
R;Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotidic sequence analysis of the variable domains of four human monoclonal
A;Reference number: S34001; MUID:93209281; PMID:7681398
A;Accession: S34005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <MAR>
A;Cross-references: UNIPARC:UPI0000176D33; EMBL:Z18330
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 51; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 98 FGQGTKVEIK 107

RESULT 11
S36268
Ig lambda chain V region (clone alpha-THY-33) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36268
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36268
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
A;Cross-references: UNIPARC:UPI0000176CD6; EMBL:Z18837
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 51; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 98 FGQGTKVEIK 107

RESULT 12
S36275
Ig lambda chain V region (clone alpha-FOG1-A4) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36275
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36275
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
A;Cross-references: UNIPARC:UPI0000118DED; EMBL:Z18827; NID:g33416; PIDN:CAA79279.1; PIE
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 51; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 97 FGQGTKVEIK 106

RESULT 13
PH0965
Ig kappa chain V region (G6+ CLL-BRA) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: PH0965
R;Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
J. Exp. Med. 175, 983-991, 1992
A;Title: Evidence for somatic selection of natural autoantibodies.
A;Reference number: PH0952; MUID:92202880; PMID:1552291
A;Accession: PH0965
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-107 <MAR>
A;Cross-references: UNIPROT:Q9UL78; UNIPARC:UPI0000176A2B
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

F;1-21/Region: framework 1
F;14-89/Domain: immunoglobulin homology <IMM>
F;22-32/Region: complementarity-determining 1
F;33-48/Region: framework 2
F;49-54/Region: complementarity-determining 2
F;55-87/Region: framework 3
F;88-95/Region: complementarity-determining 3

Query Match 100.0%; Score 51; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 97 FGQGTKVEIK 106

RESULT 14
K1HUAU
Ig kappa chain V-I region (Au) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: A91653; A01862; S02573
R;Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub
A;Reference number: A91653; MUID:72189444; PMID:5028201
A;Accession: A91653
A;Molecule type: protein
A;Residues: 1-108 <SCH>
A;Cross-references: UNIPROT:P01594; UNIPARC:UPI000012E13E
A;Note: the C region of this chain has the Inv (3) marker
R;Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Stei
Biophys. Struct. Mech. 1, 139-146, 1975
A;Title: The structure determination of the variable portion of the Bence-Jones protein
A;Reference number: A90729; MUID:77022433; PMID:1234024
A;Contents: annotation; X-ray crystallography
A;Note: the structure of the V region was determined by molecular replacement methods us
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 100.0%; Score 51; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 98 FGQGTKVEIK 107

RESULT 15
K1HUGL
Ig kappa chain V-I region (Gal) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01867
R;Laure, C.J.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973
A;Title: The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal), I
A;Reference number: A01867; MUID:75059122; PMID:4215718
A;Accession: A01867
A;Molecule type: protein
A;Residues: 1-108 <LAU>
A;Cross-references: UNIPROT:P01599; UNIPARC:UPI000012E142
A;Note: the C region of this chain has the Inv (3) marker
C;Comment: This chain was isolated from a Waldenstrom's macroglobulin.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 100.0%; Score 51; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 98 FGQGTKVEIK 107

Search completed: March 25, 2006, 09:15:45
Job time : 6.75916 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:40 ; Search time 36.0209 Seconds
(without alignments)
195.866 Million cell updates/sec

Title: US-10-755-382-29
Perfect score: 51
Sequence: 1 FGQGTKVEIK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	108	1	KV1B_HUMAN	P01594 homo sapien
2	51	100.0	108	1	KV1G_HUMAN	P01599 homo sapien
3	51	100.0	108	2	Q9UL79_HUMAN	Q9ul79 homo sapien
4	51	100.0	109	1	KV3E_HUMAN	P01623 homo sapien
5	51	100.0	109	1	KV3G_HUMAN	P04206 homo sapien
6	51	100.0	114	2	Q9UL80_HUMAN	Q9ul80 homo sapien
7	51	100.0	117	1	KV2E_HUMAN	P06309 homo sapien
8	51	100.0	129	1	KV3L_HUMAN	P18135 homo sapien
9	51	100.0	129	1	KV3M_HUMAN	P18136 homo sapien
10	51	100.0	133	1	KV2F_HUMAN	P06310 homo sapien
11	51	100.0	134	1	KV4C_HUMAN	P06314 homo sapien
12	51	100.0	234	2	Q7Z473_HUMAN	Q7z473 homo sapien
13	51	100.0	236	2	Q6PIH4_HUMAN	Q6pih4 homo sapien
14	51	100.0	236	2	Q6GMW1_HUMAN	Q6gmw1 homo sapien
15	51	100.0	236	2	Q502W4_HUMAN	Q502w4 homo sapien
16	51	100.0	239	2	Q8NEK0_HUMAN	Q8nek0 homo sapien
17	50	98.0	108	1	KV1F_HUMAN	P01598 homo sapien
18	50	98.0	108	1	KV1M_HUMAN	P01605 homo sapien
19	50	98.0	108	1	KV1R_HUMAN	P01610 homo sapien
20	49	96.1	109	1	KV3D_HUMAN	P01622 homo sapien
21	48	94.1	108	1	KV1A_HUMAN	P01593 homo sapien
22	48	94.1	108	1	KV1C_HUMAN	P01595 homo sapien
23	48	94.1	108	1	KV1H_HUMAN	P01600 homo sapien
24	48	94.1	108	1	KV1V_HUMAN	P04430 homo sapien
25	48	94.1	108	2	Q9UL77_HUMAN	Q9ul77 homo sapien
26	48	94.1	109	1	KV3F_HUMAN	P01624 homo sapien
27	48	94.1	114	1	KV4A_HUMAN	P01625 homo sapien
28	48	94.1	128	1	KV3K_HUMAN	P06311 homo sapien
29	48	94.1	129	1	KV3H_HUMAN	P04207 homo sapien
30	48	94.1	235	2	Q6GMW0_HUMAN	Q6gmw0 homo sapien
31	48	94.1	236	2	Q7Z3Y4_HUMAN	Q7z3y4 homo sapien
32	48	94.1	239	2	Q6P491_HUMAN	Q6p491 homo sapien
33	48	94.1	239	2	Q8TCD0_HUMAN	Q8tcd0 homo sapien
34	48	94.1	240	2	Q6PIH6_HUMAN	Q6pih6 homo sapien
35	47	92.2	109	1	KV3B_HUMAN	P01620 homo sapien
36	47	92.2	113	1	KV2B_HUMAN	P01615 homo sapien
37	46	90.2	108	1	KV1K_HUMAN	P01603 homo sapien
38	45	88.2	108	1	KV1L_HUMAN	P01604 homo sapien
39	45	88.2	113	1	KV2D_HUMAN	P01617 homo sapien
40	45	88.2	115	1	KV2A_HUMAN	P01614 homo sapien
41	45	88.2	129	1	KV1W_HUMAN	P04431 homo sapien
42	45	88.2	189	2	Q569I7_HUMAN	Q569i7 homo sapien
43	44	86.3	107	2	Q96SA9_HUMAN	Q96sa9 homo sapien
44	44	86.3	108	1	KV3A_HUMAN	P01619 homo sapien
45	44	86.3	109	2	Q9UL85_HUMAN	Q9ul85 homo sapien

ALIGNMENTS

RESULT 1
KV1B_HUMAN
ID KV1B_HUMAN STANDARD; PRT; 108 AA.
AC P01594;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region AU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=72189444; PubMed=5028201;
RA Schiechl H., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT protein Au).";
RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=77022433; PubMed=1234024;
RA Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA Schwager P., Steigemann W., Schramm H.J.;
RT "The structure determination of the variable portion of the Bence-
RT Jones protein Au.";
RL Biophys. Struct. Mech. 1:139-146(1975).
CC -!- MISCELLANEOUS: The structure of the V region was determined by
CC molecular replacement methods using the known structure of the V
CC region of the kappa chain REI.
CC -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC --
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC --
DR PIR; A91653; K1HUAU.
DR PDB; 1JV5; X-ray; A=1-107.
DR Ensembl; ENSG00000173782; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin domain; Immunoglobulin V region.
FT REGION 1 23 Framework-1.

```
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
FT   STRAND        4      5
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       44     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       85     90
FT   STRAND       97     98
FT   STRAND      102    106
SQ   SEQUENCE   108 AA;  11939 MW;  E8011187EE6F6FB9 CRC64;

  Query Match             100.0%;  Score 51;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db         98 FGQGTKVEIK 107


RESULT 2
KV1G_HUMAN
ID   KV1G_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01599;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Gal.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=75059122; PubMed=4215718;
RA   Laure C.J., Watanabe S., Hilschmann N.;
RT   "The primary structure of a monoclonal IgM-immunoglobulin
RT   (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT   kappa-type, subgroup I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC       macroglobulin.
CC   ---------------------------------------------------------------------
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01867; K1HUGL.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01599; 1-107.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11814 MW;  C1AD3CB0F600FF73 CRC64;

  Query Match             100.0%;  Score 51;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db         98 FGQGTKVEIK 107


RESULT 3
Q9UL79_HUMAN
ID   Q9UL79_HUMAN PRELIMINARY;      PRT;   108 AA.
AC   Q9UL79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1601042;
RA   Huber C., Klobeck H.G., Zachau H.G.;
RT   "Ongoing V kappa-J kappa recombination after formation of a productive
RT   V kappa-J kappa coding joint.";
RL   Eur. J. Immunol. 22:1561-1565(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=8436174;
RA   Wagner S.D., Luzzatto L.;
RT   "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT   distributed over a large portion of the V kappa locus and do not show
RT   somatic mutation.";
RL   Eur. J. Immunol. 23:391-397(1993).
DR   EMBL; AF035035; AAD56271.1; -; mRNA.
DR   PIR; S23638; S23638.
DR   PIR; S30521; S30521.
DR   PIR; S34090; S34090.
DR   HSSP; P01607; 1BWW.
DR   SMR; Q9UL79; 1-108.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
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DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11787 MW;  DB5845F19724FB4E CRC64;

  Query Match             100.0%;  Score 51;  DB 2;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db         98 FGQGTKVEIK 107


RESULT 4
KV3E_HUMAN
ID   KV3E_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01623;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-III region WOL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=82046598; PubMed=6794615;
RA   Andrews D.W., Capra J.D.;
RT   "Amino acid sequence of the variable regions of light chains from two
RT   idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT   group.";
RL   Biochemistry 20:5816-5822(1981).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC       globulin activity.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01896; K3HUWL.
DR   HSSP; P01625; 1LVE.
DR   SMR; P01623; 1-109.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11746 MW;  566C115E6B9CBEEE CRC64;

  Query Match             100.0%;  Score 51;  DB 1;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db         99 FGQGTKVEIK 108


RESULT 5
KV3G_HUMAN
ID   KV3G_HUMAN     STANDARD;      PRT;   109 AA.
AC   P04206;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-III region GOL (Rheumatoid factor).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=86230578; PubMed=3086710; DOI=10.1016/0161-5890(86)90049-0;
RA   Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RT   "Amino acid sequence of a light chain variable region of a human
RT   rheumatoid factor of the Wa idiotypic group, in part predicted by its
RT   reactivity with antipeptide antibodies.";
RL   Mol. Immunol. 23:239-244(1986).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01893; K3HUGO.
DR   HSSP; P01625; 1EK3.
DR   SMR; P04206; 1-109.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11830 MW;  9349A5B1D93588B6 CRC64;

  Query Match             100.0%;  Score 51;  DB 1;  Length 109;
  Best Local Similarity   100.0%;  Pred. No. 0.025;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db         99 FGQGTKVEIK 108


RESULT 6
Q9UL80_HUMAN
ID   Q9UL80_HUMAN PRELIMINARY;      PRT;   114 AA.
AC   Q9UL80;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
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RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1322670;
RA   Stuber F., Lee S.K., Bridges S.L. Jr, Koopman W.J., Schroeder H.W. Jr,
RA   Gaskin F., Fu S.M.;
RT   "A rheumatoid factor from a normal individual encoded by VH2 and V
RT   kappa II gene segments.";
RL   Arthritis Rheum. 35:900-904(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=8436174;
RA   Wagner S.D., Luzzatto L.;
RT   "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT   distributed over a large portion of the V kappa locus and do not show
RT   somatic mutation.";
RL   Eur. J. Immunol. 23:391-397(1993).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1601042;
RA   Huber C., Klobeck H.G., Zachau H.G.;
RT   "Ongoing V kappa-J kappa recombination after formation of a productive
RT   V kappa-J kappa coding joint.";
RL   Eur. J. Immunol. 22:1561-1565(1992).
DR   EMBL; AF035034; AAD56270.1; -; mRNA.
DR   PIR; B49002; B49002.
DR   PIR; S23638; S23638.
DR   PIR; S34094; S34094.
DR   PIR; S34095; S34095.
DR   HSSP; P01625; 1LVE.
DR   SMR; Q9UL80; 1-114.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     114    114
SQ   SEQUENCE   114 AA;  12775 MW;  070E31E210D1CB01 CRC64;

  Query Match             100.0%;  Score 51;  DB 2;  Length 114;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db        104 FGQGTKVEIK 113


RESULT 7
KV2E_HUMAN
ID   KV2E_HUMAN     STANDARD;      PRT;   117 AA.
AC   P06309;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-II region GM607 precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84191506; PubMed=6325927;
RA   Klobeck H.G., Solomon A., Zachau H.G.;
RT   "Contribution of human V kappa II germ-line genes to light-chain
RT   diversity.";
RL   Nature 309:73-76(1984).
CC   ----------------------------------------------------------------------
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; Z00009; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR   PIR; A01889; K2HUGM.
DR   HSSP; Q99M37; 1I9I.
DR   SMR; P06309; 5-117.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL       <1      4
FT   CHAIN         5    117       Ig kappa chain V-II region GM607.
FT   REGION        5     27       Framework-1.
FT   REGION       28     43       Complementarity-determining-1.
FT   REGION       44     58       Framework-2.
FT   REGION       59     65       Complementarity-determining-2.
FT   REGION       66     97       Framework-3.
FT   REGION       98    106       Complementarity-determining-3.
FT   REGION      107    116       Framework-4.
FT   DISULFID     27     97       By similarity.
FT   NON_TER       1      1
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12664 MW;  92C57DC719E558B1 CRC64;

  Query Match             100.0%;  Score 51;  DB 1;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db        107 FGQGTKVEIK 116


RESULT 8
KV3L_HUMAN
ID   KV3L_HUMAN     STANDARD;      PRT;   129 AA.
AC   P18135;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-III region HAH precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   J. Exp. Med. 167:840-852(1988).
CC   -!- DISEASE: The protein is one of the surface immunoglobulin M
CC       autoantibodies expressed in patients with chronic lymphocytic
CC       leukemia.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; PL0022; K3HUHA.
DR   HSSP; P01625; 1EEQ.
DR   SMR; P18135; 21-129.
DR   Ensembl; ENSG00000169769; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
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DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    129       Ig kappa chain V-III region HAH.
FT   REGION      21     43       Framework-1.
FT   REGION      44     55       Complementarity-determining-1.
FT   REGION      56     70       Framework-2.
FT   REGION      71     77       Complementarity-determining-2.
FT   REGION      78    109       Framework-3.
FT   REGION     110    118       Complementarity-determining-3.
FT   REGION     119    129       JK1 segment.
FT   DISULFID    43    109       By similarity.
FT   NON_TER    129    129
SQ   SEQUENCE   129 AA;  14073 MW;  D3C55292772774D0 CRC64;

  Query Match             100.0%;  Score 51;  DB 1;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 0.03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db        119 FGQGTKVEIK 128


RESULT 9
KV3M_HUMAN
ID   KV3M_HUMAN     STANDARD;      PRT;   129 AA.
AC   P18136;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-III region HIC precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   J. Exp. Med. 167:840-852(1988).
CC   -!- DISEASE: The protein is one of the surface immunoglobulin M
CC       autoantibodies expressed in patients with chronic lymphocytic
CC       leukemia.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; PL0021; K3HUHI.
DR   HSSP; P01625; 1EEQ.
DR   SMR; P18136; 21-129.
DR   Ensembl; ENSG00000169769; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    129       Ig kappa chain V-III region HIC.
FT   REGION      21     43       Framework-1.
FT   REGION      44     55       Complementarity-determining-1.
FT   REGION      56     70       Framework-2.
FT   REGION      71     77       Complementarity-determining-2.
FT   REGION      78    109       Framework-3.
FT   REGION     110    118       Complementarity-determining-3.
FT   REGION     119    129       JK1 segment.
FT   DISULFID    43    109       By similarity.
FT   NON_TER    129    129
SQ   SEQUENCE   129 AA;  14071 MW;  7395528EA2BB74D6 CRC64;

  Query Match             100.0%;  Score 51;  DB 1;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 0.03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db        119 FGQGTKVEIK 128


RESULT 10
KV2F_HUMAN
ID   KV2F_HUMAN     STANDARD;      PRT;   133 AA.
AC   P06310;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-II region RPMI 6410 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86041852; PubMed=2997711;
RA   Klobeck H.G., Meindl A., Combriato G., Solomon A., Zachau H.G.;
RT   "Human immunoglobulin kappa light chain genes of subgroups II and
RT   III.";
RL   Nucleic Acids Res. 13:6499-6513(1985).
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; Z00020; CAA77315.1; -; Genomic_DNA.
DR   PIR; A01890; K2HURP.
DR   HSSP; Q99M37; 1I9I.
DR   SMR; P06310; 21-133.
DR   Ensembl; ENSG00000173758; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL       1     20
FT   CHAIN       21    133       Ig kappa chain V-II region RPMI 6410.
FT   REGION      21     43       Framework-1.
FT   REGION      44     59       Complementarity-determining-1.
FT   REGION      60     74       Framework-2.
FT   REGION      75     81       Complementarity-determining-2.
FT   REGION      82    113       Framework-3.
FT   REGION     114    122       Complementarity-determining-3.
FT   REGION     123    132       Framework-4.
FT   DISULFID    43    113       By similarity.
FT   NON_TER    133    133
SQ   SEQUENCE   133 AA;  14707 MW;  513CCAF3673009EE CRC64;

  Query Match             100.0%;  Score 51;  DB 1;  Length 133;
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  Best Local Similarity   100.0%;  Pred. No. 0.031;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db        123 FGQGTKVEIK 132


RESULT 11
KV4C_HUMAN
ID   KV4C_HUMAN     STANDARD;      PRT;   134 AA.
AC   P06314;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-APR-1988 (Rel. 07, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-IV region B17 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86041854; PubMed=2997713;
RA   Marsh P., Mills F., Gould H.;
RT   "Detection of a unique human V kappa IV germline gene by a cloned cDNA
RT   probe.";
RL   Nucleic Acids Res. 13:6531-6544(1985).
RN   [2]
RP   SEQUENCE REVISION TO 76.
RA   Marsh P.;
RL   Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X02990; CAA26733.1; -; mRNA.
DR   HSSP; P01625; 1LVE.
DR   SMR; P06314; 21-134.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    134       Ig kappa chain V-IV region B17.
FT   REGION       21     43       Framework-1.
FT   REGION       44     60       Complementarity-determining-1.
FT   REGION       61     75       Framework-2.
FT   REGION       76     82       Complementarity-determining-2.
FT   REGION       83    114       Framework-3.
FT   REGION      115    121       Complementarity-determining-3.
FT   REGION      122    133       Framework-4.
FT   DISULFID     43    114       By similarity.
FT   NON_TER     134    134
SQ   SEQUENCE   134 AA;  14966 MW;  6413A22FD0738832 CRC64;

  Query Match             100.0%;  Score 51;  DB 1;  Length 134;
  Best Local Similarity   100.0%;  Pred. No. 0.032;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db        124 FGQGTKVEIK 133


RESULT 12
Q7Z473_HUMAN
ID   Q7Z473_HUMAN PRELIMINARY;      PRT;   234 AA.
AC   Q7Z473;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGKC protein.
GN   Name=IGKC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RG   NIH MGC Project;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC056256; AAH56256.1; -; mRNA.
DR   HSSP; P01834; 1HEZ.
DR   SMR; Q7Z473; 22-234.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   234 AA;  25674 MW;  1A2C259BAB51BC0F CRC64;

  Query Match             100.0%;  Score 51;  DB 2;  Length 234;
  Best Local Similarity   100.0%;  Pred. No. 0.056;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db        118 FGQGTKVEIK 127


RESULT 13
Q6PIH4_HUMAN
ID   Q6PIH4_HUMAN PRELIMINARY;      PRT;   236 AA.
AC   Q6PIH4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034146; AAH34146.1; -; mRNA.
DR   HSSP; P01607; 1AR2.
DR   SMR; Q6PIH4; 23-236.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25871 MW;  BE01A28CD06EEE26 CRC64;

  Query Match             100.0%;  Score 51;  DB 2;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 0.057;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db        120 FGQGTKVEIK 129


RESULT 14
Q6GMW1_HUMAN
ID   Q6GMW1_HUMAN PRELIMINARY;      PRT;   236 AA.
AC   Q6GMW1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGKC protein.
GN   Name=IGKC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RG   NIH MGC Project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073791; AAH73791.1; -; mRNA.
DR   SMR; Q6GMW1; 24-236.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   236 AA;  25751 MW;  5BFE6A087AFAC437 CRC64;

  Query Match             100.0%;  Score 51;  DB 2;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 0.057;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db        120 FGQGTKVEIK 129


RESULT 15
Q502W4_HUMAN
ID   Q502W4_HUMAN PRELIMINARY;      PRT;   236 AA.
AC   Q502W4;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   IGKC protein.
GN   Name=IGKC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Glandular pool- thyroid;
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RG NIH MGC Project;
RL Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC095489; AAH95489.1; -; mRNA.
DR SMR; Q502W4; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 236 AA; 25936 MW; E2DF79AC18756AA9 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 FGQGTKVEIK 10
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Db        120 FGQGTKVEIK 129
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Search completed: March 25, 2006, 09:13:49
Job time : 37.0209 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:14:16 ; Search time 9.10995 Seconds
(without alignments)
90.753 Million cell updates/sec

Title: US-10-755-382-29
Perfect score: 51
Sequence: 1 FGQGTKVEIK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	10	1	US-07-946-421-10	Sequence 10, Appl
2	51	100.0	10	1	US-08-137-117D-123	Sequence 123, App
3	51	100.0	10	1	US-08-137-117D-142	Sequence 142, App
4	51	100.0	10	1	US-08-436-717-123	Sequence 123, App
5	51	100.0	10	1	US-08-436-717-142	Sequence 142, App
6	51	100.0	10	1	US-08-553-501A-68	Sequence 68, Appl
7	51	100.0	10	1	US-08-553-501A-72	Sequence 72, Appl
8	51	100.0	10	1	US-08-318-157B-29	Sequence 29, Appl
9	51	100.0	10	1	US-08-765-783A-90	Sequence 90, Appl
10	51	100.0	10	2	US-09-205-231-68	Sequence 68, Appl
11	51	100.0	10	2	US-09-205-231-72	Sequence 72, Appl
12	51	100.0	10	2	US-08-646-265A-124	Sequence 124, App
13	51	100.0	10	2	US-09-416-557-90	Sequence 90, Appl
14	51	100.0	10	2	US-09-443-199C-1271	Sequence 1271, Ap
15	51	100.0	10	2	US-09-253-794-29	Sequence 29, Appl
16	51	100.0	10	2	US-09-563-222C-77	Sequence 77, Appl
17	51	100.0	11	1	US-08-470-139-15	Sequence 15, Appl
18	51	100.0	11	2	US-08-569-147-42	Sequence 42, Appl
19	51	100.0	11	2	US-09-347-061-15	Sequence 15, Appl
20	51	100.0	11	2	US-09-313-942-5	Sequence 5, Appli
21	51	100.0	11	2	US-09-855-271-15	Sequence 15, Appl
22	51	100.0	11	2	US-10-282-162-5	Sequence 5, Appli
23	51	100.0	13	2	US-10-194-975-95	Sequence 95, Appl
24	51	100.0	17	2	US-08-783-853A-70	Sequence 70, Appl
25	51	100.0	17	2	US-09-344-050-70	Sequence 70, Appl
26	51	100.0	80	1	US-08-553-501A-85	Sequence 85, Appl
27	51	100.0	80	1	US-08-765-783A-104	Sequence 104, App
28	51	100.0	80	2	US-09-205-231-85	Sequence 85, Appl
29	51	100.0	80	2	US-09-416-557-104	Sequence 104, App
30	51	100.0	80	2	US-09-269-921-130	Sequence 130, App
31	51	100.0	80	2	US-09-269-921-131	Sequence 131, App
32	51	100.0	81	1	US-08-497-312-19	Sequence 19, Appl
33	51	100.0	81	2	US-09-254-180C-160	Sequence 160, App
34	51	100.0	81	2	US-09-254-180C-161	Sequence 161, App
35	51	100.0	87	2	US-08-646-265A-112	Sequence 112, App
36	51	100.0	98	1	US-08-553-501A-87	Sequence 87, Appl
37	51	100.0	98	2	US-09-205-231-87	Sequence 87, Appl
38	51	100.0	106	1	US-08-561-521-7	Sequence 7, Appli
39	51	100.0	106	1	US-08-553-501A-86	Sequence 86, Appl
40	51	100.0	106	1	US-08-318-157B-19	Sequence 19, Appl
41	51	100.0	106	2	US-09-205-231-86	Sequence 86, Appl
42	51	100.0	106	2	US-09-253-794-19	Sequence 19, Appl
43	51	100.0	106	2	US-08-844-215-14	Sequence 14, Appl
44	51	100.0	106	4	PCT-US95-01219-7	Sequence 7, Appli
45	51	100.0	107	1	US-07-634-278-63	Sequence 63, Appl

ALIGNMENTS

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RESULT 1
US-07-946-421-10
; Sequence 10, Application US/07946421
; Patent No. 5558864
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Kettleborough, Catherine A.
;    APPLICANT:  Saldanha, Jose
;    TITLE OF INVENTION:  Humanized and Chimeric Monoclonal
;    TITLE OF INVENTION:  Antibodies
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Millen, White, Zelano & Branigan, P.C.
;      STREET:  2200 Clarendon Boulevard, Suite 1400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/946,421
;      FILING DATE:  06-NOV-1992
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/EP92/00480
;      FILING DATE:  04-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 911933892
;      FILING DATE:  06-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hamlet-King, Diana
;      REGISTRATION NUMBER:  33,302
;      REFERENCE/DOCKET NUMBER:  Merck 1430
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-243-6333
;      TELEFAX:  703-243-6410
;      TELEX:  64191
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-07-946-421-10

  Query Match             100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 2
US-08-137-117D-123
; Sequence 123, Application US/08137117D
; Patent No. 5795965
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  BENDIG, Mary
;    APPLICANT:  JONES, Steven
;    APPLICANT:  SALDANHA, Jose
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6 RECEPTOR
;    NUMBER OF SEQUENCES:  158
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,117D
;      FILING DATE:  20-DEC-1993
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP92/00544
;      FILING DATE:  24-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 4-32084
;      FILING DATE:  19-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 3-95476
;      FILING DATE:  25-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/126/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  123:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-137-117D-123

  Query Match             100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 3
US-08-137-117D-142
; Sequence 142, Application US/08137117D
; Patent No. 5795965
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  BENDIG, Mary
;    APPLICANT:  JONES, Steven
;    APPLICANT:  SALDANHA, Jose
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6 RECEPTOR
;    NUMBER OF SEQUENCES:  158
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,117D
;      FILING DATE:  20-DEC-1993
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP92/00544
;      FILING DATE:  24-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 4-32084
;      FILING DATE:  19-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 3-95476
;      FILING DATE:  25-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/126/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  142:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-137-117D-142

  Query Match             100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 4
US-08-436-717-123
; Sequence 123, Application US/08436717
; Patent No. 5817790
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  BENDIG, Mary
;    APPLICANT:  JONES, Steven
;    APPLICANT:  SALDANHA, Jose
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6 RECEPTOR
;    NUMBER OF SEQUENCES:  158
```

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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/436,717
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,117
;      FILING DATE:  20-DEC-1993
;      APPLICATION NUMBER:  WO PCT/JP92/00544
;      FILING DATE:  24-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 4-32084
;      FILING DATE:  19-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 3-95476
;      FILING DATE:  25-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/126/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  123:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-436-717-123

  Query Match             100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 5
US-08-436-717-142
; Sequence 142, Application US/08436717
; Patent No. 5817790
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  BENDIG, Mary
;    APPLICANT:  JONES, Steven
;    APPLICANT:  SALDANHA, Jose
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6 RECEPTOR
;    NUMBER OF SEQUENCES:  158
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/436,717
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,117
;      FILING DATE:  20-DEC-1993
;      APPLICATION NUMBER:  WO PCT/JP92/00544
;      FILING DATE:  24-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 4-32084
;      FILING DATE:  19-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 3-95476
;      FILING DATE:  25-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/126/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  142:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-436-717-142

  Query Match             100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 6
US-08-553-501A-68
; Sequence 68, Application US/08553501A
; Patent No. 5856135
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  HIRATA, Yuichi
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,501A
;      FILING DATE:  20-FEB-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/00859
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;      FILING DATE:  30-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-129787
;      FILING DATE:  31-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/177/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-553-501A-68

  Query Match             100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 7
US-08-553-501A-72
; Sequence 72, Application US/08553501A
; Patent No. 5856135
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  HIRATA, Yuichi
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,501A
;      FILING DATE:  20-FEB-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/00859
;      FILING DATE:  30-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-129787
;      FILING DATE:  31-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/177/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  72:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-553-501A-72

  Query Match             100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 8
US-08-318-157B-29
; Sequence 29, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  29:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-29

  Query Match             100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 9
US-08-765-783A-90
; Sequence 90, Application US/08765783A
; Patent No. 5994524
;  GENERAL INFORMATION:
;    APPLICANT:  Matsushima, Kouji
;    APPLICANT:  Matsumoto, Yoshihiro
```

```
;    APPLICANT:  Yamada, Yoshiki
;    APPLICANT:  Sato, Koh
;    APPLICANT:  Tsuchiya, Masayuki
;    APPLICANT:  Yamazaki, Tatsumi
;    TITLE OF INVENTION:  Reshaped Human Antibody to
;    TITLE OF INVENTION:  Interleukin-8
;    NUMBER OF SEQUENCES:  105
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/765,783A
;      FILING DATE:  07-MAR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  35029-20001.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-822-0168
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  90:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-765-783A-90

  Query Match             100.0%;  Score 51;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 10
US-09-205-231-68
; Sequence 68, Application US/09205231
; Patent No. 6121423
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  HIRATA, Yuichi
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/205,231
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,501
;      FILING DATE:  20-FEB-1996
;      APPLICATION NUMBER:  WO PCT/JP94/00859
;      FILING DATE:  30-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-129787
;      FILING DATE:  31-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/177/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-205-231-68

  Query Match             100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 11
US-09-205-231-72
; Sequence 72, Application US/09205231
; Patent No. 6121423
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  HIRATA, Yuichi
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/205,231
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,501
;      FILING DATE:  20-FEB-1996
;      APPLICATION NUMBER:  WO PCT/JP94/00859
;      FILING DATE:  30-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-129787
;      FILING DATE:  31-MAY-1993
```

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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/177/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  72:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-205-231-72

  Query Match             100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 12
US-08-646-265A-124
; Sequence 124, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  124:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-646-265A-124

  Query Match             100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 13
US-09-416-557-90
; Sequence 90, Application US/09416557
; Patent No. 6245894
;  GENERAL INFORMATION:
;    APPLICANT:  Matsushima, Kouji
;    APPLICANT:  Matsumoto, Yoshihiro
;    APPLICANT:  Yamada, Yoshiki
;    APPLICANT:  Sato, Koh
;    APPLICANT:  Tsuchiya, Masayuki
;    APPLICANT:  Yamazaki, Tatsumi
;    TITLE OF INVENTION:  Reshaped Human Antibody to
;    TITLE OF INVENTION:  Interleukin-8
;    NUMBER OF SEQUENCES:  105
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/416,557
;      FILING DATE:  12-October-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/765,783
;      FILING DATE:  7-March-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  35029-20001.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-822-0168
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  90:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-416-557-90

  Query Match             100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 14
US-09-443-199C-1271
; Sequence 1271, Application US/09443199C
; Patent No. 6670464
; GENERAL INFORMATION:
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;  APPLICANT: Shimkets, Richard A.
;  APPLICANT:  Leach, Martin
;  TITLE OF INVENTION: Nucleic Acids Containing Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms and Methods of Use Thereof
;  FILE REFERENCE: 15966-534A
;  CURRENT APPLICATION NUMBER: US/09/443,199C
;  CURRENT FILING DATE:  1999-11-16
;  PRIOR APPLICATION NUMBER: 60/109,024
;  PRIOR FILING DATE: 1998-11-17
;  NUMBER OF SEQ ID NOS: 1272
;  SOFTWARE: CuraGen Patent Formatter Version 0.9
; SEQ ID NO 1271
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: (7)...(0)
;   OTHER INFORMATION: cSNP translation
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Peptide 1 of 2 allelic variants (1272 is other peptide)
US-09-443-199C-1271

  Query Match             100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 15
US-09-253-794-29
; Sequence 29, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 29:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 10 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-253-794-29

  Query Match             100.0%;  Score 51;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.009;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


Search completed: March 25, 2006, 09:18:45
Job time : 9.10995 secs
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:55:36 ; Search time 29.8429 Seconds
(without alignments)
140.009 Million cell updates/sec

Title: US-10-755-382-29
Perfect score: 51
Sequence: 1 FGQGTKVEIK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	10	3	US-09-253-794-29	Sequence 29, Appl
2	51	100.0	10	3	US-09-730-857-90	Sequence 90, Appl
3	51	100.0	10	3	US-09-749-873-124	Sequence 124, App
4	51	100.0	10	3	US-09-563-222-77	Sequence 77, Appl
5	51	100.0	10	3	US-09-563-222-81	Sequence 81, Appl
6	51	100.0	10	3	US-09-563-222-85	Sequence 85, Appl
7	51	100.0	10	3	US-09-563-222-89	Sequence 89, Appl
8	51	100.0	10	4	US-10-412-703A-136	Sequence 136, App
9	51	100.0	10	4	US-10-663-244-36	Sequence 36, Appl
10	51	100.0	10	4	US-10-338-552-60	Sequence 60, Appl
11	51	100.0	10	4	US-10-338-627-60	Sequence 60, Appl
12	51	100.0	10	4	US-10-783-950-77	Sequence 77, Appl
13	51	100.0	10	5	US-10-755-382-29	Sequence 29, Appl
14	51	100.0	10	5	US-10-984-960A-18	Sequence 18, Appl
15	51	100.0	10	5	US-10-984-960A-36	Sequence 36, Appl
16	51	100.0	10	5	US-10-984-960A-54	Sequence 54, Appl
17	51	100.0	11	3	US-09-313-942-5	Sequence 5, Appli
18	51	100.0	11	3	US-09-855-271-15	Sequence 15, Appl
19	51	100.0	11	3	US-09-949-559-93	Sequence 93, Appl
20	51	100.0	11	3	US-09-935-868-5	Sequence 5, Appli
21	51	100.0	11	3	US-09-875-221A-93	Sequence 93, Appl
22	51	100.0	11	4	US-10-287-035-5	Sequence 5, Appli
23	51	100.0	11	4	US-10-282-162-5	Sequence 5, Appli
24	51	100.0	11	4	US-10-428-408A-18	Sequence 18, Appl
25	51	100.0	11	4	US-10-428-894-18	Sequence 18, Appl
26	51	100.0	11	4	US-10-307-276B-43	Sequence 43, Appl
27	51	100.0	11	4	US-10-632-706-250	Sequence 250, App
28	51	100.0	11	4	US-10-632-706-253	Sequence 253, App
29	51	100.0	11	4	US-10-632-706-256	Sequence 256, App
30	51	100.0	11	4	US-10-632-706-259	Sequence 259, App
31	51	100.0	11	4	US-10-632-706-262	Sequence 262, App
32	51	100.0	11	4	US-10-699-874-18	Sequence 18, Appl
33	51	100.0	11	5	US-10-728-420B-89	Sequence 89, Appl
34	51	100.0	11	5	US-10-914-015-89	Sequence 89, Appl
35	51	100.0	11	5	US-10-877-773-119	Sequence 119, App
36	51	100.0	11	5	US-10-877-774-119	Sequence 119, App
37	51	100.0	11	6	US-11-061-956-43	Sequence 43, Appl
38	51	100.0	11	6	US-11-134-114-5	Sequence 5, Appli
39	51	100.0	12	4	US-10-308-817-145	Sequence 145, App
40	51	100.0	12	4	US-10-443-466A-53	Sequence 53, Appl
41	51	100.0	12	4	US-10-443-466A-61	Sequence 61, Appl
42	51	100.0	12	4	US-10-443-466A-86	Sequence 86, Appl
43	51	100.0	12	4	US-10-443-466A-94	Sequence 94, Appl
44	51	100.0	12	4	US-10-443-466A-102	Sequence 102, App
45	51	100.0	12	4	US-10-443-466A-110	Sequence 110, App

ALIGNMENTS

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RESULT 1
US-09-253-794-29
; Sequence 29, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 29:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 10 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-253-794-29

  Query Match           100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 2
US-09-730-857-90
; Sequence 90, Application US/09730857
; Patent No. US20020082396A1
;   GENERAL INFORMATION:
;        APPLICANT: Matsushima, Kouji
;                   Matsumoto, Yoshihiro
;                   Yamada, Yoshiki
;                   Sato, Koh
;                   Tsuchiya, Masayuki
;                   Yamazaki, Tatsumi
;        TITLE OF INVENTION: Reshaped Human Antibody to
;                            Interleukin-8
;        NUMBER OF SEQUENCES: 105
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORRISON & FOERSTER
;             STREET: 2000 Pennsylvania Avenue, NW, suite 5500
;             CITY: Washington
;             STATE: DC
;             COUNTRY: USA
;             ZIP: 20006-1888
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/730,857
;             FILING DATE: 07-Dec-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/416,557
;             FILING DATE: 1999-10-12
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Murashige, Kate H
;             REGISTRATION NUMBER: 29,959
;             REFERENCE/DOCKET NUMBER: 35029-20001.10
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-887-1500
;             TELEFAX: 202-822-0168
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 90:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 10 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 90:
US-09-730-857-90

  Query Match             100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 3
US-09-749-873-124
; Sequence 124, Application US/09749873
; Publication No. US20030023045A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/749,873
;             FILING DATE: 29-Dec-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/646,265
;             FILING DATE: 1996-09-09
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 124:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 10 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 124:
US-09-749-873-124

  Query Match             100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 4
US-09-563-222-77
; Sequence 77, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
;  APPLICANT:  Hiatt, Andrew
;  APPLICANT:  Hein, Mich B.
;  TITLE OF INVENTION:  IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
;  TITLE OF INVENTION:  EUKARYOTIC CELLS
;  FILE REFERENCE:  310098.406
;  CURRENT APPLICATION NUMBER: US/09/563,222
;  CURRENT FILING DATE:  2000-05-02
;  NUMBER OF SEQ ID NOS:  197
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 77
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-563-222-77

  Query Match             100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 5
US-09-563-222-81
; Sequence 81, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
;  APPLICANT:  Hiatt, Andrew
;  APPLICANT:  Hein, Mich B.
;  TITLE OF INVENTION:  IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
;  TITLE OF INVENTION:  EUKARYOTIC CELLS
;  FILE REFERENCE:  310098.406
;  CURRENT APPLICATION NUMBER: US/09/563,222
;  CURRENT FILING DATE:  2000-05-02
;  NUMBER OF SEQ ID NOS:  197
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 81
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-563-222-81

  Query Match             100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 6
US-09-563-222-85
; Sequence 85, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
;  APPLICANT:  Hiatt, Andrew
;  APPLICANT:  Hein, Mich B.
;  TITLE OF INVENTION:  IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
;  TITLE OF INVENTION:  EUKARYOTIC CELLS
;  FILE REFERENCE:  310098.406
;  CURRENT APPLICATION NUMBER: US/09/563,222
;  CURRENT FILING DATE:  2000-05-02
;  NUMBER OF SEQ ID NOS:  197
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 85
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-563-222-85

  Query Match             100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
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Db          1 FGQGTKVEIK 10


RESULT 7
US-09-563-222-89
; Sequence 89, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
;  APPLICANT:  Hiatt, Andrew
;  APPLICANT:  Hein, Mich B.
;  TITLE OF INVENTION:  IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
;  TITLE OF INVENTION:  EUKARYOTIC CELLS
;  FILE REFERENCE:  310098.406
;  CURRENT APPLICATION NUMBER: US/09/563,222
;  CURRENT FILING DATE:  2000-05-02
;  NUMBER OF SEQ ID NOS:  197
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 89
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-563-222-89

  Query Match             100.0%;  Score 51;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 8
US-10-412-703A-136
; Sequence 136, Application US/10412703A
; Publication No. US20030219439A1
; GENERAL INFORMATION:
;  APPLICANT: Reed et al.
;  TITLE OF INVENTION: Recombinant Anti-Interleukin-9 Antibodies
;  FILE REFERENCE: IL400US
;  CURRENT APPLICATION NUMBER: US/10/412,703A
;  CURRENT FILING DATE:  2003-04-11
;  PRIOR APPLICATION NUMBER: 60/371,728
;  PRIOR FILING DATE: 2002-04-12
;  PRIOR APPLICATION NUMBER: 60/371,683
;  PRIOR FILING DATE: 2002-04-12
;  NUMBER OF SEQ ID NOS: 140
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 136
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-412-703A-136

  Query Match             100.0%;  Score 51;  DB 4;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 9
US-10-663-244-36
; Sequence 36, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
;  APPLICANT: Rondon, Isaac J.
;  APPLICANT:  Edge,  Albert
;  APPLICANT:  Kent, Rachel Baribault
;  TITLE OF INVENTION: CD44 LIGANDS
;  FILE REFERENCE: 10280-063001
;  CURRENT APPLICATION NUMBER: US/10/663,244
;  CURRENT FILING DATE:  2003-09-15
;  PRIOR APPLICATION NUMBER: US 60/410,758
;  PRIOR FILING DATE: 2002-09-13
;  PRIOR APPLICATION NUMBER: US 60/469,123
;  PRIOR FILING DATE: 2003-05-09
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-36

 Query Match 100.0%; Score 51; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
 ||||||||||
Db 1 FGQGTKVEIK 10

RESULT 10
US-10-338-552-60
; Sequence 60, Application US/10338552
; Publication No. US20040131612A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffry D.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Marquis, David
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: TNF-alpha Binding Molecules
; FILE REFERENCE: AME-06971
; CURRENT APPLICATION NUMBER: US/10/338,552
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-552-60

 Query Match 100.0%; Score 51; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
 ||||||||||
Db 1 FGQGTKVEIK 10

RESULT 11
US-10-338-627-60
; Sequence 60, Application US/10338627
; Publication No. US20040131613A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffry D.
; APPLICANT: Vasserot, Alain P.
; APPLICANT: Marquis, David
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: TNF-alpha Binding Molecules
; FILE REFERENCE: AME-07497
; CURRENT APPLICATION NUMBER: US/10/338,627
; CURRENT FILING DATE: 2003-01-08
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 60
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-627-60

 Query Match 100.0%; Score 51; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
 ||||||||||
Db 1 FGQGTKVEIK 10

RESULT 12
US-10-783-950-77
; Sequence 77, Application US/10783950
; Publication No. US20040199945A1
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/10/783,950
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-783-950-77

 Query Match 100.0%; Score 51; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
 ||||||||||
Db 1 FGQGTKVEIK 10

RESULT 13
US-10-755-382-29
; Sequence 29, Application US/10755382
; Publication No. US20050089538A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/755,382
; FILING DATE: 13-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399

```
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 29:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 10 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-10-755-382-29

  Query Match            100.0%;  Score 51;  DB 5;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 14
US-10-984-960A-18
; Sequence 18, Application US/10984960A
; Publication No. US20050142137A1
; GENERAL INFORMATION:
;  APPLICANT: Gallo, Michael
;  APPLICANT:  Chui, Daniel
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Ara, Gulshan
;  APPLICANT:  LaRochelle, William J.
;  TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
;  FILE REFERENCE: Cura 970
;  CURRENT APPLICATION NUMBER: US/10/984,960A
;  CURRENT FILING DATE:  2004-11-08
;  PRIOR APPLICATION NUMBER: 60/518,275
;  PRIOR FILING DATE: 2003-11-07
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 18
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-984-960A-18

  Query Match            100.0%;  Score 51;  DB 5;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


RESULT 15
US-10-984-960A-36
; Sequence 36, Application US/10984960A
; Publication No. US20050142137A1
; GENERAL INFORMATION:
;  APPLICANT: Gallo, Michael
;  APPLICANT:  Chui, Daniel
;  APPLICANT:  Zhong, Haihong
;  APPLICANT:  Ara, Gulshan
;  APPLICANT:  LaRochelle, William J.
;  TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
;  FILE REFERENCE: Cura 970
;  CURRENT APPLICATION NUMBER: US/10/984,960A
;  CURRENT FILING DATE:  2004-11-08
;  PRIOR APPLICATION NUMBER: 60/518,275
;  PRIOR FILING DATE: 2003-11-07
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 36
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-984-960A-36

  Query Match            100.0%;  Score 51;  DB 5;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.013;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          1 FGQGTKVEIK 10


Search completed: March 25, 2006, 10:08:04
Job time : 30.8429 secs
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:58:56 ; Search time 3.61257 Seconds
(without alignments)
81.644 Million cell updates/sec

Title: US-10-755-382-29
Perfect score: 51
Sequence: 1 FGQGTKVEIK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	10	6	US-10-839-799-124	Sequence 124, App
2	51	100.0	12	7	US-11-051-453-79	Sequence 79, Appl
3	51	100.0	12	7	US-11-004-590-99	Sequence 99, Appl
4	51	100.0	13	7	US-11-054-669-95	Sequence 95, Appl
5	51	100.0	13	7	US-11-061-848-74	Sequence 74, Appl
6	51	100.0	17	7	US-11-240-195-70	Sequence 70, Appl
7	51	100.0	58	6	US-10-925-366A-308	Sequence 308, App
8	51	100.0	58	6	US-10-925-366A-325	Sequence 325, App
9	51	100.0	58	6	US-10-925-366A-328	Sequence 328, App
10	51	100.0	74	6	US-10-925-366A-295	Sequence 295, App
11	51	100.0	76	6	US-10-925-366A-319	Sequence 319, App
12	51	100.0	76	6	US-10-925-366A-322	Sequence 322, App
13	51	100.0	78	6	US-10-925-366A-302	Sequence 302, App
14	51	100.0	78	6	US-10-925-366A-311	Sequence 311, App
15	51	100.0	78	6	US-10-925-366A-314	Sequence 314, App
16	51	100.0	80	6	US-10-982-357-43	Sequence 43, Appl
17	51	100.0	80	6	US-10-982-357-49	Sequence 49, Appl
18	51	100.0	80	7	US-11-226-325-131	Sequence 131, App
19	51	100.0	80	7	US-11-226-325-132	Sequence 132, App
20	51	100.0	87	6	US-10-839-799-112	Sequence 112, App
21	51	100.0	91	6	US-10-999-866-12	Sequence 12, Appl
22	51	100.0	91	6	US-10-935-005B-42	Sequence 42, Appl
23	51	100.0	91	7	US-11-144-248-22	Sequence 22, Appl
24	51	100.0	91	7	US-11-061-821-12	Sequence 12, Appl
25	51	100.0	91	7	US-11-144-222-22	Sequence 22, Appl
26	51	100.0	91	7	US-11-182-343-22	Sequence 22, Appl
27	51	100.0	92	6	US-10-999-866-11	Sequence 11, Appl
28	51	100.0	92	6	US-10-935-005B-41	Sequence 41, Appl
29	51	100.0	92	7	US-11-061-821-11	Sequence 11, Appl
30	51	100.0	93	6	US-10-999-866-10	Sequence 10, Appl
31	51	100.0	93	6	US-10-935-005B-40	Sequence 40, Appl
32	51	100.0	93	7	US-11-061-821-10	Sequence 10, Appl
33	51	100.0	104	7	US-11-155-775-28	Sequence 28, Appl
34	51	100.0	104	7	US-11-250-411-104	Sequence 104, App
35	51	100.0	104	7	US-11-250-411-105	Sequence 105, App
36	51	100.0	104	7	US-11-250-411-107	Sequence 107, App
37	51	100.0	105	7	US-11-096-074-55	Sequence 55, Appl
38	51	100.0	105	7	US-11-155-775-16	Sequence 16, Appl
39	51	100.0	105	7	US-11-155-775-44	Sequence 44, Appl
40	51	100.0	105	7	US-11-095-822-55	Sequence 55, Appl
41	51	100.0	105	7	US-11-250-411-109	Sequence 109, App
42	51	100.0	105	7	US-11-250-411-110	Sequence 110, App
43	51	100.0	105	7	US-11-250-411-111	Sequence 111, App
44	51	100.0	106	6	US-10-850-635-10	Sequence 10, Appl
45	51	100.0	106	7	US-11-155-775-20	Sequence 20, Appl

ALIGNMENTS

```
RESULT 1
US-10-839-799-124
; Sequence 124, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 124:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 10 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
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; SEQUENCE DESCRIPTION: SEQ ID NO: 124:
US-10-839-799-124

 Query Match 100.0%; Score 51; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
 ||||||||||
Db 1 FGQGTKVEIK 10

RESULT 2
US-11-051-453-79
; Sequence 79, Application US/11051453
; Publication No. US20050287150A1
; GENERAL INFORMATION:
; APPLICANT: AMBROSINO, DONNA
; APPLICANT: BABCOCK, GREGORY J.
; APPLICANT: BROERING, THERESA
; APPLICANT: GRAZIANO, ROBERT
; APPLICANT: HERNANDEZ, HECTOR JAVIER
; APPLICANT: LOWY, ISRAEL
; APPLICANT: MANDELL, ROBERT
; APPLICANT: MOLRINE, DEBORAH
; APPLICANT: THOMAS, JR., WILLIAM D.
; APPLICANT: ZHANG, HUI-FEN
; TITLE OF INVENTION: ANTIBODIES AGAINST CLOSTRIDIUM DIFFICILE TOXINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: MJI-001
; CURRENT APPLICATION NUMBER: US/11/051,453
; CURRENT FILING DATE: 2005-02-04
; PRIOR APPLICATION NUMBER: 60/542,357
; PRIOR FILING DATE: 2004-02-06
; PRIOR APPLICATION NUMBER: 60/613,854
; PRIOR FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 79
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-051-453-79

 Query Match 100.0%; Score 51; DB 7; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
 ||||||||||
Db 3 FGQGTKVEIK 12

RESULT 3
US-11-004-590-99
; Sequence 99, Application US/11004590
; Publication No. US20060008883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 99
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-590-99

 Query Match 100.0%; Score 51; DB 7; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
 ||||||||||
Db 3 FGQGTKVEIK 12

RESULT 4
US-11-054-669-95
; Sequence 95, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 95
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-95

 Query Match 100.0%; Score 51; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
 ||||||||||
Db 3 FGQGTKVEIK 12

RESULT 5
US-11-061-848-74
; Sequence 74, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, David S.
; APPLICANT: Nock, Steffen
; APPLICANT: Larrick, James W.
; TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
; FILE REFERENCE: 186280/US
; CURRENT APPLICATION NUMBER: US/11/061,848
; CURRENT FILING DATE: 2005-02-17
; PRIOR APPLICATION NUMBER: US 60/545,011
; PRIOR FILING DATE: 2004-02-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 74
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-061-848-74

 Query Match 100.0%; Score 51; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0016;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          3 FGQGTKVEIK 12
```

RESULT 6
US-11-240-195-70
; Sequence 70, Application US/11240195
; Publication No. US20060057140A1
; GENERAL INFORMATION:
; APPLICANT: Feuerstein, Giora Z.
; TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
; TITLE OF INVENTION: OF THROMBOSIS
; FILE REFERENCE: P50816-1
; CURRENT APPLICATION NUMBER: US/11/240,195
; CURRENT FILING DATE: 2005-09-30
; PRIOR APPLICATION NUMBER: US/10/430,176
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 09/817,960
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/359,202
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 60/095,714
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 10/051,852
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 09/344,050
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 08/783,853
; PRIOR FILING DATE: 1997-01-06
; PRIOR APPLICATION NUMBER: 60/010,108
; PRIOR FILING DATE: 1996-01-17
; PRIOR APPLICATION NUMBER: 60/029,119
; PRIOR FILING DATE: 1996-10-24
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-240-195-70

Query Match 100.0%; Score 51; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 FGQGTKVEIK 10
              ||||||||||
Db          3 FGQGTKVEIK 12
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RESULT 7
US-10-925-366A-308
; Sequence 308, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: DeWildt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Basran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 308
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-308

Query Match 100.0%; Score 51; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 FGQGTKVEIK 10
              ||||||||||
Db         48 FGQGTKVEIK 57
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RESULT 8
US-10-925-366A-325
; Sequence 325, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: DeWildt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Basran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 325
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-325

Query Match 100.0%; Score 51; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 48 FGQGTKVEIK 57

RESULT 9
US-10-925-366A-328
; Sequence 328, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: DeWildt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Basran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 328
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-328

Query Match 100.0%; Score 51; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 48 FGQGTKVEIK 57

RESULT 10
US-10-925-366A-295
; Sequence 295, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: DeWildt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Basran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 295
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-295

Query Match 100.0%; Score 51; DB 6; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 64 FGQGTKVEIK 73

RESULT 11
US-10-925-366A-319
; Sequence 319, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: DeWildt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Basran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804

; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 319
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-319

Query Match 100.0%; Score 51; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 66 FGQGTKVEIK 75

RESULT 12
US-10-925-366A-322
; Sequence 322, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: DeWildt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Basran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 322
; LENGTH: 76
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-322

Query Match 100.0%; Score 51; DB 6; Length 76;
Best Local Similarity 100.0%; Pred. No. 0.0093;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 66 FGQGTKVEIK 75

RESULT 13
US-10-925-366A-302
; Sequence 302, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: DeWildt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Basran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 302
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-302

Query Match 100.0%; Score 51; DB 6; Length 78;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FGQGTKVEIK 10
||||||||||
Db 68 FGQGTKVEIK 77

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RESULT 14
US-10-925-366A-311
; Sequence 311, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
;  APPLICANT: Ignatovich, Olga
;  APPLICANT:  DeWildt, Rudolph M.T.
;  APPLICANT:  Benjamin, Woolven
;  APPLICANT:  Grant, Steven
;  APPLICANT:  Jones, Philip
;  APPLICANT:  Basran, Amrik
;  APPLICANT:  Brewis, Neil
;  TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
;  FILE REFERENCE: 8039/2105
;  CURRENT APPLICATION NUMBER: US/10/925,366A
;  CURRENT FILING DATE:  2004-08-24
;  PRIOR APPLICATION NUMBER: US 10/744,774
;  PRIOR FILING DATE: 2003-12-23
;  PRIOR APPLICATION NUMBER: PCT/GB2003/002804
;  PRIOR FILING DATE: 2003-06-30
;  PRIOR APPLICATION NUMBER: PCT/GB2002/03014
;  PRIOR FILING DATE: 2002-06-28
;  PRIOR APPLICATION NUMBER: GB 0230202.4
;  PRIOR FILING DATE: 2002-12-27
;  PRIOR APPLICATION NUMBER: GB 115841.9
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: PCT/GB2004/002829
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/535,076
;  PRIOR FILING DATE: 2004-01-08
;  PRIOR APPLICATION NUMBER: PCT/GB2003/005646
;  PRIOR FILING DATE: 2003-12-24
;  PRIOR APPLICATION NUMBER: GB 0327706.8
;  PRIOR FILING DATE: 2003-11-28
;  PRIOR APPLICATION NUMBER: US 60/509,613
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 368
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 311
;   LENGTH: 78
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-311

  Query Match             100.0%;  Score 51;  DB 6;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 0.0095;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db         68 FGQGTKVEIK 77


RESULT 15
US-10-925-366A-314
; Sequence 314, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
;  APPLICANT: Ignatovich, Olga
;  APPLICANT:  DeWildt, Rudolph M.T.
;  APPLICANT:  Benjamin, Woolven
;  APPLICANT:  Grant, Steven
;  APPLICANT:  Jones, Philip
;  APPLICANT:  Basran, Amrik
;  APPLICANT:  Brewis, Neil
;  TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
;  FILE REFERENCE: 8039/2105
;  CURRENT APPLICATION NUMBER: US/10/925,366A
;  CURRENT FILING DATE:  2004-08-24
;  PRIOR APPLICATION NUMBER: US 10/744,774
;  PRIOR FILING DATE: 2003-12-23
;  PRIOR APPLICATION NUMBER: PCT/GB2003/002804
;  PRIOR FILING DATE: 2003-06-30
;  PRIOR APPLICATION NUMBER: PCT/GB2002/03014
;  PRIOR FILING DATE: 2002-06-28
;  PRIOR APPLICATION NUMBER: GB 0230202.4
;  PRIOR FILING DATE: 2002-12-27
;  PRIOR APPLICATION NUMBER: GB 115841.9
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: PCT/GB2004/002829
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/535,076
;  PRIOR FILING DATE: 2004-01-08
;  PRIOR APPLICATION NUMBER: PCT/GB2003/005646
;  PRIOR FILING DATE: 2003-12-24
;  PRIOR APPLICATION NUMBER: GB 0327706.8
;  PRIOR FILING DATE: 2003-11-28
;  PRIOR APPLICATION NUMBER: US 60/509,613
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 368
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 314
;   LENGTH: 78
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-314

  Query Match             100.0%;  Score 51;  DB 6;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 0.0095;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 FGQGTKVEIK 10
              ||||||||||
Db         68 FGQGTKVEIK 77


Search completed: March 25, 2006, 10:09:19
Job time : 4.61257 secs
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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:10 ; Search time 110.576 Seconds
(without alignments)
119.206 Million cell updates/sec

Title: US-10-755-382-30
Perfect score: 151
Sequence: 1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	151	100.0	30	2	AAR97323	Aar97323 Humanised
2	148	98.0	30	2	AAR97324	Aar97324 Humanised
3	148	98.0	118	6	ABR42755	Abr42755 Anti-CEA
4	148	98.0	119	8	ADM95101	Adm95101 Humanised
5	148	98.0	119	8	ADM98324	Adm98324 Humanised
6	148	98.0	138	6	ABG76489	Abg76489 Heavy cha
7	148	98.0	254	2	AAR94557	Aar94557 Humanised
8	148	98.0	256	6	ABR42757	Abr42757 Anti-CEA
9	148	98.0	257	6	ABR42758	Abr42758 Anti-CEA
10	148	98.0	261	6	ABR42289	Abr42289 Diabody 6
11	148	98.0	261	6	ABR42754	Abr42754 Anti-CEA
12	148	98.0	261	6	ABR83645	Abr83645 hMN14-scF
13	148	98.0	267	6	ABR42292	Abr42292 Bispecifi
14	148	98.0	267	6	ABR42299	Abr42299 Bispecifi
15	148	98.0	267	6	ABR42296	Abr42296 Bispecifi
16	148	98.0	267	6	ABR42294	Abr42294 Bispecifi
17	148	98.0	358	8	ADU26571	Adu26571 Chimeric
18	148	98.0	363	8	ADU26561	Adu26561 Chimeric
19	148	98.0	364	8	ADU26570	Adu26570 Chimeric
20	148	98.0	370	8	ADU26560	Adu26560 Chimeric
21	148	98.0	415	6	ABR83648	Abr83648 TS1 VH ch
22	148	98.0	443	6	ABG76488	Abg76488 Humanised
23	148	98.0	443	6	ABG74240	Abg74240 Chimaeric
24	148	98.0	468	7	ADE64201	Ade64201 MN14HCF p
25	148	98.0	468	7	ADF60815	Adf60815 hMN-14 he
26	148	98.0	669	9	ADY97271	Ady97271 Exemplary
27	144	95.4	119	2	AAR97336	Aar97336 Humanised
28	140	92.7	117	2	AAR77305	Aar77305 Variable
29	140	92.7	119	2	AAR82964	Aar82964 3S193HuVH
30	140	92.7	119	2	AAR82965	Aar82965 3S193HuVH
31	140	92.7	119	2	AAR82966	Aar82966 3S193HuVH
32	140	92.7	119	2	AAR82962	Aar82962 Humanised
33	140	92.7	244	5	ABP45899	Abp45899 Human BLy
34	140	92.7	244	7	ADG96726	Adg96726 Single ch
35	138	91.4	119	2	AAR13092	Aar13092 Grafted h
36	138	91.4	119	2	AAR13102	Aar13102 Grafted h
37	138	91.4	119	2	AAR67447	Aar67447 OKT3 huma
38	138	91.4	119	2	AAW11919	Aaw11919 Humanised
39	138	91.4	119	2	AAW73529	Aaw73529 Humanised
40	138	91.4	120	2	AAR54930	Aar54930 Fc recept
41	138	91.4	300	2	AAW11503	Aaw11503 Humanised
42	138	91.4	300	2	AAW73218	Aaw73218 H22-HRG f
43	138	91.4	300	4	AAB61954	Aab61954 Amino aci
44	138	91.4	300	4	AAB85449	Aab85449 H22-HRG f
45	138	91.4	352	2	AAY06272	Aay06272 Anti-Fc g

ALIGNMENTS

RESULT 1
AAR97323
ID AAR97323 standard; peptide; 30 AA.
XX
AC AAR97323;
XX
DT 15-OCT-1996 (first entry)
XX
DE Humanised monoclonal antibody heavy chain framework region.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Homo sapiens.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Claim 7; Page 39; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. This sequence corresponds to the first framework region of the
CC heavy chain of the humanised MAb. See AAR97313-97333

```
XX
SQ   Sequence 30 AA;

  Query Match             100.0%;  Score 151;  DB 2;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 2
AAR97324
ID   AAR97324 standard; peptide; 30 AA.
XX
AC   AAR97324;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Humanised monoclonal antibody heavy chain framework region.
XX
KW   Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW   complementary determining region; anti-carcinoembryonic antigen; CEA;
KW   diagnosis; imaging; therapy; immune response.
XX
OS   Homo sapiens.
XX
PN   WO9611013-A1.
XX
PD   18-APR-1996.
XX
PF   28-SEP-1995;   95WO-US011964.
XX
PR   05-OCT-1994;   94US-00318157.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Hansen HJ,  Armour KL;
XX
DR   WPI; 1996-209653/21.
XX
PT   New humanised anti-CEA monoclonal antibody - having engrafted murine
PT   CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS   Claim 7; Page 39; 62pp; English.
XX
CC   New humanised monoclonal antibodies (MAbs) comprising the complementary
CC   determining regions (CDRs) of a parental murine class III anti-
CC   carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC   heterologous antibody which can be derived from any species including
CC   human, retain the anti-CEA binding specificity of the parental murine MAb
CC   but are less immunogenic in a human subject than the parental MAb. The
CC   humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC   -producing cancers and patients receiving the humanised antibodies and
CC   conjugates show improved therapeutic results, decreased immune responses
CC   and decreased immune-mediated adverse effects compared to the parent
CC   antibody. This sequence corresponds to the first framework region of the
CC   heavy chain of the humanised MAb. See AAR97313-97333
XX
SQ   Sequence 30 AA;

  Query Match             98.0%;  Score 148;  DB 2;  Length 30;
  Best Local Similarity   96.7%;  Pred. No. 4e-12;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 3
ABR42755
ID   ABR42755 standard; protein; 118 AA.
XX
AC   ABR42755;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14 VH region.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Disclosure; Fig 12; 62pp; English.
XX
CC   The present sequence is the protein sequence of the heavy chain variable
CC   region of anti-carcinoembryonic antigen (CEA) humanized monoclonal
CC   antibody hMN-14. scFv constructs comprising the hMN-14 VH and Vkappa
CC   regions are used in novel multivalent, monospecific binding proteins
CC   (diabody, triabody and tetrabody) of the invention (see also ABR42754,
CC   ABR42757 and ABR42758). Claimed binding proteins are specific for a
CC   tumour-associated antigen, and are used in the diagnosis and treatment of
CC   a tumour, carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma,
CC   lymphoma or myeloma, or a cancer selected from acute lymphoblastic
CC   leukaemia, acute myelogenous leukaemia, biliary, breast, cervical,
CC   chronic lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 118 AA;

  Query Match             98.0%;  Score 148;  DB 6;  Length 118;
  Best Local Similarity   96.7%;  Pred. No. 1.6e-11;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 4
ADM95101
ID   ADM95101 standard; protein; 119 AA.
XX
AC   ADM95101;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 MAb heavy chain variable region coding sequence.
```

```
XX
KW   non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW   complementarity determining region; pancreatic cancer; breast cancer;
KW   ovarian cancer.
XX
OS   Mus sp.
OS   Homo sapiens.
XX
PN   WO2004032962-A1.
XX
PD   22-APR-2004.
XX
PF   11-OCT-2002; 2002WO-US032307.
XX
PR   08-OCT-2002; 2002US-0416531P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-364813/34.
DR   N-PSDB; ADM95099.
XX
PT   Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT   comprises administering, either concurrently or sequentially, Class III
PT   anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT   therapeutic agent(s).
XX
PS   Claim 14; Fig 16B; 88pp; English.
XX
CC   The invention relates to a method of treating a non-medullary thyroid
CC   carcinoma or treating medullary thyroid carcinoma involves administering
CC   to a subject, either concurrently or sequentially, a Class III anti-CEA
CC   (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC   least one therapeutic agent. The antibody or its fragment comprises the
CC   complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC   antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC   medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC   ovarian cancer, in a subject. This sequence corresponds to the humanised
CC   murine MN-14 antibody heavy chain variable region.
XX
SQ   Sequence 119 AA;

  Query Match             98.0%;  Score 148;  DB 8;  Length 119;
  Best Local Similarity   96.7%;  Pred. No. 1.6e-11;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 5
ADM98324
ID   ADM98324 standard; protein; 119 AA.
XX
AC   ADM98324;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 antibody heavy chain variable region protein.
XX
KW   carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW   antibody; MN-14; non-medullary thyroid carcinoma;
KW   medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW   hepatocellular carcinoma; breast cancer; lung cancer;
KW   antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW   apoptosis; humanised.
XX
OS   Mus sp.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 33. .34
FT                   /note= "Encoded by TGGGATAGCAGTACGATTAACTATGCGATG"
FT   Misc-difference 53. .62
FT                   /note= "Encoded by CCACCG"
XX
PN   WO2004032857-A2.
XX
PD   22-APR-2004.
XX
PF   08-OCT-2003; 2003WO-US031801.
XX
PR   08-OCT-2002; 2002US-0416531P.
PR   11-OCT-2002; 2002WO-US032307.
PR   02-MAY-2003; 2003US-0467161P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-340797/31.
DR   N-PSDB; ADM98323.
XX
PT   Treating non-medullary or medullary thyroid carcinoma, involves
PT   administering to subject, either concurrently or sequentially, anti-
PT   carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS   Disclosure; Fig 23b; 122pp; English.
XX
CC   This invention relates to methods for treating cancers that express
CC   carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC   therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC   antibodies that can be used following administration of an agent that
CC   will increase antibody effector functions or following administration of
CC   an amount of interferon effective to upregulate CEA expression in tumour
CC   cells. The present invention describes the anti-CEA antibody as a class
CC   III humanised murine monoclonal antibody that retains specificity for CEA
CC   binding and is preferably an MN-14 antibody or fragment thereof.
CC   Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC   composition useful for the treatment of non-medullary or medullary
CC   thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC   carcinoma, as well as breast or lung cancer. Furthermore, it can
CC   stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC   mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC   cell growth and angiogenesis. This polypeptide sequence is the humanised
CC   murine MN-14 antibody heavy chain variable region protein of the
CC   invention.
XX
SQ   Sequence 119 AA;

  Query Match             98.0%;  Score 148;  DB 8;  Length 119;
  Best Local Similarity   96.7%;  Pred. No. 1.6e-11;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 6
ABG76489
ID   ABG76489 standard; protein; 138 AA.
XX
AC   ABG76489;
XX
DT   13-MAY-2003  (first entry)
XX
DE   Heavy chain variable, VH, region of antibody hMN14.
XX
KW   CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW   colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW   human; zeta signalling chain; CD8alpha hinge; humanised antibody;
KW   heavy chain variable region; VH.
XX
```

```
OS   Homo sapiens.
OS   Mus sp.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT   Protein         20. .138
FT                   /label= Mature_VH_of_hMN14
XX
PN   US2002165360-A1.
XX
PD   07-NOV-2002.
XX
PF   10-DEC-2001; 2001US-00006771.
XX
PR   30-NOV-2000; 2000US-0250087P.
PR   30-NOV-2000; 2000US-0250090P.
XX
PA   (JUNG/) JUNGHANS R P.
XX
PI   Junghans RP;
XX
DR   WPI; 2003-298705/29.
DR   N-PSDB; ABX13169.
XX
PT   New chimeric molecule from humanized antibody against carcinoembryonic
PT   antigen and having signaling molecules of T cells and other effector
PT   cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS   Disclosure; Page 9; 20pp; English.
XX
CC   The invention relates to a chimaeric molecule comprising the
CC   carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC   as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC   chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC   which the cysteine residues have been mutated, with the IgTCR molecule
CC   occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC   appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC   NK (not defined) or other effector cells are useful in treating patients
CC   with cancers expressing the CEA antigen, together with other or with
CC   heterologous constructs to engage additional stimulatory and functional
CC   properties of the effector cells to enhance the anti-tumour therapeutic
CC   efficacy. The cancer disorder includes colorectal, breast and lung
CC   cancers. The present sequence represents the heavy chain variable, VH,
CC   region of antibody hMN14. The VH protein is humanised (complementarity
CC   determining region-grafted) and has a leader peptide
XX
SQ   Sequence 138 AA;

  Query Match             98.0%;  Score 148;  DB 6;  Length 138;
  Best Local Similarity   96.7%;  Pred. No. 1.8e-11;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||:||||||
Db         20 EVQLVESGGGVVQPGRSLRLSCASGFDFT 49


RESULT 7
AAR94557
ID   AAR94557 standard; protein; 254 AA.
XX
AC   AAR94557;
XX
DT   19-JUN-1996  (first entry)
XX
DE   Humanised antibody MN14 heavy chain.
XX
KW   Cancer; therapy; radiotherapy; radiolabelling; phosphorus;
KW   humanised antibody; complementarity determining region; CDR; targetting;
KW   protein kinase; Fab; F(ab')2; Escherichia coli; vector; MN14pBEV;
KW   carcinoembryonic antigen; CEA; MN14-Kemptide.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Sig_peptide
FT                   /note= "PelB signal peptide"
FT   Protein         23. .254
FT                   /label= Mat_protein
FT   Region          53. .57
FT                   /label= CDR-H1
FT   Region          72. .88
FT                   /label= CDR-H2
FT   Region          121. .130
FT                   /label= CDR-H3
FT   Domain          240. .254
FT                   /label= Hinge_domain
XX
PN   WO9608506-A1.
XX
PD   21-MAR-1996.
XX
PF   18-SEP-1995;   95WO-US011405.
XX
PR   16-SEP-1994;   94US-00308103.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Leung S,  Hansen HJ,  Griffiths GL;
XX
DR   WPI; 1996-179897/18.
DR   N-PSDB; AAT14493.
XX
PT   Phosphorus labelled antibodies for use in cancer therapy - comprise
PT   protein kinase peptide substrate sequence and specific targetting CDR,
PT   for radio-labelling diseased cells with a phosphorus isotope.
XX
PS   Example 1 (ix); Fig 5; 62pp; English.
XX
CC   The heavy chain and hinge region (AAR94557) and light chain (AAR94558) of
CC   humanised anti-CEA antibody MN14 are the products of an Fab'/F(ab')2
CC   dicistronic gene (AAT14493). They are derived from anti-CEA murine
CC   monoclonal antibody MN14 following cloning and humanisation of
CC   complementarity determining regions. The dicistronic gene was used to
CC   construct vector MN14pBEV. A protein kinase substrate (see AAR94550)
CC   encoding sequence was incorporated into the vector, and MN14-Kemptide
CC   fusion protein was secreted from E. coli BMH71-18 mutS. The fusion
CC   protein can be radiolabelled with 32P or 33P and used for targetted
CC   radiotherapy of tumours or infectious lesions
XX
SQ   Sequence 254 AA;

  Query Match             98.0%;  Score 148;  DB 2;  Length 254;
  Best Local Similarity   96.7%;  Pred. No. 3.3e-11;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||:||||||
Db         23 EVQLVESGGGVVQPGRSLRLSCASGFDFT 52


RESULT 8
ABR42757
ID   ABR42757 standard; protein; 256 AA.
XX
AC   ABR42757;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-0.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-0;
```

```
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; triabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .256
FT                   /label= hMN-14-0
FT   Region          142. .250
FT                   /label= hMN-14Vkappa
FT   Region          251. .256
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
DR   N-PSDB; ACC58722.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 39; Fig 13; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-0, which is
CC   designed to form an hMN-14 triabody. The hMN-14-0 polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa without a peptide linker. The use of the zero linker enables the
CC   secreted polypeptide to form a triabody, forming 3 binding sites for CEA.
CC   The polypeptide also includes a pelB signal peptide, which precedes the
CC   VH moiety to facilitate synthesis of the polypeptide in the periplasmic
CC   space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific triabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 256 AA;

  Query Match             98.0%;  Score 148;  DB 6;  Length 256;
  Best Local Similarity   96.7%;  Pred. No. 3.3e-11;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||||:||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53


RESULT 9
ABR42758
ID   ABR42758 standard; protein; 257 AA.
XX
AC   ABR42758;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-1G.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-1G;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; tetrabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .257
FT                   /label= hMN-14-0
FT   Region          142
FT                   /label= 1G_linker
FT   Region          143. .251
FT                   /label= hMN-14Vkappa
FT   Region          252. .257
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 48; Fig 14; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-1G, which is
CC   designed to form an hMN-14 tetrabody. The hMN-14-1G polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa via a single glycine residues. Use of the 1G linker enables some
CC   of the the secreted polypeptide to form a tetrabody with 4 binding sites
CC   for CEA. The polypeptide also includes a pelB signal peptide, which
CC   precedes the VH moiety to facilitate synthesis of the polypeptide in the
CC   periplasmic space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific tetrabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
```

```
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 257 AA;

  Query Match             98.0%;  Score 148;  DB 6;  Length 257;
  Best Local Similarity   96.7%;  Pred. No. 3.4e-11;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||||||:||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53


RESULT 10
ABR42289
ID   ABR42289 standard; protein; 261 AA.
XX
AC   ABR42289;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Diabody 679-scFv-L5 polypeptide (VH-I3Q/C101S mutant).
XX
KW   Diabody; antibody; 679-scFv-L5; histamine-succinyl-glycyl; HSG;
KW   affinity enhancement system; tumour; targeting; mutant; mutein.
XX
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB signal peptide"
FT   Misc-difference 3
FT                   /note= "wild-type Ile substituted by Gln"
FT   Protein         23. .268
FT                   /label= 679-scFv-L5
FT   Region          23. .142
FT                   /label= 679VH(I3Q/C101S)
FT   Misc-difference 101
FT                   /note= "wild-type Cys substituted by Ser"
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .260
FT                   /label= 679Vk
FT   Region          261. .268
FT                   /label= 6His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57803.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Disclosure; Fig 28; 87pp; English.
XX
CC   The present sequence is the protein sequence of a 679 mutant diabody in
CC   which antibody 679 VH has a Gln for Ile amino acid substitution at
CC   position 3 and a Ser for Gln amino acid substitution at position 101.
CC   Murine monoclonal antibody 679 binds with high affinity to molecules
CC   containing the moiety histamine-succinyl-glycyl (HSG). The present
CC   polypeptide comprises: 679 VH(I3Q) linked to 679 Vk via a peptide linker
CC   (enables the secreted polypeptide to dimerise into a diabody, forming 2
CC   sites for HSG); a pelB leader signal peptide (facilitates transport of
CC   the polypeptide into the periplasmic space of Escherichia coli); and 6
CC   His residues (allows purification by IMAC). The 679 diabody was expressed
CC   in E. coli at a level of 10 ug/l of culture, compared with 1 ug/l for the
CC   non-mutant polypeptide. The invention provides a bispecific diabody
CC   comprising an HSG binding site and a carcinoembryonic antigen (CEA)
CC   binding site. The HSG antigen binding site may comprise the VH and Vk
CC   polypeptides of 679 MAb. These diabodies are produced via recombinant DNA
CC   technology and create a novel affinity enhancement system that shows
CC   specific affinity for HSG and CEA. They pre-target CEA positive tumours
CC   for subsequent specific delivery of therapeutic radioisotopes carried by
CC   HSG-carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 261 AA;

  Query Match             98.0%;  Score 148;  DB 6;  Length 261;
  Best Local Similarity   96.7%;  Pred. No. 3.4e-11;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||||||:||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53


RESULT 11
ABR42754
ID   ABR42754 standard; protein; 261 AA.
XX
AC   ABR42754;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-scFv-L5.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-scFv-15;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .261
FT                   /label= hMN-14-scFv-L5
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .255
FT                   /label= hMN-14Vkappa
FT   Region          256. .261
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
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XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032718.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
PR 08-JAN-2002; 2002US-0345641P.
PR 22-AUG-2002; 2002US-0404919P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg DM;
XX
DR WPI; 2003-513460/48.
DR N-PSDB; ACC58721.
XX
PT New multivalent, monospecific binding protein comprising two or more
PT binding sites having affinity for the same single target antigen, where
PT each binding site is associated with scFv fragments, useful for
PT diagnosing or treating tumor.
XX
PS Claim 31; Fig 11; 62pp; English.
XX
CC The present sequence is the protein sequence of hMN-14-scFv-L5, which was
CC designed to form an hMN-14 diabody. The hMN-14-scFv-L5 polypeptide
CC comprises the C-terminal end of anti-carcinoembryonic antigen (CEA)
CC humanized monoclonal antibody hMN-14 VH linked to the N-terminal part of
CC hMN-14 Vkappa by a peptide linker that enables the secreted polypeptide
CC to dimerize into a diabody, forming 2 binding sites for CEA. The
CC polypeptide also includes a pelB signal peptide, which precedes the VH
CC moiety to facilitate synthesis of the polypeptide in the periplasmic
CC space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC purification. In the claimed monospecific diabody, each scFv comprises
CC the present sequence. The diabody is an example of claimed multivalent
CC binding proteins specific for a tumour-associated antigen. The binding
CC proteins are used in the diagnosis and treatment of a tumour, carcinoma,
CC melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma or myeloma,
CC or a cancer selected from acute lymphoblastic leukaemia, acute
CC myelogenous leukaemia, biliary, breast, cervical, chronic lymphocytic
CC leukaemia, chronic myelogenous leukaemia, colorectal, endometrial,
CC oesophageal, gastric, head and neck, Hodgkin's lymphoma, lung, medullary
CC thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic, prostate and
CC bladder
XX
SQ Sequence 261 AA;

Query Match 98.0%; Score 148; DB 6; Length 261;
Best Local Similarity 96.7%; Pred. No. 3.4e-11;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
||||||||||||||||||||||||:||||||
Db 24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53

RESULT 12
ABR83645
ID ABR83645 standard; protein; 261 AA.
XX
AC ABR83645;
XX
DT 16-OCT-2003 (first entry)
XX
DE hMN14-scFv-L5 amino acid sequence.
XX
KW Multispecific binding protein; multivalent; target antigen; cytostatic;
KW immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW immunotherapy; autoimmune disease; infectious disease;
KW cardiovascular disease; inflammatory disease.
XX
OS Escherichia coli.
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003057829-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US038985.
XX
PR 26-DEC-2001; 2001US-0342103P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg D;
XX
DR WPI; 2003-607997/57.
DR N-PSDB; ACF57430.
XX
PT Novel multivalent, multi-specific binding protein useful for treating
PT cancer, has first binding site having affinity towards hapten group and
PT second and third binding sites each having affinity towards target
PT antigen.
XX
PS Claim 11; Fig 6; 43pp; English.
XX
CC The present invention describes a multivalent, multi-specific binding
CC protein (I) comprising a first binding site having an affinity towards a
CC hapten group and a second and a third binding sites each having affinity
CC towards a target antigen, which may be the same or a different target
CC antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC useful for delivering a diagnostic agent, a therapeutic agent, or its
CC combination to a target, which involves administering (I) to a subject,
CC waiting for a sufficient amount of time for an amount of the non-binding
CC protein to clear the subject's blood stream, and administering to the
CC subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC agent, or its combination, that binds to a binding site of the binding
CC protein. (I) is also useful for detecting or treating a human disorder,
CC preferably cancer, autoimmune diseases, infectious diseases,
CC cardiovascular diseases and inflammatory diseases. The present sequence
CC represents a hMN14-scFv-L5 amino acid sequence, which is used in the
CC exemplification of the present invention
XX
SQ Sequence 261 AA;

Query Match 98.0%; Score 148; DB 6; Length 261;
Best Local Similarity 96.7%; Pred. No. 3.4e-11;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
||||||||||||||||||||||||:||||||
Db 24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53

RESULT 13
ABR42292
ID ABR42292 standard; protein; 267 AA.
XX
AC ABR42292;
XX
DT 11-AUG-2003 (first entry)
XX
DE Bispecific diabody polypeptide #2.
XX
KW Diabody; antibody; carcinoembryonic antigen; CEA;
KW histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW targeting.
XX
OS Homo sapiens.
OS Mus sp.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX

```
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .267
FT                   /label= BSI_polypeptide#1
FT   Region          24. .141
FT                   /label= hMN14_VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .259
FT                   /label= 679_Vk
FT   Region          262. .267
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57806.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 31; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of a
CC   novel bispecific diabody comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen. The bispecific diabody can be produced using
CC   recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC   a novel affinity enhancement system that shows specific affinity for HSG
CC   and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC   subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC   carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             98.0%;  Score 148;  DB 6;  Length 267;
  Best Local Similarity   96.7%;  Pred. No. 3.5e-11;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||||||:||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53


RESULT 14
ABR42299
ID   ABR42299 standard; protein; 267 AA.
XX
AC   ABR42299;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS1.5H polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BS1.5H_polypeptide#2
FT   Region          24. .142
FT                   /label= hMN14_VH
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
FT                   /label= h679_Vk
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57813.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 38; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of novel
CC   bispecific diabody BS1.5H comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). A humanised version of its VH and Vk sequences
CC   have been used in BS1.5H. Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC   using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC   provides a novel affinity enhancement system that shows specific affinity
CC   for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC   tumours for subsequent specific delivery of therapeutic radioisotopes
CC   carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC   disease, cardiovascular diseases and inflammatory diseases can be
CC   detected or treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             98.0%;  Score 148;  DB 6;  Length 267;
  Best Local Similarity   96.7%;  Pred. No. 3.5e-11;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||||||:||||||
```

```
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53

RESULT 15
ABR42296
ID   ABR42296 standard; protein; 267 AA.
XX
AC   ABR42296;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS2 polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .267
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FT                   /label= 679_Vk
FT   Region          262. .267
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57810.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 35; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of novel
CC   bispecific diabody BS2 comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC   using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC   provides a novel affinity enhancement system that shows specific affinity
CC   for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC   tumours for subsequent specific delivery of therapeutic radioisotopes
CC   carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC   disease, cardiovascular diseases and inflammatory diseases can be
CC   detected or treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             98.0%;  Score 148;  DB 6;  Length 267;
  Best Local Similarity   96.7%;  Pred. No. 3.5e-11;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||:||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53


Search completed: March 25, 2006, 09:02:21
Job time : 112.701 secs
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:02:50 ; Search time 17.2775 Seconds
(without alignments)
167.067 Million cell updates/sec

Title: US-10-755-382-30
Perfect score: 151
Sequence: 1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	135	89.4	126	1	G1HUKL	Ig heavy chain V-I
2	134	88.7	97	2	S44115	Ig heavy chain V r
3	134	88.7	114	2	S46390	Ig heavy chain V r
4	133	88.1	100	2	S69896	Ig heavy chain V r
5	131	86.8	94	2	PL0120	Ig heavy chain V-I
6	131	86.8	98	2	PL0116	Ig heavy chain V-I
7	131	86.8	98	2	S29546	Ig heavy chain V r
8	131	86.8	113	2	S57410	Ig heavy chain V-J
9	131	86.8	113	2	S38490	Ig heavy chain - h
10	131	86.8	118	2	S31116	Ig heavy chain - h
11	131	86.8	119	2	S31111	Ig heavy chain - h
12	131	86.8	119	2	F36005	Ig heavy chain V r
13	131	86.8	120	2	S31112	Ig heavy chain - h
14	131	86.8	121	2	G36005	Ig heavy chain V r
15	131	86.8	122	2	S31117	Ig heavy chain - h
16	131	86.8	122	2	E36005	Ig heavy chain V r
17	131	86.8	122	2	S31119	Ig heavy chain - h
18	131	86.8	128	2	S48797	Ig heavy chain V r
19	131	86.8	130	2	S31601	Ig heavy chain V r
20	131	86.8	130	2	PL0098	Ig heavy chain pre
21	131	86.8	132	2	S31603	Ig heavy chain V r
22	131	86.8	133	2	S31590	Ig heavy chain V r
23	131	86.8	133	2	A49028	Ig heavy chain V-I
24	131	86.8	134	2	S31679	Ig heavy chain V r
25	131	86.8	137	2	S31701	Ig heavy chain V r
26	131	86.8	139	2	S31674	Ig heavy chain V r
27	130	86.1	98	2	S26927	Ig heavy chain V r
28	130	86.1	121	2	S31118	Ig heavy chain - h
29	130	86.1	121	2	S31104	Ig heavy chain (su
30	130	86.1	123	2	S30532	Ig heavy chain V r
31	130	86.1	128	2	S31595	Ig heavy chain V r
32	130	86.1	145	2	S11239	Ig heavy chain V r
33	129	85.4	96	2	PH0873	Ig heavy chain V r
34	128	84.8	116	1	M3HUGL	Ig heavy chain V-I
35	128	84.8	119	1	G1HUNI	Ig heavy chain V-I
36	128	84.8	121	2	S19666	Ig heavy chain V r
37	126	83.4	98	2	S54856	Ig heavy chain V r
38	126	83.4	121	2	S26798	Ig heavy chain V r
39	126	83.4	122	1	M3HUAM	Ig heavy chain V-I
40	125	82.8	115	2	S57445	Ig heavy chain V-J
41	125	82.8	118	2	A47329	Ig heavy chain V r
42	125	82.8	119	2	S24491	Ig heavy chain V r
43	125	82.8	119	2	S24524	Ig heavy chain V r
44	125	82.8	119	2	S24511	Ig heavy chain V r
45	125	82.8	119	2	S24520	Ig heavy chain V r

ALIGNMENTS

RESULT 1
G1HUKL
Ig heavy chain V-III region (Kol) - human
C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C;Accession: A02055
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KO
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Accession: A02055
A;Molecule type: protein
A;Residues: 1-126 <SCH>
A;Cross-references: UNIPROT:P01772; UNIPARC:UPI000002D0C3
C;Genetics:
A;Gene: GDB:IGHV@
A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;15-98/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96,105-110/Disulfide bonds: #status experimental

Query Match 89.4%; Score 135; DB 1; Length 126;
Best Local Similarity 90.0%; Pred. No. 3e-11;
Matches 27; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|||||||||||||||||||||||||||| |:
Db          1 QVQLVESGGGVVQPGRSLRLSCSSSGFIFS 30
```

RESULT 2
S44115
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44115
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
A;Accession: S44115
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <HAW>
A;Cross-references: UNIPARC:UPI000011662B; EMBL:Z31384; NID:g472969; PIDN:CAA83259.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 88.7%; Score 134; DB 2; Length 97;

```
  Best Local Similarity   86.7%;  Pred. No. 3.2e-11;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||::||| |:
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 3
S46390
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46390
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46390
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <FIG>
A;Cross-references: UNIPARC:UPI000011663F; EMBL:Z31686; NID:g509782; PIDN:CAA83491.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             88.7%;  Score 134;  DB 2;  Length 114;
  Best Local Similarity   86.7%;  Pred. No. 3.7e-11;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||::||| |:
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 4
S69896
Ig heavy chain V region (clone RFKL5H), rheumatoid factor - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: S69896
R;Randen, I.; Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig, J
Eur. J. Immunol. 23, 1220-1225, 1993
A;Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune respo
A;Reference number: S69896; MUID:93272805; PMID:8500520
A;Accession: S69896
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-100 <RAN>
A;Cross-references: UNIPARC:UPI0000116198; EMBL:X73605; NID:g509797; PIDN:CAA51998.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             88.1%;  Score 133;  DB 2;  Length 100;
  Best Local Similarity   86.2%;  Pred. No. 4.5e-11;
  Matches   25;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDF 29
              |||||||||:|||||||||||::|||:|
Db          1 EVQLVESGGGLVQPGRSLRLSCAASGFEF 29


RESULT 5
PL0120
Ig heavy chain V-III region (TD-Vo) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 31-Dec-2004
C;Accession: PL0120
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A;Reference number: PL0116; MUID:88286083; PMID:2840480
A;Accession: PL0120
A;Molecule type: mRNA
A;Residues: 1-94 <BIR>
A;Cross-references: UNIPROT:Q8WUK1; UNIPROT:Q9UL93; UNIPARC:UPI0000176A2C
A;Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A;Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement f
C;Superfamily: immunoglobulin homology
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2

  Query Match             86.8%;  Score 131;  DB 2;  Length 94;
  Best Local Similarity   83.3%;  Pred. No. 7.9e-11;
  Matches   25;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|||||||||||||||||||::||| |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 6
PL0116
Ig heavy chain V-III region (AW-Vx) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PL0116; S26892
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A;Reference number: PL0116; MUID:88286083; PMID:2840480
A;Accession: PL0116
A;Molecule type: mRNA
A;Residues: 1-98 <BIR>
A;Cross-references: UNIPARC:UPI0000031F3A
A;Experimental source: B cells from patient AW with acute lymphoblastic leukemia, ALL
A;Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA rearrangement f
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26892
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI0000031F3A; EMBL:Z12349; NID:g32918; PIDN:CAA78219.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2

  Query Match             86.8%;  Score 131;  DB 2;  Length 98;
  Best Local Similarity   83.3%;  Pred. No. 8.3e-11;
  Matches   25;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|||||||||||||||||||::||| |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 7
S29546
Ig heavy chain V region (COS-8 / DP-46) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29546; S26888
R;Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Accession: S29546
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI000002DD16; EMBL:Z17394; NID:g32843; PIDN:CAA78997.1; PI
```

```
A;Note: designated COS-8
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TO2>
A;Cross-references: UNIPARC:UPI000002DD16; EMBL:Z12346; NID:g32912; PIDN:CAA78216.1; PID
A;Note: designated DP-46
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.8%;  Score 131;  DB 2;  Length 98;
  Best Local Similarity   83.3%;  Pred. No. 8.3e-11;
  Matches   25;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|||||||||||||||||||::|||  |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 8
S57410
Ig heavy chain V-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S57410
R;Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.
submitted to the EMBL Data Library, June 1995
A;Description: Analysis of anti-GM1 ganglioside IgM antibodies cloned from motor neuropa
A;Reference number: S57408
A;Accession: S57410
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <PAT>
A;Cross-references: UNIPARC:UPI00001137A9; EMBL:X87893; NID:g871363; PIDN:CAA61144.1; PI
C;Genetics:
A;Introns: 99/2
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.8%;  Score 131;  DB 2;  Length 113;
  Best Local Similarity   83.3%;  Pred. No. 9.5e-11;
  Matches   25;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|||||||||||||||||||::|||  |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 9
S38490
Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38490
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a p
A;Reference number: S38488
A;Accession: S38490
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <MAR>
A;Cross-references: UNIPARC:UPI0000116549; EMBL:Z23030; NID:g414027; PIDN:CAA80565.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.8%;  Score 131;  DB 2;  Length 113;
  Best Local Similarity   83.3%;  Pred. No. 9.5e-11;
  Matches   25;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|||||||||||||||||||::|||  |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 10
S31116
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C;Accession: S31116
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31116
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-118 <RAA>
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176E37; EMBL:X62966
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.8%;  Score 131;  DB 2;  Length 118;
  Best Local Similarity   83.3%;  Pred. No. 9.9e-11;
  Matches   25;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|||||||||||||||||||::|||  |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 11
S31111
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31111
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31111
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-119 <RAA>
A;Cross-references: UNIPARC:UPI0000176DC2; EMBL:X62959
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.8%;  Score 131;  DB 2;  Length 119;
  Best Local Similarity   83.3%;  Pred. No. 1e-10;
  Matches   25;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|||||||||||||||||||::|||  |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 12
F36005
Ig heavy chain V region (M49) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 31-Dec-2004
C;Accession: F36005
R;Schroeder Jr., H.W.; Wang, J.Y.
```

```
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: F36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C32; GB:M34026
C;Genetics:
A;Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.8%;  Score 131;  DB 2;  Length 119;
  Best Local Similarity   83.3%;  Pred. No. 1e-10;
  Matches   25;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|||||||||||||||||||::|||  |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 13
S31112
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31112
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31112
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-120 <RAA>
A;Cross-references: UNIPARC:UPI0000176C8C; EMBL:X62961
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.8%;  Score 131;  DB 2;  Length 120;
  Best Local Similarity   83.3%;  Pred. No. 1e-10;
  Matches   25;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|||||||||||||||||||::|||  |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 14
G36005
Ig heavy chain V region (M74) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 31-Dec-2004
C;Accession: G36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: G36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C2C; GB:M34031
C;Genetics:
A;Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.8%;  Score 131;  DB 2;  Length 121;
  Best Local Similarity   83.3%;  Pred. No. 1e-10;
  Matches   25;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|||||||||||||||||||::|||  |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 15
S31117
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31117
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman,
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third compleme
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31117
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-122 <RAA>
A;Cross-references: UNIPARC:UPI0000176C8D; EMBL:X62967
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             86.8%;  Score 131;  DB 2;  Length 122;
  Best Local Similarity   83.3%;  Pred. No. 1e-10;
  Matches   25;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|||||||||||||||||||::|||  |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


Search completed: March 25, 2006, 09:15:45
Job time : 17.2775 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:40 ; Search time 108.063 Seconds
(without alignments)
195.866 Million cell updates/sec

Title: US-10-755-382-30
Perfect score: 151
Sequence: 1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	135	89.4	126	1	HV3K_HUMAN	P01772 homo sapien
2	132	87.4	470	2	Q68CN4_HUMAN	Q68cn4 homo sapien
3	131	86.8	613	2	Q8WUK1_HUMAN	Q8wuk1 homo sapien
4	130	86.1	472	2	Q6N089_HUMAN	Q6n089 homo sapien
5	130	86.1	475	2	Q5EFE5_HUMAN	Q5efe5 homo sapien
6	130	86.1	573	2	Q8WU38_HUMAN	Q8wu38 homo sapien
7	129	85.4	116	2	Q9UL93_HUMAN	Q9ul93 homo sapien
8	128	84.8	116	1	HV3T_HUMAN	P01781 homo sapien
9	128	84.8	119	1	HV3I_HUMAN	P01770 homo sapien
10	128	84.8	461	2	Q5M7V3_RAT	Q5m7v3 rattus norv
11	128	84.8	479	2	Q5BK12_RAT	Q5bk12 rattus norv
12	127	84.1	113	2	Q9UL90_HUMAN	Q9ul90 homo sapien
13	126	83.4	122	1	HV3G_HUMAN	P01768 homo sapien
14	126	83.4	122	2	Q9UL84_HUMAN	Q9ul84 homo sapien
15	126	83.4	465	2	Q5I0J0_RAT	Q5i0j0 rattus norv
16	125	82.8	120	1	HV3U_HUMAN	P01782 homo sapien
17	125	82.8	479	2	Q5PQK9_RAT	Q5pqk9 rattus norv
18	124	82.1	117	1	HV17_MOUSE	P01786 mus musculu
19	124	82.1	118	2	Q9UL91_HUMAN	Q9ul91 homo sapien
20	124	82.1	119	1	HV3P_HUMAN	P01777 homo sapien
21	124	82.1	120	1	HV3E_HUMAN	P01766 homo sapien
22	124	82.1	478	2	Q6PI81_HUMAN	Q6pi81 homo sapien
23	123	81.5	122	1	HV3H_HUMAN	P01769 homo sapien
24	123	81.5	473	2	Q6MZV7_HUMAN	Q6mzv7 homo sapien
25	122	80.8	117	1	HV3O_HUMAN	P01776 homo sapien
26	122	80.8	147	2	Q9Y509_HUMAN	Q9y509 homo sapien
27	122	80.8	467	2	Q4VBH1_RAT	Q4vbh1 rattus norv
28	122	80.8	493	2	Q6GMX2_HUMAN	Q6gmx2 homo sapien
29	122	80.8	499	2	Q8N5K4_HUMAN	Q8n5k4 homo sapien
30	122	80.8	597	2	Q96BB9_HUMAN	Q96bb9 homo sapien
31	121	80.1	115	1	HV3D_HUMAN	P01765 homo sapien
32	121	80.1	116	1	HV36_MOUSE	P01806 mus musculu
33	121	80.1	116	1	HV3R_HUMAN	P01779 homo sapien
34	121	80.1	117	1	HV3C_HUMAN	P01764 homo sapien
35	121	80.1	117	1	HV41_MOUSE	P01811 mus musculu
36	121	80.1	118	1	HV3V_HUMAN	P80419 homo sapien
37	121	80.1	119	1	HV37_MOUSE	P01807 mus musculu
38	121	80.1	119	1	HV38_MOUSE	P01808 mus musculu
39	121	80.1	119	1	HV3M_HUMAN	P01774 homo sapien
40	121	80.1	119	1	HV40_MOUSE	P01810 mus musculu
41	121	80.1	236	2	Q6ZP85_HUMAN	Q6zp85 homo sapien
42	121	80.1	476	2	Q4V9Z4_MOUSE	Q4v9z4 mus musculu
43	121	80.1	483	2	Q566J7_MOUSE	Q566j7 mus musculu
44	120	79.5	112	2	Q9HCC1_HUMAN	Q9hcc1 homo sapien
45	120	79.5	121	2	Q9UL71_HUMAN	Q9ul71 homo sapien

ALIGNMENTS

```
RESULT 1
HV3K_HUMAN
ID   HV3K_HUMAN     STANDARD;      PRT;   126 AA.
AC   P01772;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region KOL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE, AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6884994;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=81072295; PubMed=7441755;
RA   Marquart M., Deisenhofer J., Huber R., Palm W.;
RT   "Crystallographic refinement and atomic models of the intact
RT   immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
RT   and 1.0-A resolution.";
RL   J. Mol. Biol. 141:369-391(1980).
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A02055; G1HUKL.
DR   PDB; 2FB4; X-ray; H=2-126.
DR   PDB; 2IG2; X-ray; H=2-126.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   DISULFID     22     96
FT   DISULFID    105    110
FT   NON_TER     126    126
FT   STRAND        3      7
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FT   STRAND       11     12
FT   TURN         14     15
FT   STRAND       18     25
FT   HELIX        29     31
FT   STRAND       34     39
FT   TURN         41     42
FT   STRAND       45     51
FT   TURN         53     54
FT   STRAND       58     60
FT   HELIX        62     64
FT   STRAND       65     65
FT   TURN         66     67
FT   STRAND       68     73
FT   TURN         74     77
FT   STRAND       78     83
FT   HELIX        88     90
FT   STRAND       92     99
FT   STRAND      106    106
FT   TURN        107    108
FT   STRAND      109    109
FT   STRAND      113    116
FT   STRAND      120    124
SQ   SEQUENCE   126 AA;  13718 MW;  E4D71B52B16F8776 CRC64;

  Query Match             89.4%;  Score 135;  DB 1;  Length 126;
  Best Local Similarity   90.0%;  Pred. No. 1.7e-10;
  Matches   27;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|||||||||||||||||||||||||| |:
Db          1 QVQLVESGGGVVQPGRSLRLSCSSSGFIFS 30


RESULT 2
Q68CN4_HUMAN
ID   Q68CN4_HUMAN PRELIMINARY;      PRT;   470 AA.
AC   Q68CN4;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein DKFZp686E23209.
GN   Name=DKFZp686E23209;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Rectum tumor;
RG   The German cDNA Consortium;
RA   Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA   Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CR749861; CAH18705.2; -; mRNA.
DR   SMR; Q68CN4; 43-493.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   470 AA;  51536 MW;  7CB061DFC03D0B2B CRC64;

  Query Match             87.4%;  Score 132;  DB 2;  Length 470;
  Best Local Similarity   80.0%;  Pred. No. 1.7e-09;
  Matches   24;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|||||||||||||||:|:||||::|||||:
Db         20 QVQLVESGGGVVQPGKSVRLSCAASGFDFS 49


RESULT 3
Q8WUK1_HUMAN
ID   Q8WUK1_HUMAN PRELIMINARY;      PRT;   613 AA.
AC   Q8WUK1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
GN   Name=IGHM;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RG   NIH MGC Project;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2117273;
RA   Schroeder H.W. Jr, Wang J.Y.;
RT   "Preferential utilization of conserved immunoglobulin heavy chain
RT   variable gene segments during human fetal life.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1383695; DOI=10.1016/0161-5890(92)90173-U;
RA   Cuisinier A.M., Fumoux F., Fougereau M., Tonnelle C.;
RT   "IGM kappa/lambda EBV human B cell clone: an early step of
RT   differentiation of fetal B cells or a distinct B lineage?";
RL   Mol. Immunol. 29:1363-1373(1992).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1730252;
RA   Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA   Schuurman R.K.;
RT   "Restricted utilization of germ-line VH3 genes and short diverse third
RT   complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT   immunoglobulin heavy chain rearrangements.";
RL   Eur. J. Immunol. 22:247-251(1992).
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RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1904154;
RA   Neale G.A., Kitchingman G.R.;
RT   "mRNA transcripts initiating within the human immunoglobulin mu heavy
RT   chain enhancer region contain a non-translatable exon and are
RT   extremely heterogeneous at the 5' end.";
RL   Nucleic Acids Res. 19:2427-2433(1991).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2840480; DOI=10.1084/jem.168.1.229;
RA   Bird J., Galili N., Link M., Stites D., Sklar J.;
RT   "Continuing rearrangement but absence of somatic hypermutation in
RT   immunoglobulin genes of human B cell precursor leukemia.";
RL   J. Exp. Med. 168:229-245(1988).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2538551; DOI=10.1084/jem.169.4.1391;
RA   Nickerson K.G., Berman J., Glickman E., Chess L., Alt F.W.;
RT   "Early human IgH gene assembly in Epstein-Barr virus-transformed fetal
RT   B cell lines. Preferential utilization of the most JH-proximal D
RT   segment (DQ52) and two unusual VH-related rearrangements.";
RL   J. Exp. Med. 169:1391-1403(1989).
RN   [9]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA   Hillson J.L., Karr N.S., Oppliger I.R., Mannik M., Sasso E.H.;
RT   "The structural basis of germline-encoded VH3 immunoglobulin binding
RT   to staphylococcal protein A.";
RL   J. Exp. Med. 178:331-336(1993).
DR   EMBL; BC020240; AAH20240.1; -; mRNA.
DR   PIR; F36005; F36005.
DR   PIR; G36005; G36005.
DR   PIR; PH1642; PH1642.
DR   PIR; PH1643; PH1643.
DR   PIR; PH1645; PH1645.
DR   PIR; PH1646; PH1646.
DR   PIR; PL0098; PL0098.
DR   PIR; PL0120; PL0120.
DR   PIR; S15590; S15590.
DR   PIR; S31116; S31116.
DR   PIR; S31119; S31119.
DR   PIR; S70442; S70442.
DR   HSSP; P01861; 1ADQ.
DR   SMR; Q8WUK1; 20-242.
DR   Ensembl; ENSG00000130076; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Immunoglobulin domain.
SQ   SEQUENCE   613 AA;  67296 MW;  60C7F5950671E315 CRC64;

  Query Match             86.8%;  Score 131;  DB 2;  Length 613;
  Best Local Similarity   83.3%;  Pred. No. 3e-09;
  Matches   25;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|||||||||||||||||||||::||| |:
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 49


RESULT 4
Q6N089_HUMAN
ID   Q6N089_HUMAN PRELIMINARY;      PRT;   472 AA.
AC   Q6N089;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686P15220.
GN   Name=DKFZp686P15220;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Rectum tumor;
RG   The German cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640627; CAE45781.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA;  51724 MW;  26CB340D0046D279 CRC64;

  Query Match             86.1%;  Score 130;  DB 2;  Length 472;
  Best Local Similarity   86.2%;  Pred. No. 3.2e-09;
  Matches   25;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDF 29
              |||||||||||:|||||||||||::||| |
Db         20 EVQLVESGGGLVQPGRSLRLSCAASGFTF 48


RESULT 5
Q5EFE5_HUMAN
ID   Q5EFE5_HUMAN PRELIMINARY;      PRT;   475 AA.
AC   Q5EFE5;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Anti-RhD monoclonal T125 gamma1 heavy chain precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Gaucher C., Klein P., Beliard R.;
RT   "Sequence determination of the recombinant human anti-RhD monoclonal
RT   antibody T125.";
RL   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY894992; AAW82028.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF07686; V-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Signal.
FT   SIGNAL        1     19       Potential.
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FT   CHAIN        20    475       anti-RhD monoclonal T125 gamma1 heavy
FT                                chain.
SQ   SEQUENCE   475 AA;  52362 MW;  1367D400DC7D2859 CRC64;

  Query Match             86.1%;  Score 130;  DB 2;  Length 475;
  Best Local Similarity   86.2%;  Pred. No. 3.2e-09;
  Matches   25;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDF 29
              :|||||||||||||||||||::||| |
Db         20 QVQLVESGGGVVQPGRSLRLSCTASGFTF 48


RESULT 6
Q8WU38_HUMAN
ID   Q8WU38_HUMAN PRELIMINARY;      PRT;   573 AA.
AC   Q8WU38;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHD protein.
GN   Name=IGHD;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RA   Director MGC Project;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   PROTEIN SEQUENCE.
RX   PubMed=1555592;
RA   Makiya R., Stigbrand T.;
RT   "Placental alkaline phosphatase has a binding site for the human
RT   immunoglobulin-G Fc portion.";
RL   Eur. J. Biochem. 205:341-345(1992).
DR   EMBL; BC021276; AAH21276.1; -; mRNA.
DR   PIR; S21205; S21205.
DR   PIR; S30532; S30532.
DR   HSSP; P18529; 1I8K.
DR   Ensembl; ENSG00000196122; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Immunoglobulin domain; Repeat.
SQ   SEQUENCE   573 AA;  62967 MW;  FD072344033AC530 CRC64;

  Query Match             86.1%;  Score 130;  DB 2;  Length 573;
  Best Local Similarity   86.2%;  Pred. No. 3.9e-09;
  Matches   25;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDF 29
              ||||||||||:|||||||||||::||| |
Db         20 EVQLVESGGGLVQPGRSLRLSCAASGFTF 48


RESULT 7
Q9UL93_HUMAN
ID   Q9UL93_HUMAN PRELIMINARY;      PRT;   116 AA.
AC   Q9UL93;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA   Hillson J.L., Karr N.S., Oppliger I.R., Mannik M., Sasso E.H.;
RT   "The structural basis of germline-encoded VH3 immunoglobulin binding
RT   to staphylococcal protein A.";
RL   J. Exp. Med. 178:331-336(1993).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2840480;
RA   Bird J., Galili N., Link M., Stites D., Sklar J.;
RT   "Continuing rearrangement but absence of somatic hypermutation in
RT   immunoglobulin genes of human B cell precursor leukemia.";
RL   J. Exp. Med. 168:229-245(1988).
DR   EMBL; AF035021; AAD56257.1; -; mRNA.
DR   PIR; PH1644; PH1644.
DR   PIR; PL0120; PL0120.
DR   HSSP; P01772; 2FB4.
DR   SMR; Q9UL93; 1-116.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12434 MW;  0DA0348154DD6061 CRC64;

  Query Match             85.4%;  Score 129;  DB 2;  Length 116;
  Best Local Similarity   86.2%;  Pred. No. 1e-09;
  Matches   25;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||::||| |:
Db          1 VQLVESGGGVVQPGRSLRLSCAASGFTFS 29
```

```
RESULT 8
HV3T_HUMAN
ID   HV3T_HUMAN     STANDARD;      PRT;   116 AA.
AC   P01781;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region GAL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=75059123; PubMed=4803843;
RA   Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT   "The primary structure of a monoclonal IgM-immunoglobulin
RT   (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT   type), subgroup H III. Architecture of the complete IgM-molecule.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN   [2]
RP   SEQUENCE REVISION TO 28-33.
RA   Hilschmann N.;
RL   Submitted (JUN-1975) to the PIR data bank.
CC   -!- MISCELLANEOUS: This mu chain was isolated from a Waldenstrom's
CC       macroglobulin.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A02064; M3HUGL.
DR   HSSP; P01772; 2FB4.
DR   SMR; P01781; 1-116.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    112       Ig-like.
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12731 MW;  2C67CA9AAAAA1282 CRC64;

  Query Match             84.8%;  Score 128;  DB 1;  Length 116;
  Best Local Similarity   82.8%;  Pred. No. 1.4e-09;
  Matches   24;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDF 29
              ||||||||| :|||||||||||::|||:|
Db          1 EVQLVESGGDLVQPGRSLRLSCAASGFBF 29


RESULT 9
HV3I_HUMAN
ID   HV3I_HUMAN     STANDARD;      PRT;   119 AA.
AC   P01770;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region NIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT   peptides of the H-chain, alignment of the tryptic peptides and
RT   discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT   characterization of the protein, the L- and H-chains, the cyanogen
RT   bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC       protein.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A91668; G1HUNI.
DR   HSSP; P01772; 2FB4.
DR   SMR; P01770; 1-119.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   DISULFID     22     96
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13243 MW;  C96935A6E55E165B CRC64;

  Query Match             84.8%;  Score 128;  DB 1;  Length 119;
  Best Local Similarity   80.0%;  Pred. No. 1.5e-09;
  Matches   24;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :||||:||||||||||||||::||| |:
Db          1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 10
Q5M7V3_RAT
ID   Q5M7V3_RAT  PRELIMINARY;      PRT;   461 AA.
AC   Q5M7V3;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   LOC367586 protein.
GN   Name=LOC367586;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
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RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RG   NIH MGC Project;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC       histocompatibility complex class I molecules (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; BC088423; AAH88423.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
KW   Immunoglobulin domain; Repeat.
SQ   SEQUENCE   461 AA;  50949 MW;  25EA4ECE6FE0F5A9 CRC64;

  Query Match             84.8%;  Score 128;  DB 2;  Length 461;
  Best Local Similarity   80.0%;  Pred. No. 5.9e-09;
  Matches   24;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              ||||||||||:|||||||:|||::||| |:
Db         20 EVQLVESGGGLVQPGRSLKLSCAASGFTFS 49


RESULT 11
Q5BK12_RAT
ID   Q5BK12_RAT  PRELIMINARY;      PRT;   479 AA.
AC   Q5BK12;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Igha protein.
GN   Name=Igha;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RG   NIH MGC Project;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC091247; AAH91247.1; -; mRNA.
DR   SMR; Q5BK12; 20-241.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   479 AA;  52329 MW;  8B146164AE8437C5 CRC64;

  Query Match             84.8%;  Score 128;  DB 2;  Length 479;
  Best Local Similarity   80.0%;  Pred. No. 6.1e-09;
  Matches   24;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              ||||||||||:|||||||:|||::||| |:
Db         20 EVQLVESGGGLVQPGRSLKLSCTASGFTFS 49


RESULT 12
Q9UL90_HUMAN
ID   Q9UL90_HUMAN PRELIMINARY;      PRT;   113 AA.
AC   Q9UL90;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1730252;
RA   Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA   Schuurman R.K.;
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RT   "Restricted utilization of germ-line VH3 genes and short diverse third
RT   complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT   immunoglobulin heavy chain rearrangements.";
RL   Eur. J. Immunol. 22:247-251(1992).
DR   EMBL; AF035024; AAD56260.1; -; mRNA.
DR   PIR; S78486; S78486.
DR   HSSP; P01772; 2FB4.
DR   SMR; Q9UL90; 1-113.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     113    113
SQ   SEQUENCE   113 AA;  12437 MW;  ED57FDD19086D07F CRC64;

  Query Match             84.1%;  Score 127;  DB 2;  Length 113;
  Best Local Similarity   83.3%;  Pred. No. 1.9e-09;
  Matches   25;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||| ||||||::||| |:
Db          1 EVQLVESGGGVVQPGGSLRLSCAASGFTFS 30


RESULT 13
HV3G_HUMAN
ID   HV3G_HUMAN     STANDARD;      PRT;   122 AA.
AC   P01768;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region CAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=81013859; PubMed=6774332;
RA   Lehman D.W., Putnam F.W.;
RT   "Amino acid sequence of the variable region of a human mu chain:
RT   location of a possible JH segment.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC   -!- MISCELLANEOUS: This mu chain was isolated from the plasma of a
CC       patient with macroglobulinemia.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A02051; M3HUAM.
DR   HSSP; P01772; 2FB4.
DR   SMR; P01768; 2-122.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13668 MW;  A42D0F17D252F1C2 CRC64;

  Query Match             83.4%;  Score 126;  DB 1;  Length 122;
  Best Local Similarity   76.7%;  Pred. No. 2.8e-09;
  Matches   23;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              :|:|||||||||:||||||||::||| |:
Db          1 QVELVESGGGVVZPGRSLRLSCAASGFTFS 30


RESULT 14
Q9UL84_HUMAN
ID   Q9UL84_HUMAN PRELIMINARY;      PRT;   122 AA.
AC   Q9UL84;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035030; AAD56266.1; -; mRNA.
DR   HSSP; P01772; 2FB4.
DR   SMR; Q9UL84; 1-122.
DR   Ensembl; ENSG00000130076; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13579 MW;  36054D41366545B8 CRC64;

  Query Match             83.4%;  Score 126;  DB 2;  Length 122;
  Best Local Similarity   83.3%;  Pred. No. 2.8e-09;
  Matches   25;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

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Db          1 EVQLVESGGGVVQPGRSLRLSCAASRFTFS 30


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ID   Q5I0J0_RAT  PRELIMINARY;      PRT;   465 AA.
AC   Q5I0J0;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical LOC299354.
GN   Name=LOC299354;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Thymus;
RG NIH MGC Project;
RL Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC histocompatibility complex class I molecules (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR EMBL; BC088271; AAH88271.1; -; mRNA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 2.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
KW Hypothetical protein; Immunoglobulin domain; Repeat.
SQ SEQUENCE 465 AA; 51699 MW; 97C4533A213A424F CRC64;

Query Match 83.4%; Score 126; DB 2; Length 465;
Best Local Similarity 76.7%; Pred. No. 1.1e-08;
Matches 23; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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Search completed: March 25, 2006, 09:13:50
Job time : 109.063 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: March 25, 2006, 09:14:16 ; Search time 27.3298 Seconds
(without alignments)
90.753 Million cell updates/sec

Title: US-10-755-382-30
Perfect score: 151
Sequence: 1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	151	100.0	30	1	US-08-318-157B-30	Sequence 30, Appl
2	151	100.0	30	2	US-09-253-794-30	Sequence 30, Appl
3	151	100.0	119	1	US-08-318-157B-12	Sequence 12, Appl
4	151	100.0	119	1	US-08-318-157B-17	Sequence 17, Appl
5	151	100.0	119	2	US-09-253-794-12	Sequence 12, Appl
6	151	100.0	119	2	US-09-253-794-17	Sequence 17, Appl
7	148	98.0	30	1	US-08-318-157B-31	Sequence 31, Appl
8	148	98.0	30	2	US-09-253-794-31	Sequence 31, Appl
9	148	98.0	119	1	US-08-318-157B-13	Sequence 13, Appl
10	148	98.0	119	1	US-08-318-157B-14	Sequence 14, Appl
11	148	98.0	119	1	US-08-318-157B-15	Sequence 15, Appl
12	148	98.0	119	2	US-09-253-794-13	Sequence 13, Appl
13	148	98.0	119	2	US-09-253-794-14	Sequence 14, Appl
14	148	98.0	119	2	US-09-253-794-15	Sequence 15, Appl
15	148	98.0	489	4	PCT-US95-11405-35	Sequence 35, Appl
16	140	92.7	117	1	US-08-652-558-3	Sequence 3, Appli
17	140	92.7	117	1	US-08-652-558-45	Sequence 45, Appl
18	140	92.7	117	1	US-08-652-558-46	Sequence 46, Appl
19	140	92.7	119	1	US-08-859-649-20	Sequence 20, Appl
20	140	92.7	119	1	US-08-859-649-22	Sequence 22, Appl
21	140	92.7	119	1	US-08-859-649-23	Sequence 23, Appl
22	140	92.7	119	1	US-08-859-649-24	Sequence 24, Appl
23	140	92.7	119	1	US-08-859-649-31	Sequence 31, Appl
24	140	92.7	119	2	US-08-207-861-20	Sequence 20, Appl
25	140	92.7	119	2	US-08-207-861-22	Sequence 22, Appl
26	140	92.7	119	2	US-08-207-861-23	Sequence 23, Appl
27	140	92.7	119	2	US-08-207-861-24	Sequence 24, Appl
28	140	92.7	119	2	US-08-207-861-31	Sequence 31, Appl
29	140	92.7	119	2	US-08-859-648-20	Sequence 20, Appl
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31	140	92.7	119	2	US-08-859-648-23	Sequence 23, Appl
32	140	92.7	119	2	US-08-859-648-24	Sequence 24, Appl
33	140	92.7	119	2	US-08-859-648-31	Sequence 31, Appl
34	138	91.4	119	1	US-08-303-569B-11	Sequence 11, Appl
35	138	91.4	119	1	US-08-303-569B-21	Sequence 21, Appl
36	138	91.4	119	1	US-08-318-157B-58	Sequence 58, Appl
37	138	91.4	119	1	US-08-070-116A-12	Sequence 12, Appl
38	138	91.4	119	1	US-08-116-247-12	Sequence 12, Appl
39	138	91.4	119	1	US-08-116-247-22	Sequence 22, Appl
40	138	91.4	119	2	US-08-557-050-12	Sequence 12, Appl
41	138	91.4	119	2	US-09-795-515-11	Sequence 11, Appl
42	138	91.4	119	2	US-09-795-515-21	Sequence 21, Appl
43	138	91.4	119	2	US-09-253-794-58	Sequence 58, Appl
44	138	91.4	119	2	US-09-348-224-12	Sequence 12, Appl
45	138	91.4	119	2	US-09-348-224-22	Sequence 22, Appl

ALIGNMENTS

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RESULT 1
US-08-318-157B-30
; Sequence 30, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-30

  Query Match           100.0%;  Score 151;  DB 1;  Length 30;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
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RESULT 2
US-09-253-794-30
; Sequence 30, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 30:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 30 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-253-794-30

  Query Match             100.0%;  Score 151;  DB 2;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 3
US-08-318-157B-12
; Sequence 12, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-12

  Query Match             100.0%;  Score 151;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 4
US-08-318-157B-17
; Sequence 17, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-17

  Query Match             100.0%;  Score 151;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 5
US-09-253-794-12
; Sequence 12, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-253-794-12

  Query Match             100.0%;  Score 151;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
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Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 6
US-09-253-794-17
; Sequence 17, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-253-794-17

  Query Match             100.0%;  Score 151;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
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Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 7
US-08-318-157B-31
; Sequence 31, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/318,157B
;       FILING DATE:  05-OCT-1994
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  SAXE, Bernhard D.
;       REGISTRATION NUMBER:  28,665
;       REFERENCE/DOCKET NUMBER:  18733/464
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)672-5300
;       TELEFAX:  (202)672-5399
;       TELEX:  904136
;   INFORMATION FOR SEQ ID NO:  31:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  30 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-318-157B-31

  Query Match             98.0%;  Score 148;  DB 1;  Length 30;
  Best Local Similarity   96.7%;  Pred. No. 6.3e-14;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 8
US-09-253-794-31
; Sequence 31, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 31:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 30 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-253-794-31

  Query Match             98.0%;  Score 148;  DB 2;  Length 30;
  Best Local Similarity   96.7%;  Pred. No. 6.3e-14;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 9
US-08-318-157B-13
; Sequence 13, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-13

  Query Match             98.0%;  Score 148;  DB 1;  Length 119;
  Best Local Similarity   96.7%;  Pred. No. 2.9e-13;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 10
US-08-318-157B-14
; Sequence 14, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
```

```
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-14

  Query Match             98.0%;  Score 148;  DB 1;  Length 119;
  Best Local Similarity   96.7%;  Pred. No. 2.9e-13;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 11
US-08-318-157B-15
; Sequence 15, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-15

  Query Match             98.0%;  Score 148;  DB 1;  Length 119;
  Best Local Similarity   96.7%;  Pred. No. 2.9e-13;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 12
US-09-253-794-13
; Sequence 13, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-253-794-13

  Query Match             98.0%;  Score 148;  DB 2;  Length 119;
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  Best Local Similarity   96.7%;  Pred. No. 2.9e-13;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 13
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

  Query Match             98.0%;  Score 148;  DB 2;  Length 119;
  Best Local Similarity   96.7%;  Pred. No. 2.9e-13;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 14
US-09-253-794-15
; Sequence 15, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-253-794-15

  Query Match             98.0%;  Score 148;  DB 2;  Length 119;
  Best Local Similarity   96.7%;  Pred. No. 2.9e-13;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
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Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 15
PCT-US95-11405-35
; Sequence 35, Application PC/TUS9511405
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  PHOSPHOROUS-32 LABELING OF ANTIBODIES
;    TITLE OF INVENTION:  FOR CANCER THERAPY
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/11405
;      FILING DATE:  18-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/308,103
;      FILING DATE:  16-SEP-1994
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/599/IMIN
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  489 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-11405-35

  Query Match             98.0%;  Score 148;  DB 4;  Length 489;
  Best Local Similarity   96.7%;  Pred. No. 1.4e-12;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||:||||||
Db         23 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 52


Search completed: March 25, 2006, 09:18:45
Job time : 27.3298 secs
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:55:36 ; Search time 89.5288 Seconds
(without alignments)
140.009 Million cell updates/sec

Title: US-10-755-382-30
Perfect score: 151
Sequence: 1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	151	100.0	30	3	US-09-253-794-30	Sequence 30, Appl
2	151	100.0	30	5	US-10-755-382-30	Sequence 30, Appl
3	151	100.0	119	3	US-09-253-794-12	Sequence 12, Appl
4	151	100.0	119	3	US-09-253-794-17	Sequence 17, Appl
5	151	100.0	119	4	US-10-680-734-12	Sequence 12, Appl
6	151	100.0	119	5	US-10-755-382-12	Sequence 12, Appl
7	151	100.0	119	5	US-10-755-382-17	Sequence 17, Appl
8	148	98.0	30	3	US-09-253-794-31	Sequence 31, Appl
9	148	98.0	30	5	US-10-755-382-31	Sequence 31, Appl
10	148	98.0	118	4	US-10-270-073-3	Sequence 3, Appli
11	148	98.0	119	3	US-09-253-794-13	Sequence 13, Appl
12	148	98.0	119	3	US-09-253-794-14	Sequence 14, Appl
13	148	98.0	119	3	US-09-253-794-15	Sequence 15, Appl
14	148	98.0	119	4	US-10-680-734-13	Sequence 13, Appl
15	148	98.0	119	4	US-10-680-734-14	Sequence 14, Appl
16	148	98.0	119	4	US-10-680-734-15	Sequence 15, Appl
17	148	98.0	119	4	US-10-680-734-17	Sequence 17, Appl
18	148	98.0	119	5	US-10-755-382-13	Sequence 13, Appl
19	148	98.0	119	5	US-10-755-382-14	Sequence 14, Appl
20	148	98.0	119	5	US-10-755-382-15	Sequence 15, Appl
21	148	98.0	138	4	US-10-006-771A-4	Sequence 4, Appli
22	148	98.0	256	4	US-10-270-073-6	Sequence 6, Appli
23	148	98.0	257	4	US-10-270-073-8	Sequence 8, Appli
24	148	98.0	261	4	US-10-270-071-18	Sequence 18, Appl
25	148	98.0	261	4	US-10-270-073-2	Sequence 2, Appli
26	148	98.0	261	4	US-10-328-190-6	Sequence 6, Appli
27	148	98.0	267	4	US-10-270-071-22	Sequence 22, Appl
28	148	98.0	267	4	US-10-270-071-26	Sequence 26, Appl
29	148	98.0	267	4	US-10-270-071-30	Sequence 30, Appl
30	148	98.0	267	4	US-10-270-071-36	Sequence 36, Appl
31	148	98.0	358	5	US-10-829-388-12	Sequence 12, Appl
32	148	98.0	363	5	US-10-829-388-2	Sequence 2, Appli
33	148	98.0	364	5	US-10-829-388-11	Sequence 11, Appl
34	148	98.0	370	5	US-10-829-388-1	Sequence 1, Appli
35	148	98.0	415	4	US-10-328-190-12	Sequence 12, Appl
36	148	98.0	443	4	US-10-006-773-2	Sequence 2, Appli
37	148	98.0	443	4	US-10-006-771A-2	Sequence 2, Appli
38	148	98.0	468	4	US-10-377-109-2	Sequence 2, Appli
39	148	98.0	669	5	US-10-900-928-3	Sequence 3, Appli
40	140	92.7	244	3	US-09-880-748-1910	Sequence 1910, Ap
41	140	92.7	244	4	US-10-293-418-1910	Sequence 1910, Ap
42	138	91.4	119	3	US-09-253-794-58	Sequence 58, Appl
43	138	91.4	119	3	US-09-795-515-11	Sequence 11, Appl
44	138	91.4	119	3	US-09-795-515-21	Sequence 21, Appl
45	138	91.4	119	4	US-10-267-286A-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-253-794-30
; Sequence 30, Application US/09253794
; Patent No. US20020018750A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-253-794-30

Query Match 100.0%; Score 151; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.1e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 2
US-10-755-382-30
; Sequence 30, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 30:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 30 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-755-382-30

  Query Match             100.0%;  Score 151;  DB 5;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 3
US-09-253-794-12
; Sequence 12, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-253-794-12

  Query Match             100.0%;  Score 151;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 4
US-09-253-794-17
; Sequence 17, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
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;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-253-794-17

  Query Match             100.0%;  Score 151;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 5
US-10-680-734-12
; Sequence 12, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-12

  Query Match             100.0%;  Score 151;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 6
US-10-755-382-12
; Sequence 12, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-755-382-12

  Query Match             100.0%;  Score 151;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 7
US-10-755-382-17
; Sequence 17, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
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;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-755-382-17

  Query Match             100.0%;  Score 151;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 8
US-09-253-794-31
; Sequence 31, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 31:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 30 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-253-794-31

  Query Match             98.0%;  Score 148;  DB 3;  Length 30;
  Best Local Similarity   96.7%;  Pred. No. 1e-12;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              ||||||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 9
US-10-755-382-31
; Sequence 31, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 31:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 30 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-755-382-31

  Query Match             98.0%;  Score 148;  DB 5;  Length 30;
  Best Local Similarity   96.7%;  Pred. No. 1e-12;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
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Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
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RESULT 10
US-10-270-073-3
; Sequence 3, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14VH deduced amino acid sequence
US-10-270-073-3

  Query Match             98.0%;  Score 148;  DB 4;  Length 118;
  Best Local Similarity   96.7%;  Pred. No. 4.3e-12;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 11
US-09-253-794-13
; Sequence 13, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-253-794-13

  Query Match             98.0%;  Score 148;  DB 3;  Length 119;
  Best Local Similarity   96.7%;  Pred. No. 4.4e-12;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              |||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 12
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

  Query Match             98.0%;  Score 148;  DB 3;  Length 119;
  Best Local Similarity   96.7%;  Pred. No. 4.4e-12;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
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RESULT 13
US-09-253-794-15
; Sequence 15, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-253-794-15

  Query Match             98.0%;  Score 148;  DB 3;  Length 119;
  Best Local Similarity   96.7%;  Pred. No. 4.4e-12;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 14
US-10-680-734-13
; Sequence 13, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-13

  Query Match             98.0%;  Score 148;  DB 4;  Length 119;
  Best Local Similarity   96.7%;  Pred. No. 4.4e-12;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 15
US-10-680-734-14
; Sequence 14, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-14

  Query Match             98.0%;  Score 148;  DB 4;  Length 119;
  Best Local Similarity   96.7%;  Pred. No. 4.4e-12;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


Search completed: March 25, 2006, 10:08:04
Job time : 89.5288 secs
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:58:56 ; Search time 10.8377 Seconds
(without alignments)
81.644 Million cell updates/sec

Title: US-10-755-382-30
Perfect score: 151
Sequence: 1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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6: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	140	92.7	244	7	US-11-054-515-1910	Sequence 1910, Ap
2	138	91.4	119	7	US-11-221-900-12	Sequence 12, Appl
3	137	90.7	449	7	US-11-080-587-6	Sequence 6, Appli
4	135	89.4	126	7	US-11-221-900-11	Sequence 11, Appl
5	135	89.4	249	7	US-11-054-515-1956	Sequence 1956, Ap
6	135	89.4	253	7	US-11-054-515-1628	Sequence 1628, Ap
7	134	88.7	122	6	US-10-982-440-53	Sequence 53, Appl
8	134	88.7	123	6	US-10-982-440-1	Sequence 1, Appli
9	134	88.7	124	7	US-11-040-159-14	Sequence 14, Appl
10	134	88.7	124	7	US-11-040-159-16	Sequence 16, Appl
11	134	88.7	251	7	US-11-054-515-955	Sequence 955, App
12	134	88.7	252	7	US-11-054-515-988	Sequence 988, App
13	134	88.7	254	7	US-11-054-515-1428	Sequence 1428, Ap
14	133	88.1	254	7	US-11-054-515-1302	Sequence 1302, Ap
15	133	88.1	254	7	US-11-054-515-1796	Sequence 1796, Ap
16	132	87.4	118	6	US-10-648-816-10	Sequence 10, Appl
17	132	87.4	118	6	US-10-648-816-12	Sequence 12, Appl
18	132	87.4	118	6	US-10-648-816-13	Sequence 13, Appl
19	132	87.4	121	6	US-10-648-816-16	Sequence 16, Appl
20	132	87.4	122	7	US-11-051-453-1	Sequence 1, Appli
21	132	87.4	124	7	US-11-064-174-2	Sequence 2, Appli
22	132	87.4	124	7	US-11-064-174-4	Sequence 4, Appli
23	132	87.4	124	7	US-11-064-174-5	Sequence 5, Appli
24	132	87.4	124	7	US-11-064-174-6	Sequence 6, Appli
25	132	87.4	124	7	US-11-064-174-7	Sequence 7, Appli
26	132	87.4	125	7	US-11-064-174-151	Sequence 151, App
27	132	87.4	141	7	US-11-051-453-49	Sequence 49, Appl
28	132	87.4	251	7	US-11-054-515-1320	Sequence 1320, Ap
29	131	86.8	98	7	US-11-054-669-23	Sequence 23, Appl
30	131	86.8	98	7	US-11-054-669-24	Sequence 24, Appl
31	131	86.8	98	7	US-11-054-669-25	Sequence 25, Appl
32	131	86.8	98	7	US-11-054-669-26	Sequence 26, Appl
33	131	86.8	98	7	US-11-084-554-34	Sequence 34, Appl
34	131	86.8	98	7	US-11-084-554-35	Sequence 35, Appl
35	131	86.8	98	7	US-11-093-274-31	Sequence 31, Appl
36	131	86.8	98	7	US-11-004-590-24	Sequence 24, Appl
37	131	86.8	98	7	US-11-004-590-25	Sequence 25, Appl
38	131	86.8	98	7	US-11-004-590-26	Sequence 26, Appl
39	131	86.8	98	7	US-11-136-250-34	Sequence 34, Appl
40	131	86.8	98	7	US-11-136-250-35	Sequence 35, Appl
41	131	86.8	117	6	US-10-771-257-9	Sequence 9, Appli
42	131	86.8	117	6	US-10-771-257-18	Sequence 18, Appl
43	131	86.8	117	7	US-11-093-274-19	Sequence 19, Appl
44	131	86.8	117	7	US-11-127-677-9	Sequence 9, Appli
45	131	86.8	117	7	US-11-127-677-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-11-054-515-1910
; Sequence 1910, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1910
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1910

Query Match 92.7%; Score 140; DB 7; Length 244;
Best Local Similarity 93.1%; Pred. No. 7.8e-12;
Matches 27; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFDF 29
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RESULT 2

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US-11-221-900-12
; Sequence 12, Application US/11221900
; Publication No. US20060002933A1
; GENERAL INFORMATION:
;  APPLICANT: BLUESTONE, JEFFREY A.
;  APPLICANT:  ZIVIN, ROBERT A.
;  APPLICANT:  JOLLIFFE, LINDA K.
;  TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
;  TITLE OF INVENTION:  IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: TOLT:004USC1
;  CURRENT APPLICATION NUMBER: US/11/221,900
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: US/10/267,286
;  PRIOR FILING DATE: 2003-01-28
;  PRIOR APPLICATION NUMBER: 08/557,050
;  PRIOR FILING DATE: 1998-10-09
;  PRIOR APPLICATION NUMBER: PCT/US94/06198
;  PRIOR FILING DATE: 1994-06-01
;  PRIOR APPLICATION NUMBER: 08/070,116
;  PRIOR FILING DATE: 1993-06-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-11-221-900-12

  Query Match             91.4%;  Score 138;  DB 7;  Length 119;
  Best Local Similarity   90.0%;  Pred. No. 7.2e-12;
  Matches   27;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT 3
US-11-080-587-6
; Sequence 6, Application US/11080587
; Publication No. US20060002942A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  TITLE OF INVENTION: Calicheamicin Conjugates
;  FILE REFERENCE: AM101462
;  CURRENT APPLICATION NUMBER: US/11/080,587
;  CURRENT FILING DATE:  2005-03-15
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Human/murine chimera
;   FEATURE:
;   OTHER INFORMATION: Human/Murine Chimera G193 Heavy Chain
US-11-080-587-6

  Query Match             90.7%;  Score 137;  DB 7;  Length 449;
  Best Local Similarity   90.0%;  Pred. No. 3.6e-11;
  Matches   27;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
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Db          1 EVQLVESGGGVVQPGRSLRLSCSTSGFTFS 30


RESULT 4
US-11-221-900-11
; Sequence 11, Application US/11221900
; Publication No. US20060002933A1
; GENERAL INFORMATION:
;  APPLICANT: BLUESTONE, JEFFREY A.
;  APPLICANT:  ZIVIN, ROBERT A.
;  APPLICANT:  JOLLIFFE, LINDA K.
;  TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
;  TITLE OF INVENTION:  IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: TOLT:004USC1
;  CURRENT APPLICATION NUMBER: US/11/221,900
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: US/10/267,286
;  PRIOR FILING DATE: 2003-01-28
;  PRIOR APPLICATION NUMBER: 08/557,050
;  PRIOR FILING DATE: 1998-10-09
;  PRIOR APPLICATION NUMBER: PCT/US94/06198
;  PRIOR FILING DATE: 1994-06-01
;  PRIOR APPLICATION NUMBER: 08/070,116
;  PRIOR FILING DATE: 1993-06-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-11-221-900-11

  Query Match             89.4%;  Score 135;  DB 7;  Length 126;
  Best Local Similarity   90.0%;  Pred. No. 1.9e-11;
  Matches   27;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

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              :|||||||||||||||||||||||||||| |:
Db          1 QVQLVESGGGVVQPGRSLRLSCSSSGFIFS 30


RESULT 5
US-11-054-515-1956
; Sequence 1956, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1956
;   LENGTH: 249
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1956

  Query Match             89.4%;  Score 135;  DB 7;  Length 249;
  Best Local Similarity   86.7%;  Pred. No. 3.8e-11;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

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RESULT 6
US-11-054-515-1628
; Sequence 1628, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PP523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1628
;   LENGTH: 253
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1628

  Query Match             89.4%;  Score 135;  DB 7;  Length 253;
  Best Local Similarity   86.7%;  Pred. No. 3.9e-11;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

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Db          1 EVQLVQSGGGVVQPGRSLRLSCAASGFTFT 30


RESULT 7
US-10-982-440-53
; Sequence 53, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
;  APPLICANT: Oliner, John
;  APPLICANT:  Graham, Kevin
;  TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
;  FILE REFERENCE: 04-881-A
;  CURRENT APPLICATION NUMBER: US/10/982,440
;  CURRENT FILING DATE:  2004-11-04
;  PRIOR APPLICATION NUMBER: 60/620,161
;  PRIOR FILING DATE: 2004-10-19
;  NUMBER OF SEQ ID NOS: 215
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 53
;   LENGTH: 122
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-982-440-53

  Query Match             88.7%;  Score 134;  DB 6;  Length 122;
  Best Local Similarity   86.7%;  Pred. No. 2.6e-11;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
              ||||||||||||||||||||::||| |:
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 8
US-10-982-440-1
; Sequence 1, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
;  APPLICANT: Oliner, John
;  APPLICANT:  Graham, Kevin
;  TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
;  FILE REFERENCE: 04-881-A
;  CURRENT APPLICATION NUMBER: US/10/982,440
;  CURRENT FILING DATE:  2004-11-04
;  PRIOR APPLICATION NUMBER: 60/620,161
;  PRIOR FILING DATE: 2004-10-19
;  NUMBER OF SEQ ID NOS: 215
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
;   LENGTH: 123
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-982-440-1

  Query Match             88.7%;  Score 134;  DB 6;  Length 123;
  Best Local Similarity   86.7%;  Pred. No. 2.6e-11;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
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Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 9
US-11-040-159-14
; Sequence 14, Application US/11040159
; Publication No. US20050255552A1
; GENERAL INFORMATION:
;  APPLICANT: Flynn, Peter
;  APPLICANT:  Luehrsen, Kenneth
;  APPLICANT:  Balint, Robert F.
;  APPLICANT:  Her, Jeng-Horng
;  APPLICANT:  Bebbington, Christopher R.
;  APPLICANT:  Yarranton, Geoffrey T.
;  APPLICANT:  KaloBios, Inc.
;  TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
;  TITLE OF INVENTION:  Binding Determinants
;  FILE REFERENCE: 021167-001730US
;  CURRENT APPLICATION NUMBER: US/11/040,159
;  CURRENT FILING DATE:  2005-01-20
;  PRIOR APPLICATION NUMBER: US 60/537,364
;  PRIOR FILING DATE: 2004-01-20
;  PRIOR APPLICATION NUMBER: US 60/546,216
;  PRIOR FILING DATE: 2004-02-23
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 124
;   TYPE: PRT
```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:V-region of
; OTHER INFORMATION: anti-PcrV antibody F6 VH
US-11-040-159-14

Query Match 88.7%; Score 134; DB 7; Length 124;
Best Local Similarity 86.7%; Pred. No. 2.6e-11;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
||||||||||||||||||||||::||| |:
Db 1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30

RESULT 10
US-11-040-159-16
; Sequence 16, Application US/11040159
; Publication No. US20050255552A1
; GENERAL INFORMATION:
; APPLICANT: Flynn, Peter
; APPLICANT: Luehrsen, Kenneth
; APPLICANT: Balint, Robert F.
; APPLICANT: Her, Jeng-Horng
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Yarranton, Geoffrey T.
; APPLICANT: KaloBios, Inc.
; TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
; TITLE OF INVENTION: Binding Determinants
; FILE REFERENCE: 021167-001730US
; CURRENT APPLICATION NUMBER: US/11/040,159
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US 60/537,364
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/546,216
; PRIOR FILING DATE: 2004-02-23
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:V-region of
; OTHER INFORMATION: anti-PcrV antibody 1F1 VH
US-11-040-159-16

Query Match 88.7%; Score 134; DB 7; Length 124;
Best Local Similarity 86.7%; Pred. No. 2.6e-11;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
||||||||||||||||||||||::||| |:
Db 1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30

RESULT 11
US-11-054-515-955
; Sequence 955, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 955
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-955

Query Match 88.7%; Score 134; DB 7; Length 251;
Best Local Similarity 86.7%; Pred. No. 5.2e-11;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
||||||||||||||||||||||::||| |:
Db 1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30

RESULT 12
US-11-054-515-988
; Sequence 988, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 988
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-988

Query Match 88.7%; Score 134; DB 7; Length 252;
Best Local Similarity 86.7%; Pred. No. 5.2e-11;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30

```
                     ||||||||||||||||||||||::||| |:
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 13
US-11-054-515-1428
; Sequence 1428, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1428
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1428

  Query Match             88.7%;  Score 134;  DB 7;  Length 254;
  Best Local Similarity   86.7%;  Pred. No. 5.3e-11;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
                ||||||||||||||||||||||::||| |:
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 14
US-11-054-515-1302
; Sequence 1302, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1302
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1302

  Query Match             88.1%;  Score 133;  DB 7;  Length 254;
  Best Local Similarity   86.2%;  Pred. No. 7.2e-11;
  Matches   25;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
                ||||:||||||||||||||||::|||||:
Db          2 VQLVQSGGGVVQPGRSLRLSCAASGFDFS 30


RESULT 15
US-11-054-515-1796
; Sequence 1796, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1796
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1796

  Query Match             88.1%;  Score 133;  DB 7;  Length 254;
  Best Local Similarity   89.7%;  Pred. No. 7.2e-11;
  Matches   26;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDF 29
                ||||||||||||||||||||||::||| |
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTF 29


Search completed: March 25, 2006, 10:09:19
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Job time : 10.8377 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:10 ; Search time 110.576 Seconds
(without alignments)
119.206 Million cell updates/sec

Title: US-10-755-382-31
Perfect score: 151
Sequence: 1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	151	100.0	30	2	AAR97324	Aar97324 Humanised
2	151	100.0	118	6	ABR42755	Abr42755 Anti-CEA
3	151	100.0	119	8	ADM95101	Adm95101 Humanised
4	151	100.0	119	8	ADM98324	Adm98324 Humanised
5	151	100.0	138	6	ABG76489	Abg76489 Heavy cha
6	151	100.0	254	2	AAR94557	Aar94557 Humanised
7	151	100.0	256	6	ABR42757	Abr42757 Anti-CEA
8	151	100.0	257	6	ABR42758	Abr42758 Anti-CEA
9	151	100.0	261	6	ABR42289	Diabody 6
10	151	100.0	261	6	ABR42754	Abr42754 Anti-CEA
11	151	100.0	261	6	ABR83645	Abr83645 hMN14-scF
12	151	100.0	267	6	ABR42292	Abr42292 Bispecifi
13	151	100.0	267	6	ABR42299	Abr42299 Bispecifi
14	151	100.0	267	6	ABR42296	Abr42296 Bispecifi
15	151	100.0	267	6	ABR42294	Abr42294 Bispecifi
16	151	100.0	358	8	ADU26571	Adu26571 Chimeric
17	151	100.0	363	8	ADU26561	Adu26561 Chimeric
18	151	100.0	364	8	ADU26570	Adu26570 Chimeric
19	151	100.0	370	8	ADU26560	Adu26560 Chimeric
20	151	100.0	415	6	ABR83648	Abr83648 TS1 VH ch
21	151	100.0	443	6	ABG76488	Abg76488 Humanised
22	151	100.0	443	6	ABG74240	Abg74240 Chimaeric
23	151	100.0	468	7	ADE64201	Ade64201 MN14HCF p
24	151	100.0	468	7	ADF60815	Adf60815 hMN-14 he
25	151	100.0	669	9	ADY97271	Ady97271 Exemplary
26	148	98.0	30	2	AAR97323	Aar97323 Humanised
27	143	94.7	244	5	ABP45899	Abp45899 Human BLy
28	143	94.7	244	7	ADG96726	Adg96726 Single ch
29	141	93.4	119	2	AAR97336	Aar97336 Humanised
30	140	92.7	119	2	AAR82982	Aar82982 LK26 huma
31	138	91.4	119	2	AAR13101	Aar13101 Grafted h
32	138	91.4	119	9	AEA62457	Aea62457 Human ant
33	138	91.4	123	9	AEA40499	Aea40499 Anti-VEGF
34	138	91.4	249	5	ABP45945	Abp45945 Human BLy
35	138	91.4	249	7	ADG96772	Adg96772 Single ch
36	138	91.4	253	5	ABP45617	Abp45617 Human BLy
37	138	91.4	253	7	ADG96444	Adg96444 Single ch
38	137	90.7	113	4	AAU02538	Aau02538 Anti-adip
39	137	90.7	113	4	AAU02537	Aau02537 Anti-adip
40	137	90.7	115	2	AAW15522	Aaw15522 Anti-TGF
41	137	90.7	116	5	ABB07234	Abb07234 Anti-IL-4
42	137	90.7	116	9	AEA08939	Aea08939 Antibody
43	137	90.7	117	2	AAR77305	Aar77305 Variable
44	137	90.7	118	9	ADZ08173	Adz08173 IGF-speci
45	137	90.7	119	2	AAR82964	Aar82964 3S193HuVH

ALIGNMENTS

RESULT 1
AAR97324
ID AAR97324 standard; peptide; 30 AA.
XX
AC AAR97324;
XX
DT 15-OCT-1996 (first entry)
XX
DE Humanised monoclonal antibody heavy chain framework region.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Homo sapiens.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Claim 7; Page 39; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. This sequence corresponds to the first framework region of the
CC heavy chain of the humanised MAb. See AAR97313-97333

```
XX
SQ   Sequence 30 AA;

  Query Match             100.0%;  Score 151;  DB 2;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 2
ABR42755
ID   ABR42755 standard; protein; 118 AA.
XX
AC   ABR42755;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14 VH region.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Disclosure; Fig 12; 62pp; English.
XX
CC   The present sequence is the protein sequence of the heavy chain variable
CC   region of anti-carcinoembryonic antigen (CEA) humanized monoclonal
CC   antibody hMN-14. scFv constructs comprising the hMN-14 VH and Vkappa
CC   regions are used in novel multivalent, monospecific binding proteins
CC   (diabody, triabody and tetrabody) of the invention (see also ABR42754,
CC   ABR42757 and ABR42758). Claimed binding proteins are specific for a
CC   tumour-associated antigen, and are used in the diagnosis and treatment of
CC   a tumour, carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma,
CC   lymphoma or myeloma, or a cancer selected from acute lymphoblastic
CC   leukaemia, acute myelogenous leukaemia, biliary, breast, cervical,
CC   chronic lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 118 AA;

  Query Match             100.0%;  Score 151;  DB 6;  Length 118;
  Best Local Similarity   100.0%;  Pred. No. 3e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 3
ADM95101
ID   ADM95101 standard; protein; 119 AA.
XX
AC   ADM95101;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 MAb heavy chain variable region coding sequence.
XX
KW   non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW   complementarity determining region; pancreatic cancer; breast cancer;
KW   ovarian cancer.
XX
OS   Mus sp.
OS   Homo sapiens.
XX
PN   WO2004032962-A1.
XX
PD   22-APR-2004.
XX
PF   11-OCT-2002; 2002WO-US032307.
XX
PR   08-OCT-2002; 2002US-0416531P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-364813/34.
DR   N-PSDB; ADM95099.
XX
PT   Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT   comprises administering, either concurrently or sequentially, Class III
PT   anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT   therapeutic agent(s).
XX
PS   Claim 14; Fig 16B; 88pp; English.
XX
CC   The invention relates to a method of treating a non-medullary thyroid
CC   carcinoma or treating medullary thyroid carcinoma involves administering
CC   to a subject, either concurrently or sequentially, a Class III anti-CEA
CC   (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC   least one therapeutic agent. The antibody or its fragment comprises the
CC   complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC   antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC   medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC   ovarian cancer, in a subject. This sequence corresponds to the humanised
CC   murine MN-14 antibody heavy chain variable region.
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 151;  DB 8;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 3e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 4
ADM98324
ID   ADM98324 standard; protein; 119 AA.
XX
AC   ADM98324;
XX
DT   15-JUL-2004  (first entry)
```

```
XX
DE   Humanised murine MN-14 antibody heavy chain variable region protein.
XX
KW   carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW   antibody; MN-14; non-medullary thyroid carcinoma;
KW   medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW   hepatocellular carcinoma; breast cancer; lung cancer;
KW   antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW   apoptosis; humanised.
XX
OS   Mus sp.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 33. .34
FT                   /note= "Encoded by TGGGATAGCAGTACGATTAACTATGCGATG"
FT   Misc-difference 53. .62
FT                   /note= "Encoded by CCACCG"
XX
PN   WO2004032857-A2.
XX
PD   22-APR-2004.
XX
PF   08-OCT-2003; 2003WO-US031801.
XX
PR   08-OCT-2002; 2002US-0416531P.
PR   11-OCT-2002; 2002WO-US032307.
PR   02-MAY-2003; 2003US-0467161P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-340797/31.
DR   N-PSDB; ADM98323.
XX
PT   Treating non-medullary or medullary thyroid carcinoma, involves
PT   administering to subject, either concurrently or sequentially, anti-
PT   carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS   Disclosure; Fig 23b; 122pp; English.
XX
CC   This invention relates to methods for treating cancers that express
CC   carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC   therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC   antibodies that can be used following administration of an agent that
CC   will increase antibody effector functions or following administration of
CC   an amount of interferon effective to upregulate CEA expression in tumour
CC   cells. The present invention describes the anti-CEA antibody as a class
CC   III humanised murine monoclonal antibody that retains specificity for CEA
CC   binding and is preferably an MN-14 antibody or fragment thereof.
CC   Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC   composition useful for the treatment of non-medullary or medullary
CC   thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC   carcinoma, as well as breast or lung cancer. Furthermore, it can
CC   stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC   mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC   cell growth and angiogenesis. This polypeptide sequence is the humanised
CC   murine MN-14 antibody heavy chain variable region protein of the
CC   invention.
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 151;  DB 8;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 3e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 5
ABG76489
ID   ABG76489 standard; protein; 138 AA.
XX
AC   ABG76489;
XX
DT   13-MAY-2003  (first entry)
XX
DE   Heavy chain variable, VH, region of antibody hMN14.
XX
KW   CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW   colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW   human; zeta signalling chain; CD8alpha hinge; humanised antibody;
KW   heavy chain variable region; VH.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT   Protein         20. .138
FT                   /label= Mature_VH_of_hMN14
XX
PN   US2002165360-A1.
XX
PD   07-NOV-2002.
XX
PF   10-DEC-2001; 2001US-00006771.
XX
PR   30-NOV-2000; 2000US-0250087P.
PR   30-NOV-2000; 2000US-0250090P.
XX
PA   (JUNG/) JUNGHANS R P.
XX
PI   Junghans RP;
XX
DR   WPI; 2003-298705/29.
DR   N-PSDB; ABX13169.
XX
PT   New chimeric molecule from humanized antibody against carcinoembryonic
PT   antigen and having signaling molecules of T cells and other effector
PT   cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS   Disclosure; Page 9; 20pp; English.
XX
CC   The invention relates to a chimaeric molecule comprising the
CC   carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC   as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC   chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC   which the cysteine residues have been mutated, with the IgTCR molecule
CC   occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC   appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC   NK (not defined) or other effector cells are useful in treating patients
CC   with cancers expressing the CEA antigen, together with other or with
CC   heterologous constructs to engage additional stimulatory and functional
CC   properties of the effector cells to enhance the anti-tumour therapeutic
CC   efficacy. The cancer disorder includes colorectal, breast and lung
CC   cancers. The present sequence represents the heavy chain variable, VH,
CC   region of antibody hMN14. The VH protein is humanised (complementarity
CC   determining region-grafted) and has a leader peptide
XX
SQ   Sequence 138 AA;

  Query Match             100.0%;  Score 151;  DB 6;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db         20 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 49
```

```
RESULT 6
AAR94557
ID   AAR94557 standard; protein; 254 AA.
XX
AC   AAR94557;
XX
DT   19-JUN-1996  (first entry)
XX
DE   Humanised antibody MN14 heavy chain.
XX
KW   Cancer; therapy; radiotherapy; radiolabelling; phosphorus;
KW   humanised antibody; complementarity determining region; CDR; targetting;
KW   protein kinase; Fab; F(ab')2; Escherichia coli; vector; MN14pBEV;
KW   carcinoembryonic antigen; CEA; MN14-Kemptide.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Sig_peptide
FT                   /note= "PelB signal peptide"
FT   Protein         23. .254
FT                   /label= Mat_protein
FT   Region          53. .57
FT                   /label= CDR-H1
FT   Region          72. .88
FT                   /label= CDR-H2
FT   Region          121. .130
FT                   /label= CDR-H3
FT   Domain          240. .254
FT                   /label= Hinge_domain
XX
PN   WO9608506-A1.
XX
PD   21-MAR-1996.
XX
PF   18-SEP-1995;   95WO-US011405.
XX
PR   16-SEP-1994;   94US-00308103.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Leung S,  Hansen HJ,  Griffiths GL;
XX
DR   WPI; 1996-179897/18.
DR   N-PSDB; AAT14493.
XX
PT   Phosphorus labelled antibodies for use in cancer therapy - comprise
PT   protein kinase peptide substrate sequence and specific targetting CDR,
PT   for radio-labelling diseased cells with a phosphorus isotope.
XX
PS   Example 1 (ix); Fig 5; 62pp; English.
XX
CC   The heavy chain and hinge region (AAR94557) and light chain (AAR94558) of
CC   humanised anti-CEA antibody MN14 are the products of an Fab'/F(ab')2
CC   dicistronic gene (AAT14493). They are derived from anti-CEA murine
CC   monoclonal antibody MN14 following cloning and humanisation of
CC   complementarity determining regions. The dicistronic gene was used to
CC   construct vector MN14pBEV. A protein kinase substrate (see AAR94550)
CC   encoding sequence was incorporated into the vector, and MN14-Kemptide
CC   fusion protein was secreted from E. coli BMH71-18 mutS. The fusion
CC   protein can be radiolabelled with 32P or 33P and used for targetted
CC   radiotherapy of tumours or infectious lesions
XX
SQ   Sequence 254 AA;

  Query Match             100.0%;  Score 151;  DB 2;  Length 254;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db         23 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 52


RESULT 7
ABR42757
ID   ABR42757 standard; protein; 256 AA.
XX
AC   ABR42757;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-0.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-0;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; triabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .256
FT                   /label= hMN-14-0
FT   Region          142. .250
FT                   /label= hMN-14Vkappa
FT   Region          251. .256
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
DR   N-PSDB; ACC58722.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 39; Fig 13; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-0, which is
CC   designed to form an hMN-14 triabody. The hMN-14-0 polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa without a peptide linker. The use of the zero linker enables the
CC   secreted polypeptide to form a triabody, forming 3 binding sites for CEA.
CC   The polypeptide also includes a pelB signal peptide, which precedes the
CC   VH moiety to facilitate synthesis of the polypeptide in the periplasmic
CC   space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific triabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
```

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CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 256 AA;

  Query Match             100.0%;  Score 151;  DB 6;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53


RESULT 8
ABR42758
ID   ABR42758 standard; protein; 257 AA.
XX
AC   ABR42758;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-1G.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-1G;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; tetrabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .257
FT                   /label= hMN-14-0
FT   Region          142
FT                   /label= 1G_linker
FT   Region          143. .251
FT                   /label= hMN-14Vkappa
FT   Region          252. .257
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 48; Fig 14; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-1G, which is
CC   designed to form an hMN-14 tetrabody. The hMN-14-1G polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa via a single glycine residues. Use of the 1G linker enables some
CC   of the the secreted polypeptide to form a tetrabody with 4 binding sites
CC   for CEA. The polypeptide also includes a pelB signal peptide, which
CC   precedes the VH moiety to facilitate synthesis of the polypeptide in the
CC   periplasmic space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific tetrabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 257 AA;

  Query Match             100.0%;  Score 151;  DB 6;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53


RESULT 9
ABR42289
ID   ABR42289 standard; protein; 261 AA.
XX
AC   ABR42289;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Diabody 679-scFv-L5 polypeptide (VH-I3Q/C101S mutant).
XX
KW   Diabody; antibody; 679-scFv-L5; histamine-succinyl-glycyl; HSG;
KW   affinity enhancement system; tumour; targeting; mutant; mutein.
XX
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB signal peptide"
FT   Misc-difference 3
FT                   /note= "wild-type Ile substituted by Gln"
FT   Protein         23. .268
FT                   /label= 679-scFv-L5
FT   Region          23. .142
FT                   /label= 679VH(I3Q/C101S)
FT   Misc-difference 101
FT                   /note= "wild-type Cys substituted by Ser"
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .260
FT                   /label= 679Vk
FT   Region          261. .268
FT                   /label= 6His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
```

```
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57803.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Disclosure; Fig 28; 87pp; English.
XX
CC   The present sequence is the protein sequence of a 679 mutant diabody in
CC   which antibody 679 VH has a Gln for Ile amino acid substitution at
CC   position 3 and a Ser for Gln amino acid substitution at position 101.
CC   Murine monoclonal antibody 679 binds with high affinity to molecules
CC   containing the moiety histamine-succinyl-glycyl (HSG). The present
CC   polypeptide comprises: 679 VH(I3Q) linked to 679 Vk via a peptide linker
CC   (enables the secreted polypeptide to dimerise into a diabody, forming 2
CC   sites for HSG); a pelB leader signal peptide (facilitates transport of
CC   the polypeptide into the periplasmic space of Escherichia coli); and 6
CC   His residues (allows purification by IMAC). The 679 diabody was expressed
CC   in E. coli at a level of 10 ug/l of culture, compared with 1 ug/l for the
CC   non-mutant polypeptide. The invention provides a bispecific diabody
CC   comprising an HSG binding site and a carcinoembryonic antigen (CEA)
CC   binding site. The HSG antigen binding site may comprise the VH and Vk
CC   polypeptides of 679 MAb. These diabodies are produced via recombinant DNA
CC   technology and create a novel affinity enhancement system that shows
CC   specific affinity for HSG and CEA. They pre-target CEA positive tumours
CC   for subsequent specific delivery of therapeutic radioisotopes carried by
CC   HSG-carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 261 AA;

  Query Match             100.0%;  Score 151;  DB 6;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53


RESULT 10
ABR42754
ID   ABR42754 standard; protein; 261 AA.
XX
AC   ABR42754;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-scFv-L5.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-scFv-15;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .261
FT                   /label= hMN-14-scFv-L5
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .255
FT                   /label= hMN-14Vkappa
FT   Region          256. .261
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
DR   N-PSDB; ACC58721.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 31; Fig 11; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-scFv-L5, which was
CC   designed to form an hMN-14 diabody. The hMN-14-scFv-L5 polypeptide
CC   comprises the C-terminal end of anti-carcinoembryonic antigen (CEA)
CC   humanized monoclonal antibody hMN-14 VH linked to the N-terminal part of
CC   hMN-14 Vkappa by a peptide linker that enables the secreted polypeptide
CC   to dimerize into a diabody, forming 2 binding sites for CEA. The
CC   polypeptide also includes a pelB signal peptide, which precedes the VH
CC   moiety to facilitate synthesis of the polypeptide in the periplasmic
CC   space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. In the claimed monospecific diabody, each scFv comprises
CC   the present sequence. The diabody is an example of claimed multivalent
CC   binding proteins specific for a tumour-associated antigen. The binding
CC   proteins are used in the diagnosis and treatment of a tumour, carcinoma,
CC   melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma or myeloma,
CC   or a cancer selected from acute lymphoblastic leukaemia, acute
CC   myelogenous leukaemia, biliary, breast, cervical, chronic lymphocytic
CC   leukaemia, chronic myelogenous leukaemia, colorectal, endometrial,
CC   oesophageal, gastric, head and neck, Hodgkin's lymphoma, lung, medullary
CC   thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic, prostate and
CC   bladder
XX
SQ   Sequence 261 AA;

  Query Match             100.0%;  Score 151;  DB 6;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53


RESULT 11
ABR83645
ID   ABR83645 standard; protein; 261 AA.
```

```
XX
AC   ABR83645;
XX
DT   16-OCT-2003  (first entry)
XX
DE   hMN14-scFv-L5 amino acid sequence.
XX
KW   Multispecific binding protein; multivalent; target antigen; cytostatic;
KW   immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW   immunotherapy; autoimmune disease; infectious disease;
KW   cardiovascular disease; inflammatory disease.
XX
OS   Escherichia coli.
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003057829-A2.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-US038985.
XX
PR   26-DEC-2001; 2001US-0342103P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg D;
XX
DR   WPI; 2003-607997/57.
DR   N-PSDB; ACF57430.
XX
PT   Novel multivalent, multi-specific binding protein useful for treating
PT   cancer, has first binding site having affinity towards hapten group and
PT   second and third binding sites each having affinity towards target
PT   antigen.
XX
PS   Claim 11; Fig 6; 43pp; English.
XX
CC   The present invention describes a multivalent, multi-specific binding
CC   protein (I) comprising a first binding site having an affinity towards a
CC   hapten group and a second and a third binding sites each having affinity
CC   towards a target antigen, which may be the same or a different target
CC   antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC   and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC   useful for delivering a diagnostic agent, a therapeutic agent, or its
CC   combination to a target, which involves administering (I) to a subject,
CC   waiting for a sufficient amount of time for an amount of the non-binding
CC   protein to clear the subject's blood stream, and administering to the
CC   subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC   agent, or its combination, that binds to a binding site of the binding
CC   protein. (I) is also useful for detecting or treating a human disorder,
CC   preferably cancer, autoimmune diseases, infectious diseases,
CC   cardiovascular diseases and inflammatory diseases. The present sequence
CC   represents a hMN14-scFv-L5 amino acid sequence, which is used in the
CC   exemplification of the present invention
XX
SQ   Sequence 261 AA;

  Query Match             100.0%;  Score 151;  DB 6;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53


RESULT 12
ABR42292
ID   ABR42292 standard; protein; 267 AA.
XX
AC   ABR42292;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .267
FT                   /label= BSI_polypeptide#1
FT   Region          24. .141
FT                   /label= hMN14_VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .259
FT                   /label= 679_Vk
FT   Region          262. .267
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57806.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 31; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of a
CC   novel bispecific diabody comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen. The bispecific diabody can be produced using
CC   recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC   a novel affinity enhancement system that shows specific affinity for HSG
CC   and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC   subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC   carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             100.0%;  Score 151;  DB 6;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53
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RESULT 13
ABR42299
ID ABR42299 standard; protein; 267 AA.
XX
AC ABR42299;
XX
DT 11-AUG-2003 (first entry)
XX
DE Bispecific diabody BS1.5H polypeptide #2.
XX
KW Diabody; antibody; carcinoembryonic antigen; CEA;
KW histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW targeting; mutant; mutein.
XX
OS Homo sapiens.
OS Mus sp.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .22
FT		/label= Signal_peptide
FT		/note= "pelB leader peptide"
FT	Protein	23. .262
FT		/label= BS1.5H_polypeptide#2
FT	Region	24. .142
FT		/label= hMN14_VH
FT	Region	143. .147
FT		/label= Linker
FT	Region	148. .254
FT		/label= h679_Vk
FT	Region	257. .262
FT		/label= His_tag

XX
PN WO2003033653-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032717.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (IBCP-) IBC PHARM.
XX
PI Chang CK, Rossi E;
XX
DR WPI; 2003-393513/37.
DR N-PSDB; ACC57813.
XX
PT New kit comprising a multivalent, multi-specific binding protein and a
PT carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT for treating cancer, and cardiovascular, immune, inflammatory, or
PT infectious diseases.
XX
PS Claim 14; Fig 38; 87pp; English.
XX
CC The present sequence is the protein sequence for polypeptide #2 of novel
CC bispecific diabody BS1.5H comprising the VH region of monoclonal antibody
CC hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC binds with high affinity to molecules containing the moiety histamine-
CC succinyl-glycyl (HSG). A humanised version of its VH and Vk sequences
CC have been used in BS1.5H. Humanised antibody hMN14 binds specifically to
CC carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC provides a novel affinity enhancement system that shows specific affinity
CC for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC tumours for subsequent specific delivery of therapeutic radioisotopes
CC carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC disease, cardiovascular diseases and inflammatory diseases can be
CC detected or treated using the methods of the invention
XX
SQ Sequence 267 AA;

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  Query Match             100.0%;  Score 151;  DB 6;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53
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RESULT 14
ABR42296
ID ABR42296 standard; protein; 267 AA.
XX
AC ABR42296;
XX
DT 11-AUG-2003 (first entry)
XX
DE Bispecific diabody BS2 polypeptide #2.
XX
KW Diabody; antibody; carcinoembryonic antigen; CEA;
KW histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW targeting; mutant; mutein.
XX
OS Homo sapiens.
OS Mus sp.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .22
FT		/label= Signal_peptide
FT		/note= "pelB leader peptide"
FT	Protein	23. .267
FT		/label= BS2_polypeptide#2
FT	Region	24. .141
FT		/label= hMN14-VH
FT	Region	142. .146
FT		/label= Linker
FT	Region	147. .259
FT		/label= 679_Vk
FT	Region	262. .267
FT		/label= His_tag

XX
PN WO2003033653-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032717.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (IBCP-) IBC PHARM.
XX
PI Chang CK, Rossi E;
XX
DR WPI; 2003-393513/37.
DR N-PSDB; ACC57810.
XX
PT New kit comprising a multivalent, multi-specific binding protein and a
PT carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT for treating cancer, and cardiovascular, immune, inflammatory, or
PT infectious diseases.

```
XX
PS   Claim 14; Fig 35; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of novel
CC   bispecific diabody BS2 comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC   using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC   provides a novel affinity enhancement system that shows specific affinity
CC   for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC   tumours for subsequent specific delivery of therapeutic radioisotopes
CC   carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC   disease, cardiovascular diseases and inflammatory diseases can be
CC   detected or treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             100.0%;  Score 151;  DB 6;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53


RESULT 15
ABR42294
ID   ABR42294 standard; protein; 267 AA.
XX
AC   ABR42294;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS1.5 polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .267
FT                   /label= BS1.5_polypeptide#2
FT   Region          24. .141
FT                   /label= hMN14_VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .259
FT                   /label= 679_Vk(I3Q)
FT   Region          261. .267
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57808.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 33; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of a
CC   novel bispecific diabody comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen. The bispecific diabody can be produced using
CC   recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC   a novel affinity enhancement system that shows specific affinity for HSG
CC   and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC   subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC   carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             100.0%;  Score 151;  DB 6;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53


Search completed: March 25, 2006, 09:02:21
Job time : 110.701 secs
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:02:50 ; Search time 17.2775 Seconds
(without alignments)
167.067 Million cell updates/sec

Title: US-10-755-382-31
Perfect score: 151
Sequence: 1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	137	90.7	97	2	S44115	Ig heavy chain V r
2	137	90.7	114	2	S46390	Ig heavy chain V r
3	136	90.1	100	2	S69896	Ig heavy chain V r
4	134	88.7	94	2	PL0120	Ig heavy chain V-I
5	134	88.7	98	2	PL0116	Ig heavy chain V-I
6	134	88.7	98	2	S29546	Ig heavy chain V r
7	134	88.7	113	2	S57410	Ig heavy chain V-J
8	134	88.7	113	2	S38490	Ig heavy chain - h
9	134	88.7	118	2	S31116	Ig heavy chain - h
10	134	88.7	119	2	S31111	Ig heavy chain - h
11	134	88.7	119	2	F36005	Ig heavy chain V r
12	134	88.7	120	2	S31112	Ig heavy chain - h
13	134	88.7	121	2	G36005	Ig heavy chain V r
14	134	88.7	122	2	S31117	Ig heavy chain - h
15	134	88.7	122	2	E36005	Ig heavy chain V r
16	134	88.7	122	2	S31119	Ig heavy chain - h
17	134	88.7	128	2	S48797	Ig heavy chain V r
18	134	88.7	130	2	S31601	Ig heavy chain V r
19	134	88.7	130	2	PL0098	Ig heavy chain pre
20	134	88.7	132	2	S31603	Ig heavy chain V r
21	134	88.7	133	2	S31590	Ig heavy chain V r
22	134	88.7	133	2	A49028	Ig heavy chain V-I
23	134	88.7	134	2	S31679	Ig heavy chain V r
24	134	88.7	137	2	S31701	Ig heavy chain V r
25	134	88.7	139	2	S31674	Ig heavy chain V r
26	133	88.1	98	2	S26927	Ig heavy chain V r
27	133	88.1	121	2	S31118	Ig heavy chain - h
28	133	88.1	121	2	S31104	Ig heavy chain (su
29	133	88.1	123	2	S30532	Ig heavy chain V r
30	133	88.1	128	2	S31595	Ig heavy chain V r
31	133	88.1	145	2	S11239	Ig heavy chain V r
32	132	87.4	96	2	PH0873	Ig heavy chain V r
33	132	87.4	126	1	G1HUKL	Ig heavy chain V-I
34	131	86.8	116	1	M3HUGL	Ig heavy chain V-I
35	131	86.8	119	1	G1HUNI	Ig heavy chain V-I
36	131	86.8	121	2	S19666	Ig heavy chain V r
37	129	85.4	98	2	S54856	Ig heavy chain V r
38	129	85.4	121	2	S26798	Ig heavy chain V r
39	129	85.4	122	1	M3HUAM	Ig heavy chain V-I
40	128	84.8	115	2	S57445	Ig heavy chain V-J
41	128	84.8	118	2	A47329	Ig heavy chain V r
42	128	84.8	120	1	G1HUDB	Ig heavy chain V-I
43	128	84.8	151	2	A60943	Ig heavy chain pre
44	128	84.8	249	2	S69340	Ig heavy chain VHI
45	127	84.1	97	2	S26890	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S44115
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44115
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
A;Accession: S44115
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <HAW>
A;Cross-references: UNIPARC:UPI000011662B; EMBL:Z31384; NID:g472969; PIDN:CAA83259.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 90.7%; Score 137; DB 2; Length 97;
Best Local Similarity 90.0%; Pred. No. 1.8e-11;
Matches 27; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCASGFDFT 30
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Db 1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30

RESULT 2
S46390
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46390
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46390
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <FIG>
A;Cross-references: UNIPARC:UPI000011663F; EMBL:Z31686; NID:g509782; PIDN:CAA83491.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 90.7%; Score 137; DB 2; Length 114;
Best Local Similarity 90.0%; Pred. No. 2.1e-11;
Matches 27; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
||||||||||||||||||||||||:|||| |:

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Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 3
S69896
Ig heavy chain V region (clone RFKL5H), rheumatoid factor - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C;Accession: S69896
R;Randen, I.; Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig, J
Eur. J. Immunol. 23, 1220-1225, 1993
A;Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune respo
A;Reference number: S69896; MUID:93272805; PMID:8500520
A;Accession: S69896
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-100 <RAN>
A;Cross-references: UNIPARC:UPI0000116198; EMBL:X73605; NID:g509797; PIDN:CAA51998.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             90.1%;  Score 136;  DB 2;  Length 100;
  Best Local Similarity   89.7%;  Pred. No. 2.6e-11;
  Matches   26;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDF 29
              |||||||||:|||||||||||:||||:|
Db          1 EVQLVESGGGLVQPGRSLRLSCAASGFEF 29


RESULT 4
PL0120
Ig heavy chain V-III region (TD-Vo) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 31-Dec-2004
C;Accession: PL0120
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A;Reference number: PL0116; MUID:88286083; PMID:2840480
A;Accession: PL0120
A;Molecule type: mRNA
A;Residues: 1-94 <BIR>
A;Cross-references: UNIPROT:Q8WUK1; UNIPROT:Q9UL93; UNIPARC:UPI0000176A2C
A;Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A;Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement f
C;Superfamily: immunoglobulin homology
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2

  Query Match             88.7%;  Score 134;  DB 2;  Length 94;
  Best Local Similarity   86.7%;  Pred. No. 4.5e-11;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              :|||||||||||||||||||||:|||| |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 5
PL0116
Ig heavy chain V-III region (AW-Vx) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PL0116; S26892
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A;Reference number: PL0116; MUID:88286083; PMID:2840480
A;Accession: PL0116
A;Molecule type: mRNA
A;Residues: 1-98 <BIR>
A;Cross-references: UNIPARC:UPI0000031F3A
A;Experimental source: B cells from patient AW with acute lymphoblastic leukemia, ALL
A;Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA rearrangement f
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26892
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI0000031F3A; EMBL:Z12349; NID:g32918; PIDN:CAA78219.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2

  Query Match             88.7%;  Score 134;  DB 2;  Length 98;
  Best Local Similarity   86.7%;  Pred. No. 4.7e-11;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              :|||||||||||||||||||||:|||| |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 6
S29546
Ig heavy chain V region (COS-8 / DP-46) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29546; S26888
R;Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Accession: S29546
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI000002DD16; EMBL:Z17394; NID:g32843; PIDN:CAA78997.1; PID
A;Note: designated COS-8
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TO2>
A;Cross-references: UNIPARC:UPI000002DD16; EMBL:Z12346; NID:g32912; PIDN:CAA78216.1; PID
A;Note: designated DP-46
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             88.7%;  Score 134;  DB 2;  Length 98;
  Best Local Similarity   86.7%;  Pred. No. 4.7e-11;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              :|||||||||||||||||||||:|||| |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 7
S57410
Ig heavy chain V-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S57410
R;Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.
submitted to the EMBL Data Library, June 1995
A;Description: Analysis of anti-GM1 ganglioside IgM antibodies cloned from motor neuropa
```

```
A;Reference number: S57408
A;Accession: S57410
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <PAT>
A;Cross-references: UNIPARC:UPI00001137A9; EMBL:X87893; NID:g871363; PIDN:CAA61144.1; PI
C;Genetics:
A;Introns: 99/2
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             88.7%;  Score 134;  DB 2;  Length 113;
  Best Local Similarity   86.7%;  Pred. No. 5.4e-11;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              :|||||||||||||||||||||:|||| |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 8
S38490
Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38490
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a p
A;Reference number: S38488
A;Accession: S38490
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <MAR>
A;Cross-references: UNIPARC:UPI0000116549; EMBL:Z23030; NID:g414027; PIDN:CAA80565.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             88.7%;  Score 134;  DB 2;  Length 113;
  Best Local Similarity   86.7%;  Pred. No. 5.4e-11;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              :|||||||||||||||||||||:|||| |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 9
S31116
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C;Accession: S31116
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31116
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-118 <RAA>
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176E37; EMBL:X62966
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             88.7%;  Score 134;  DB 2;  Length 118;
  Best Local Similarity   86.7%;  Pred. No. 5.6e-11;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              :|||||||||||||||||||||:|||| |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 10
S31111
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31111
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31111
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-119 <RAA>
A;Cross-references: UNIPARC:UPI0000176DC2; EMBL:X62959
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             88.7%;  Score 134;  DB 2;  Length 119;
  Best Local Similarity   86.7%;  Pred. No. 5.7e-11;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              :|||||||||||||||||||||:|||| |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 11
F36005
Ig heavy chain V region (M49) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 31-Dec-2004
C;Accession: F36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: F36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-119 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C32; GB:M34026
C;Genetics:
A;Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             88.7%;  Score 134;  DB 2;  Length 119;
  Best Local Similarity   86.7%;  Pred. No. 5.7e-11;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              :|||||||||||||||||||||:|||| |:
Db          1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 12
S31112
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31112
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
```

A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31112
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-120 <RAA>
A;Cross-references: UNIPARC:UPI0000176C8C; EMBL:X62961
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

 Query Match 88.7%; Score 134; DB 2; Length 120;
 Best Local Similarity 86.7%; Pred. No. 5.7e-11;
 Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
 :|||||||||||||||||||:|||| |:
Db 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30

RESULT 13
G36005
Ig heavy chain V region (M74) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 31-Dec-2004
C;Accession: G36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: G36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <SCH>
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176C2C; GB:M34031
C;Genetics:
A;Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

 Query Match 88.7%; Score 134; DB 2; Length 121;
 Best Local Similarity 86.7%; Pred. No. 5.8e-11;
 Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
 :|||||||||||||||||||:|||| |:
Db 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30

RESULT 14
S31117
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31117
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31117
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-122 <RAA>
A;Cross-references: UNIPARC:UPI0000176C8D; EMBL:X62967
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

 Query Match 88.7%; Score 134; DB 2; Length 122;
 Best Local Similarity 86.7%; Pred. No. 5.8e-11;
 Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
 :|||||||||||||||||||:|||| |:
Db 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30

RESULT 15
E36005
Ig heavy chain V region (M72) - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C;Accession: E36005
R;Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A;Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A;Reference number: A36005; MUID:90349571; PMID:2117273
A;Accession: E36005
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-122 <SCH>
A;Cross-references: UNIPARC:UPI0000176C30; GB:M34030
C;Genetics:
A;Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:118731; OMIM:146910
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

 Query Match 88.7%; Score 134; DB 2; Length 122;
 Best Local Similarity 86.7%; Pred. No. 5.8e-11;
 Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
 :|||||||||||||||||||:|||| |:
Db 1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 30

Search completed: March 25, 2006, 09:15:45
Job time : 17.2775 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:40 ; Search time 108.063 Seconds
(without alignments)
195.866 Million cell updates/sec

Title: US-10-755-382-31
Perfect score: 151
Sequence: 1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	135	89.4	470	2	Q68CN4_HUMAN	Q68cn4 homo sapien
2	134	88.7	613	2	Q8WUK1_HUMAN	Q8wuk1 homo sapien
3	133	88.1	472	2	Q6N089_HUMAN	Q6n089 homo sapien
4	133	88.1	475	2	Q5EFE5_HUMAN	Q5efe5 homo sapien
5	133	88.1	573	2	Q8WU38_HUMAN	Q8wu38 homo sapien
6	132	87.4	116	2	Q9UL93_HUMAN	Q9ul93 homo sapien
7	132	87.4	126	1	HV3K_HUMAN	P01772 homo sapien
8	131	86.8	116	1	HV3T_HUMAN	P01781 homo sapien
9	131	86.8	119	1	HV3I_HUMAN	P01770 homo sapien
10	131	86.8	461	2	Q5M7V3_RAT	Q5m7v3 rattus norv
11	131	86.8	479	2	Q5BK12_RAT	Q5bk12 rattus norv
12	130	86.1	113	2	Q9UL90_HUMAN	Q9ul90 homo sapien
13	129	85.4	122	1	HV3G_HUMAN	P01768 homo sapien
14	129	85.4	122	2	Q9UL84_HUMAN	Q9ul84 homo sapien
15	129	85.4	465	2	Q5I0J0_RAT	Q5i0j0 rattus norv
16	128	84.8	120	1	HV3U_HUMAN	P01782 homo sapien
17	128	84.8	479	2	Q5PQK9_RAT	Q5pqk9 rattus norv
18	127	84.1	118	2	Q9UL91_HUMAN	Q9ul91 homo sapien
19	127	84.1	119	1	HV3P_HUMAN	P01777 homo sapien
20	127	84.1	120	1	HV3E_HUMAN	P01766 homo sapien
21	127	84.1	478	2	Q6PI81_HUMAN	Q6pi81 homo sapien
22	126	83.4	122	1	HV3H_HUMAN	P01769 homo sapien
23	126	83.4	473	2	Q6MZV7_HUMAN	Q6mzv7 homo sapien
24	125	82.8	117	1	HV3O_HUMAN	P01776 homo sapien
25	125	82.8	147	2	Q9Y509_HUMAN	Q9y509 homo sapien
26	125	82.8	467	2	Q4VBH1_RAT	Q4vbh1 rattus norv
27	125	82.8	493	2	Q6GMX2_HUMAN	Q6gmx2 homo sapien
28	125	82.8	597	2	Q96BB9_HUMAN	Q96bb9 homo sapien
29	124	82.1	115	1	HV3D_HUMAN	P01765 homo sapien
30	124	82.1	116	1	HV36_MOUSE	P01806 mus musculu
31	124	82.1	116	1	HV3R_HUMAN	P01779 homo sapien
32	124	82.1	117	1	HV3C_HUMAN	P01764 homo sapien
33	124	82.1	117	1	HV41_MOUSE	P01811 mus musculu
34	124	82.1	118	1	HV3V_HUMAN	P80419 homo sapien
35	124	82.1	119	1	HV37_MOUSE	P01807 mus musculu
36	124	82.1	119	1	HV38_MOUSE	P01808 mus musculu
37	124	82.1	119	1	HV3M_HUMAN	P01774 homo sapien
38	124	82.1	119	1	HV40_MOUSE	P01810 mus musculu
39	124	82.1	236	2	Q6ZP85_HUMAN	Q6zp85 homo sapien
40	124	82.1	476	2	Q4V9Z4_MOUSE	Q4v9z4 mus musculu
41	124	82.1	483	2	Q566J7_MOUSE	Q566j7 mus musculu
42	123	81.5	112	2	Q9HCC1_HUMAN	Q9hcc1 homo sapien
43	123	81.5	117	1	HV17_MOUSE	P01786 mus musculu
44	123	81.5	121	2	Q9UL71_HUMAN	Q9ul71 homo sapien
45	123	81.5	131	2	Q9UL88_HUMAN	Q9ul88 homo sapien

ALIGNMENTS

RESULT 1
Q68CN4_HUMAN
ID Q68CN4_HUMAN PRELIMINARY; PRT; 470 AA.
AC Q68CN4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686E23209.
GN Name=DKFZp686E23209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; CR749861; CAH18705.2; -; mRNA.
DR SMR; Q68CN4; 43-493.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51536 MW; 7CB061DFC03D0B2B CRC64;

Query Match 89.4%; Score 135; DB 2; Length 470;
Best Local Similarity 83.3%; Pred. No. 1.1e-09;
Matches 25; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              :|||||||||||||:|:||||:||||||:
Db         20 QVQLVESGGGVVQPGKSVRLSCAASGFDFS 49
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RESULT 2
Q8WUK1_HUMAN
ID Q8WUK1_HUMAN PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

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DE   IGHM protein.
GN   Name=IGHM;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RG   NIH MGC Project;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2117273;
RA   Schroeder H.W. Jr, Wang J.Y.;
RT   "Preferential utilization of conserved immunoglobulin heavy chain
RT   variable gene segments during human fetal life.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1383695; DOI=10.1016/0161-5890(92)90173-U;
RA   Cuisinier A.M., Fumoux F., Fougereau M., Tonnelle C.;
RT   "IGM kappa/lambda EBV human B cell clone: an early step of
RT   differentiation of fetal B cells or a distinct B lineage?";
RL   Mol. Immunol. 29:1363-1373(1992).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1730252;
RA   Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA   Schuurman R.K.;
RT   "Restricted utilization of germ-line VH3 genes and short diverse third
RT   complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT   immunoglobulin heavy chain rearrangements.";
RL   Eur. J. Immunol. 22:247-251(1992).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1904154;
RA   Neale G.A., Kitchingman G.R.;
RT   "mRNA transcripts initiating within the human immunoglobulin mu heavy
RT   chain enhancer region contain a non-translatable exon and are
RT   extremely heterogeneous at the 5' end.";
RL   Nucleic Acids Res. 19:2427-2433(1991).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2840480; DOI=10.1084/jem.168.1.229;
RA   Bird J., Galili N., Link M., Stites D., Sklar J.;
RT   "Continuing rearrangement but absence of somatic hypermutation in
RT   immunoglobulin genes of human B cell precursor leukemia.";
RL   J. Exp. Med. 168:229-245(1988).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2538551; DOI=10.1084/jem.169.4.1391;
RA   Nickerson K.G., Berman J., Glickman E., Chess L., Alt F.W.;
RT   "Early human IgH gene assembly in Epstein-Barr virus-transformed fetal
RT   B cell lines. Preferential utilization of the most JH-proximal D
RT   segment (DQ52) and two unusual VH-related rearrangements.";
RL   J. Exp. Med. 169:1391-1403(1989).
RN   [9]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA   Hillson J.L., Karr N.S., Oppliger I.R., Mannik M., Sasso E.H.;
RT   "The structural basis of germline-encoded VH3 immunoglobulin binding
RT   to staphylococcal protein A.";
RL   J. Exp. Med. 178:331-336(1993).
DR   EMBL; BC020240; AAH20240.1; -; mRNA.
DR   PIR; F36005; F36005.
DR   PIR; G36005; G36005.
DR   PIR; PH1642; PH1642.
DR   PIR; PH1643; PH1643.
DR   PIR; PH1645; PH1645.
DR   PIR; PH1646; PH1646.
DR   PIR; PL0098; PL0098.
DR   PIR; PL0120; PL0120.
DR   PIR; S15590; S15590.
DR   PIR; S31116; S31116.
DR   PIR; S31119; S31119.
DR   PIR; S70442; S70442.
DR   HSSP; P01861; 1ADQ.
DR   SMR; Q8WUK1; 20-242.
DR   Ensembl; ENSG00000130076; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Immunoglobulin domain.
SQ   SEQUENCE   613 AA;  67296 MW;  60C7F5950671E315 CRC64;

  Query Match             88.7%;  Score 134;  DB 2;  Length 613;
  Best Local Similarity   86.7%;  Pred. No. 1.9e-09;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              :|||||||||||||||||||||:|||| |:
Db         20 QVQLVESGGGVVQPGRSLRLSCAASGFTFS 49


RESULT 3
Q6N089_HUMAN
ID   Q6N089_HUMAN PRELIMINARY;      PRT;   472 AA.
AC   Q6N089;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686P15220.
GN   Name=DKFZp686P15220;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Rectum tumor;
RG   The German cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
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DR   EMBL; BX640627; CAE45781.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   472 AA;  51724 MW;  26CB340D0046D279 CRC64;

  Query Match             88.1%;  Score 133;  DB 2;  Length 472;
  Best Local Similarity   89.7%;  Pred. No. 2e-09;
  Matches   26;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDF 29
              ||||||||||:|||||||||||:|||| |
Db         20 EVQLVESGGGLVQPGRSLRLSCAASGFTF 48


RESULT 4
Q5EFE5_HUMAN
ID   Q5EFE5_HUMAN PRELIMINARY;      PRT;   475 AA.
AC   Q5EFE5;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Anti-RhD monoclonal T125 gamma1 heavy chain precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Gaucher C., Klein P., Beliard R.;
RT   "Sequence determination of the recombinant human anti-RhD monoclonal
RT   antibody T125.";
RL   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY894992; AAW82028.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   Pfam; PF07686; V-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Signal.
FT   SIGNAL        1     19       Potential.
FT   CHAIN        20    475       anti-RhD monoclonal T125 gamma1 heavy
FT                                chain.
SQ   SEQUENCE   475 AA;  52362 MW;  1367D400DC7D2859 CRC64;

  Query Match             88.1%;  Score 133;  DB 2;  Length 475;
  Best Local Similarity   89.7%;  Pred. No. 2e-09;
  Matches   26;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDF 29
              :||||||||||||||||||||:|||| |
Db         20 QVQLVESGGGVVQPGRSLRLSCTASGFTF 48


RESULT 5
Q8WU38_HUMAN
ID   Q8WU38_HUMAN PRELIMINARY;      PRT;   573 AA.
AC   Q8WU38;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHD protein.
GN   Name=IGHD;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RA   Director MGC Project;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   PROTEIN SEQUENCE.
RX   PubMed=1555592;
RA   Makiya R., Stigbrand T.;
RT   "Placental alkaline phosphatase has a binding site for the human
RT   immunoglobulin-G Fc portion.";
RL   Eur. J. Biochem. 205:341-345(1992).
DR   EMBL; BC021276; AAH21276.1; -; mRNA.
DR   PIR; S21205; S21205.
DR   PIR; S30532; S30532.
DR   HSSP; P18529; 1I8K.
DR   Ensembl; ENSG00000196122; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Immunoglobulin domain; Repeat.
SQ   SEQUENCE   573 AA;  62967 MW;  FD072344033AC530 CRC64;

  Query Match             88.1%;  Score 133;  DB 2;  Length 573;
  Best Local Similarity   89.7%;  Pred. No. 2.4e-09;
  Matches   26;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDF 29
              ||||||||||:|||||||||||:|||| |
Db         20 EVQLVESGGGLVQPGRSLRLSCAASGFTF 48
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RESULT 6
Q9UL93_HUMAN
ID   Q9UL93_HUMAN PRELIMINARY;      PRT;   116 AA.
AC   Q9UL93;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA   Hillson J.L., Karr N.S., Oppliger I.R., Mannik M., Sasso E.H.;
RT   "The structural basis of germline-encoded VH3 immunoglobulin binding
RT   to staphylococcal protein A.";
RL   J. Exp. Med. 178:331-336(1993).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2840480;
RA   Bird J., Galili N., Link M., Stites D., Sklar J.;
RT   "Continuing rearrangement but absence of somatic hypermutation in
RT   immunoglobulin genes of human B cell precursor leukemia.";
RL   J. Exp. Med. 168:229-245(1988).
DR   EMBL; AF035021; AAD56257.1; -; mRNA.
DR   PIR; PH1644; PH1644.
DR   PIR; PL0120; PL0120.
DR   HSSP; P01772; 2FB4.
DR   SMR; Q9UL93; 1-116.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12434 MW;  0DA0348154DD6061 CRC64;

  Query Match             87.4%;  Score 132;  DB 2;  Length 116;
  Best Local Similarity   89.7%;  Pred. No. 6.8e-10;
  Matches   26;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              |||||||||||||||||||:|||| |:
Db          1 VQLVESGGGVVQPGRSLRLSCAASGFTFS 29


RESULT 7
HV3K_HUMAN
ID   HV3K_HUMAN     STANDARD;      PRT;   126 AA.
AC   P01772;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region KOL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE, AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6884994;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=81072295; PubMed=7441755;
RA   Marquart M., Deisenhofer J., Huber R., Palm W.;
RT   "Crystallographic refinement and atomic models of the intact
RT   immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
RT   and 1.0-A resolution.";
RL   J. Mol. Biol. 141:369-391(1980).
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A02055; G1HUKL.
DR   PDB; 2FB4; X-ray; H=2-126.
DR   PDB; 2IG2; X-ray; H=2-126.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   DISULFID     22     96
FT   DISULFID    105    110
FT   NON_TER     126    126
FT   STRAND        3      7
FT   STRAND       11     12
FT   TURN         14     15
FT   STRAND       18     25
FT   HELIX        29     31
FT   STRAND       34     39
FT   TURN         41     42
FT   STRAND       45     51
FT   TURN         53     54
FT   STRAND       58     60
FT   HELIX        62     64
FT   STRAND       65     65
FT   TURN         66     67
FT   STRAND       68     73
FT   TURN         74     77
FT   STRAND       78     83
FT   HELIX        88     90
FT   STRAND       92     99
FT   STRAND      106    106
FT   TURN        107    108
FT   STRAND      109    109
FT   STRAND      113    116
FT   STRAND      120    124
SQ   SEQUENCE   126 AA;  13718 MW;  E4D71B52B16F8776 CRC64;

  Query Match             87.4%;  Score 132;  DB 1;  Length 126;
  Best Local Similarity   86.7%;  Pred. No. 7.4e-10;
  Matches   26;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              :|||||||||||||||||||||:||| |:
Db          1 QVQLVESGGGVVQPGRSLRLSCSSSGFIFS 30
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RESULT 8
HV3T_HUMAN
ID   HV3T_HUMAN     STANDARD;      PRT;   116 AA.
AC   P01781;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region GAL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=75059123; PubMed=4803843;
RA   Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT   "The primary structure of a monoclonal IgM-immunoglobulin
RT   (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT   type), subgroup H III. Architecture of the complete IgM-molecule.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN   [2]
RP   SEQUENCE REVISION TO 28-33.
RA   Hilschmann N.;
RL   Submitted (JUN-1975) to the PIR data bank.
CC   -!- MISCELLANEOUS: This mu chain was isolated from a Waldenstrom's
CC       macroglobulin.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A02064; M3HUGL.
DR   HSSP; P01772; 2FB4.
DR   SMR; P01781; 1-116.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    112       Ig-like.
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12731 MW;  2C67CA9AAAAA1282 CRC64;

  Query Match             86.8%;  Score 131;  DB 1;  Length 116;
  Best Local Similarity   86.2%;  Pred. No. 9.3e-10;
  Matches   25;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDF 29
              ||||||||| :|||||||||||:||||:|
Db          1 EVQLVESGGDLVQPGRSLRLSCAASGFBF 29


RESULT 9
HV3I_HUMAN
ID   HV3I_HUMAN     STANDARD;      PRT;   119 AA.
AC   P01770;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region NIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT   peptides of the H-chain, alignment of the tryptic peptides and
RT   discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT   characterization of the protein, the L- and H-chains, the cyanogen
RT   bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC       protein.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A91668; G1HUNI.
DR   HSSP; P01772; 2FB4.
DR   SMR; P01770; 1-119.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   DISULFID     22     96
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13243 MW;  C96935A6E55E165B CRC64;

  Query Match             86.8%;  Score 131;  DB 1;  Length 119;
  Best Local Similarity   83.3%;  Pred. No. 9.5e-10;
  Matches   25;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              :||||:||||||||||||||:|||| |:
Db          1 QVQLVQSGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 10
Q5M7V3_RAT
ID   Q5M7V3_RAT  PRELIMINARY;      PRT;   461 AA.
AC   Q5M7V3;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   LOC367586 protein.
GN   Name=LOC367586;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
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RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RG   NIH MGC Project;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC       histocompatibility complex class I molecules (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; BC088423; AAH88423.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
KW   Immunoglobulin domain; Repeat.
SQ   SEQUENCE   461 AA;  50949 MW;  25EA4ECE6FE0F5A9 CRC64;

  Query Match             86.8%;  Score 131;  DB 2;  Length 461;
  Best Local Similarity   83.3%;  Pred. No. 3.6e-09;
  Matches   25;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||:|||||||:|||:|||| |:
Db         20 EVQLVESGGGLVQPGRSLKLSCAASGFTFS 49


RESULT 11
Q5BK12_RAT
ID   Q5BK12_RAT  PRELIMINARY;      PRT;   479 AA.
AC   Q5BK12;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Igha protein.
GN   Name=Igha;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RG   NIH MGC Project;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC091247; AAH91247.1; -; mRNA.
DR   SMR; Q5BK12; 20-241.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   479 AA;  52329 MW;  8B146164AE8437C5 CRC64;

  Query Match             86.8%;  Score 131;  DB 2;  Length 479;
  Best Local Similarity   83.3%;  Pred. No. 3.8e-09;
  Matches   25;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||:|||||||:|||:|||| |:
Db         20 EVQLVESGGGLVQPGRSLKLSCTASGFTFS 49


RESULT 12
Q9UL90_HUMAN
ID   Q9UL90_HUMAN PRELIMINARY;      PRT;   113 AA.
AC   Q9UL90;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1730252;
RA   Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA   Schuurman R.K.;
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RT   "Restricted utilization of germ-line VH3 genes and short diverse third
RT   complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT   immunoglobulin heavy chain rearrangements.";
RL   Eur. J. Immunol. 22:247-251(1992).
DR   EMBL; AF035024; AAD56260.1; -; mRNA.
DR   PIR; S78486; S78486.
DR   HSSP; P01772; 2FB4.
DR   SMR; Q9UL90; 1-113.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     113    113
SQ   SEQUENCE   113 AA;  12437 MW;  ED57FDD19086D07F CRC64;

  Query Match             86.1%;  Score 130;  DB 2;  Length 113;
  Best Local Similarity   86.7%;  Pred. No. 1.2e-09;
  Matches   26;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCASGFDFT 30
              |||||||||||||||| ||||||:|||| |:
Db          1 EVQLVESGGGVVQPGGSLRLSCAASGFTFS 30


RESULT 13
HV3G_HUMAN
ID   HV3G_HUMAN     STANDARD;      PRT;   122 AA.
AC   P01768;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region CAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=81013859; PubMed=6774332;
RA   Lehman D.W., Putnam F.W.;
RT   "Amino acid sequence of the variable region of a human mu chain:
RT   location of a possible JH segment.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
CC   -!- MISCELLANEOUS: This mu chain was isolated from the plasma of a
CC       patient with macroglobulinemia.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A02051; M3HUAM.
DR   HSSP; P01772; 2FB4.
DR   SMR; P01768; 2-122.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13668 MW;  A42D0F17D252F1C2 CRC64;

  Query Match             85.4%;  Score 129;  DB 1;  Length 122;
  Best Local Similarity   80.0%;  Pred. No. 1.8e-09;
  Matches   24;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCASGFDFT 30
              :|:|||||||||:||||||||||:|||| |:
Db          1 QVELVESGGGVVZPGRSLRLSCAASGFTFS 30


RESULT 14
Q9UL84_HUMAN
ID   Q9UL84_HUMAN PRELIMINARY;      PRT;   122 AA.
AC   Q9UL84;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035030; AAD56266.1; -; mRNA.
DR   HSSP; P01772; 2FB4.
DR   SMR; Q9UL84; 1-122.
DR   Ensembl; ENSG00000130076; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13579 MW;  36054D41366545B8 CRC64;

  Query Match             85.4%;  Score 129;  DB 2;  Length 122;
  Best Local Similarity   86.7%;  Pred. No. 1.8e-09;
  Matches   26;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCASGFDFT 30
              |||||||||||||||||||||:|| | |:
Db          1 EVQLVESGGGVVQPGRSLRLSCAASRFTFS 30


RESULT 15
Q5I0J0_RAT
ID   Q5I0J0_RAT  PRELIMINARY;      PRT;   465 AA.
AC   Q5I0J0;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical LOC299354.
GN   Name=LOC299354;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC       histocompatibility complex class I molecules (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; BC088271; AAH88271.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
KW   Hypothetical protein; Immunoglobulin domain; Repeat.
SQ   SEQUENCE   465 AA;  51699 MW;  97C4533A213A424F CRC64;

  Query Match             85.4%;  Score 129;  DB 2;  Length 465;
  Best Local Similarity   80.0%;  Pred. No. 6.9e-09;
  Matches   24;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||:||||||::|||:|||| |:
Db         20 EVQLVESGGGLVQPGRSMKLSCAASGFTFS 49


Search completed: March 25, 2006, 09:13:50
Job time : 108.063 secs
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:14:16 ; Search time 27.3298 Seconds
(without alignments)
90.753 Million cell updates/sec

Title: US-10-755-382-31
Perfect score: 151
Sequence: 1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	151	100.0	30	1	US-08-318-157B-31	Sequence 31, Appl
2	151	100.0	30	2	US-09-253-794-31	Sequence 31, Appl
3	151	100.0	119	1	US-08-318-157B-13	Sequence 13, Appl
4	151	100.0	119	1	US-08-318-157B-14	Sequence 14, Appl
5	151	100.0	119	1	US-08-318-157B-15	Sequence 15, Appl
6	151	100.0	119	2	US-09-253-794-13	Sequence 13, Appl
7	151	100.0	119	2	US-09-253-794-14	Sequence 14, Appl
8	151	100.0	119	2	US-09-253-794-15	Sequence 15, Appl
9	151	100.0	489	4	PCT-US95-11405-35	Sequence 35, Appl
10	148	98.0	30	1	US-08-318-157B-30	Sequence 30, Appl
11	148	98.0	30	2	US-09-253-794-30	Sequence 30, Appl
12	148	98.0	119	1	US-08-318-157B-12	Sequence 12, Appl
13	148	98.0	119	1	US-08-318-157B-17	Sequence 17, Appl
14	148	98.0	119	2	US-09-253-794-12	Sequence 12, Appl
15	148	98.0	119	2	US-09-253-794-17	Sequence 17, Appl
16	140	92.7	119	1	US-08-207-996-22	Sequence 22, Appl
17	140	92.7	119	1	US-08-760-840A-22	Sequence 22, Appl
18	140	92.7	119	2	US-09-266-119-22	Sequence 22, Appl
19	140	92.7	119	2	US-09-602-709-22	Sequence 22, Appl
20	138	91.4	119	1	US-08-303-569B-20	Sequence 20, Appl
21	138	91.4	119	1	US-08-303-569B-23	Sequence 23, Appl
22	138	91.4	119	1	US-08-116-247-21	Sequence 21, Appl
23	138	91.4	119	1	US-08-116-247-24	Sequence 24, Appl
24	138	91.4	119	2	US-09-795-515-20	Sequence 20, Appl
25	138	91.4	119	2	US-09-795-515-23	Sequence 23, Appl
26	138	91.4	119	2	US-09-348-224-21	Sequence 21, Appl
27	138	91.4	119	2	US-09-348-224-24	Sequence 24, Appl
28	137	90.7	117	1	US-08-652-558-3	Sequence 3, Appli
29	137	90.7	117	1	US-08-652-558-44	Sequence 44, Appl
30	137	90.7	117	1	US-08-652-558-45	Sequence 45, Appl
31	137	90.7	117	1	US-08-652-558-46	Sequence 46, Appl
32	137	90.7	119	1	US-08-859-649-20	Sequence 20, Appl
33	137	90.7	119	1	US-08-859-649-22	Sequence 22, Appl
34	137	90.7	119	1	US-08-859-649-23	Sequence 23, Appl
35	137	90.7	119	1	US-08-859-649-24	Sequence 24, Appl
36	137	90.7	119	1	US-08-859-649-31	Sequence 31, Appl
37	137	90.7	119	2	US-08-207-861-20	Sequence 20, Appl
38	137	90.7	119	2	US-08-207-861-22	Sequence 22, Appl
39	137	90.7	119	2	US-08-207-861-23	Sequence 23, Appl
40	137	90.7	119	2	US-08-207-861-24	Sequence 24, Appl
41	137	90.7	119	2	US-08-207-861-31	Sequence 31, Appl
42	137	90.7	119	2	US-08-859-648-20	Sequence 20, Appl
43	137	90.7	119	2	US-08-859-648-22	Sequence 22, Appl
44	137	90.7	119	2	US-08-859-648-23	Sequence 23, Appl
45	137	90.7	119	2	US-08-859-648-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-08-318-157B-31
; Sequence 31, Application US/08318157B
; Patent No. 5874540
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; APPLICANT: ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,157B
; FILING DATE: 05-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-157B-31

Query Match 100.0%; Score 151; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.7e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
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RESULT 2
US-09-253-794-31
; Sequence 31, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 31:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 30 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-253-794-31

  Query Match             100.0%;  Score 151;  DB 2;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 3
US-08-318-157B-13
; Sequence 13, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-13

  Query Match             100.0%;  Score 151;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 4
US-08-318-157B-14
; Sequence 14, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-14

  Query Match             100.0%;  Score 151;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 5
US-08-318-157B-15
; Sequence 15, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-15

  Query Match             100.0%;  Score 151;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 6
US-09-253-794-13
; Sequence 13, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-253-794-13

  Query Match             100.0%;  Score 151;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 7
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
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;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/253,794
;              FILING DATE: 22-Feb-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US 08/318,157
;              FILING DATE: 05-OCT-1994
;         ATTORNEY/AGENT INFORMATION:
;              NAME: SAXE, Bernhard D.
;              REGISTRATION NUMBER: 28,665
;              REFERENCE/DOCKET NUMBER: 18733/464
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (202)672-5300
;              TELEFAX: (202)672-5399
;              TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 14:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 119 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: <Unknown>
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

  Query Match             100.0%;  Score 151;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 8
US-09-253-794-15
; Sequence 15, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;         APPLICANT: HANSEN, Hans J.
;                    ARMOUR, Kathryn L.
;         TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                             MOUSE MONOCLONAL ANTIBODIES
;         NUMBER OF SEQUENCES: 58
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Foley & Lardner
;              STREET: 3000 K Street, N.W., Suite 500
;              CITY: Washington
;              STATE: D.C.
;              COUNTRY: USA
;              ZIP: 20007-5109
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/253,794
;              FILING DATE: 22-Feb-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US 08/318,157
;              FILING DATE: 05-OCT-1994
;         ATTORNEY/AGENT INFORMATION:
;              NAME: SAXE, Bernhard D.
;              REGISTRATION NUMBER: 28,665
;              REFERENCE/DOCKET NUMBER: 18733/464
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (202)672-5300
;              TELEFAX: (202)672-5399
;              TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 15:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 119 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: <Unknown>
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-253-794-15

  Query Match             100.0%;  Score 151;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 7.6e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 9
PCT-US95-11405-35
; Sequence 35, Application PC/TUS9511405
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  PHOSPHOROUS-32 LABELING OF ANTIBODIES
;    TITLE OF INVENTION:  FOR CANCER THERAPY
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/11405
;      FILING DATE:  18-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/308,103
;      FILING DATE:  16-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/599/IMIN
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  489 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-11405-35

  Query Match             100.0%;  Score 151;  DB 4;  Length 489;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||||||||
Db         23 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 52


RESULT 10
US-08-318-157B-30
; Sequence 30, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  30 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-30

  Query Match             98.0%;  Score 148;  DB 1;  Length 30;
  Best Local Similarity   96.7%;  Pred. No. 4.4e-14;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 11
US-09-253-794-30
; Sequence 30, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 30:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 30 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-253-794-30

  Query Match             98.0%;  Score 148;  DB 2;  Length 30;
  Best Local Similarity   96.7%;  Pred. No. 4.4e-14;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 12
US-08-318-157B-12
; Sequence 12, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-12
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  Query Match             98.0%;  Score 148;  DB 1;  Length 119;
  Best Local Similarity   96.7%;  Pred. No. 2e-13;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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              |||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 13
US-08-318-157B-17
; Sequence 17, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-17

  Query Match             98.0%;  Score 148;  DB 1;  Length 119;
  Best Local Similarity   96.7%;  Pred. No. 2e-13;
  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 14
US-09-253-794-12
; Sequence 12, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-253-794-12

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  Matches   29;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30


RESULT 15
US-09-253-794-17
; Sequence 17, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
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; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-253-794-17

Query Match 98.0%; Score 148; DB 2; Length 119;
Best Local Similarity 96.7%; Pred. No. 2e-13;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
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Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFT 30
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Search completed: March 25, 2006, 09:18:46
Job time : 28.3298 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:55:36 ; Search time 89.5288 Seconds
(without alignments)
140.009 Million cell updates/sec

Title: US-10-755-382-31
Perfect score: 151
Sequence: 1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	151	100.0	30	3	US-09-253-794-31	Sequence 31, Appl
2	151	100.0	30	5	US-10-755-382-31	Sequence 31, Appl
3	151	100.0	118	4	US-10-270-073-3	Sequence 3, Appli
4	151	100.0	119	3	US-09-253-794-13	Sequence 13, Appl
5	151	100.0	119	3	US-09-253-794-14	Sequence 14, Appl
6	151	100.0	119	3	US-09-253-794-15	Sequence 15, Appl
7	151	100.0	119	4	US-10-680-734-13	Sequence 13, Appl
8	151	100.0	119	4	US-10-680-734-14	Sequence 14, Appl
9	151	100.0	119	4	US-10-680-734-15	Sequence 15, Appl
10	151	100.0	119	4	US-10-680-734-17	Sequence 17, Appl
11	151	100.0	119	5	US-10-755-382-13	Sequence 13, Appl
12	151	100.0	119	5	US-10-755-382-14	Sequence 14, Appl
13	151	100.0	119	5	US-10-755-382-15	Sequence 15, Appl
14	151	100.0	138	4	US-10-006-771A-4	Sequence 4, Appli
15	151	100.0	256	4	US-10-270-073-6	Sequence 6, Appli
16	151	100.0	257	4	US-10-270-073-8	Sequence 8, Appli
17	151	100.0	261	4	US-10-270-071-18	Sequence 18, Appl
18	151	100.0	261	4	US-10-270-073-2	Sequence 2, Appli
19	151	100.0	261	4	US-10-328-190-6	Sequence 6, Appli
20	151	100.0	267	4	US-10-270-071-22	Sequence 22, Appl
21	151	100.0	267	4	US-10-270-071-26	Sequence 26, Appl
22	151	100.0	267	4	US-10-270-071-30	Sequence 30, Appl
23	151	100.0	267	4	US-10-270-071-36	Sequence 36, Appl
24	151	100.0	358	5	US-10-829-388-12	Sequence 12, Appl
25	151	100.0	363	5	US-10-829-388-2	Sequence 2, Appli
26	151	100.0	364	5	US-10-829-388-11	Sequence 11, Appl
27	151	100.0	370	5	US-10-829-388-1	Sequence 1, Appli
28	151	100.0	415	4	US-10-328-190-12	Sequence 12, Appl
29	151	100.0	443	4	US-10-006-773-2	Sequence 2, Appli
30	151	100.0	443	4	US-10-006-771A-2	Sequence 2, Appli
31	151	100.0	468	4	US-10-377-109-2	Sequence 2, Appli
32	151	100.0	669	5	US-10-900-928-3	Sequence 3, Appli
33	148	98.0	30	3	US-09-253-794-30	Sequence 30, Appl
34	148	98.0	30	5	US-10-755-382-30	Sequence 30, Appl
35	148	98.0	119	3	US-09-253-794-12	Sequence 12, Appl
36	148	98.0	119	3	US-09-253-794-17	Sequence 17, Appl
37	148	98.0	119	4	US-10-680-734-12	Sequence 12, Appl
38	148	98.0	119	5	US-10-755-382-12	Sequence 12, Appl
39	148	98.0	119	5	US-10-755-382-17	Sequence 17, Appl
40	143	94.7	244	3	US-09-880-748-1910	Sequence 1910, Ap
41	143	94.7	244	4	US-10-293-418-1910	Sequence 1910, Ap
42	140	92.7	119	6	US-11-056-776-4	Sequence 4, Appli
43	140	92.7	449	6	US-11-056-776-5	Sequence 5, Appli
44	140	92.7	468	6	US-11-056-776-6	Sequence 6, Appli
45	138	91.4	119	3	US-09-795-515-20	Sequence 20, Appl

ALIGNMENTS

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RESULT 1
US-09-253-794-31
; Sequence 31, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 31:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 30 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-253-794-31

  Query Match           100.0%;  Score 151;  DB 3;  Length 30;
  Best Local Similarity  100.0%;  Pred. No. 3.5e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
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Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 2
US-10-755-382-31
; Sequence 31, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 31:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 30 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-755-382-31

  Query Match             100.0%;  Score 151;  DB 5;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-13;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
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Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 3
US-10-270-073-3
; Sequence 3, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14VH deduced amino acid sequence
US-10-270-073-3

  Query Match             100.0%;  Score 151;  DB 4;  Length 118;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
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Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 4
US-09-253-794-13
; Sequence 13, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
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;           TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-253-794-13

  Query Match             100.0%;  Score 151;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
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Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 5
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

  Query Match             100.0%;  Score 151;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
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Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 6
US-09-253-794-15
; Sequence 15, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-253-794-15

  Query Match             100.0%;  Score 151;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 7
US-10-680-734-13
; Sequence 13, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
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;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-13

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  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 8
US-10-680-734-14
; Sequence 14, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-14

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  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 9
US-10-680-734-15
; Sequence 15, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-15

  Query Match             100.0%;  Score 151;  DB 4;  Length 119;
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  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 10
US-10-680-734-17
; Sequence 17, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-17

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  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 11
US-10-755-382-13
; Sequence 13, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
```

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;            FILING DATE: 05-OCT-1994
;         ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;         TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 13:
;         SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-755-382-13

  Query Match             100.0%;  Score 151;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
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Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 12
US-10-755-382-14
; Sequence 14, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-755-382-14

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Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30


RESULT 13
US-10-755-382-15
; Sequence 15, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
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;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-755-382-15

  Query Match             100.0%;  Score 151;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 14
US-10-006-771A-4
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; Sequence 4, Application US/10006771A
; Publication No. US20020165360A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen
;  FILE REFERENCE: 002
;  CURRENT APPLICATION NUMBER: US/10/006,771A
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: 60/250,090
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 138
;   TYPE: PRT
;   ORGANISM: Homo sapiens and Mus sp.
US-10-006-771A-4

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  Best Local Similarity   100.0%;  Pred. No. 1.7e-12;
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Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
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Db         20 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 49


RESULT 15
US-10-270-073-6
; Sequence 6, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14-0 amino acid sequence
US-10-270-073-6

  Query Match             100.0%;  Score 151;  DB 4;  Length 256;
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Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 53


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Job time : 90.5288 secs
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:58:56 ; Search time 10.8377 Seconds
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81.644 Million cell updates/sec

Title: US-10-755-382-31
Perfect score: 151
Sequence: 1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30

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Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	143	94.7	244	7	US-11-054-515-1910	Sequence 1910, Ap
2	138	91.4	249	7	US-11-054-515-1956	Sequence 1956, Ap
3	138	91.4	253	7	US-11-054-515-1628	Sequence 1628, Ap
4	137	90.7	122	6	US-10-982-440-53	Sequence 53, Appl
5	137	90.7	123	6	US-10-982-440-1	Sequence 1, Appli
6	137	90.7	124	7	US-11-040-159-14	Sequence 14, Appl
7	137	90.7	124	7	US-11-040-159-16	Sequence 16, Appl
8	137	90.7	251	7	US-11-054-515-955	Sequence 955, App
9	137	90.7	252	7	US-11-054-515-988	Sequence 988, App
10	137	90.7	254	7	US-11-054-515-1428	Sequence 1428, Ap
11	136	90.1	254	7	US-11-054-515-1302	Sequence 1302, Ap
12	136	90.1	254	7	US-11-054-515-1796	Sequence 1796, Ap
13	136	90.1	449	7	US-11-080-587-6	Sequence 6, Appli
14	135	89.4	118	6	US-10-648-816-10	Sequence 10, Appl
15	135	89.4	118	6	US-10-648-816-12	Sequence 12, Appl
16	135	89.4	118	6	US-10-648-816-13	Sequence 13, Appl
17	135	89.4	119	7	US-11-221-900-12	Sequence 12, Appl
18	135	89.4	121	6	US-10-648-816-16	Sequence 16, Appl
19	135	89.4	122	7	US-11-051-453-1	Sequence 1, Appli
20	135	89.4	124	7	US-11-064-174-2	Sequence 2, Appli
21	135	89.4	124	7	US-11-064-174-4	Sequence 4, Appli
22	135	89.4	124	7	US-11-064-174-5	Sequence 5, Appli
23	135	89.4	124	7	US-11-064-174-6	Sequence 6, Appli
24	135	89.4	124	7	US-11-064-174-7	Sequence 7, Appli
25	135	89.4	125	7	US-11-064-174-151	Sequence 151, App
26	135	89.4	141	7	US-11-051-453-49	Sequence 49, Appl
27	135	89.4	251	7	US-11-054-515-1320	Sequence 1320, Ap
28	134	88.7	98	7	US-11-054-669-23	Sequence 23, Appl
29	134	88.7	98	7	US-11-054-669-24	Sequence 24, Appl
30	134	88.7	98	7	US-11-054-669-25	Sequence 25, Appl
31	134	88.7	98	7	US-11-054-669-26	Sequence 26, Appl
32	134	88.7	98	7	US-11-084-554-34	Sequence 34, Appl
33	134	88.7	98	7	US-11-084-554-35	Sequence 35, Appl
34	134	88.7	98	7	US-11-093-274-31	Sequence 31, Appl
35	134	88.7	98	7	US-11-004-590-24	Sequence 24, Appl
36	134	88.7	98	7	US-11-004-590-25	Sequence 25, Appl
37	134	88.7	98	7	US-11-004-590-26	Sequence 26, Appl
38	134	88.7	98	7	US-11-136-250-34	Sequence 34, Appl
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40	134	88.7	117	6	US-10-771-257-9	Sequence 9, Appli
41	134	88.7	117	6	US-10-771-257-18	Sequence 18, Appl
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43	134	88.7	117	7	US-11-127-677-9	Sequence 9, Appli
44	134	88.7	117	7	US-11-127-677-18	Sequence 18, Appl
45	134	88.7	117	7	US-11-165-023-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-11-054-515-1910
; Sequence 1910, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1910
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1910

Query Match 94.7%; Score 143; DB 7; Length 244;
Best Local Similarity 96.6%; Pred. No. 2.8e-12;
Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDF 29
              |||||||||||||||||||||||||||:||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFDF 29
```

RESULT 2

US-11-054-515-1956
; Sequence 1956, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1956
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1956

Query Match 91.4%; Score 138; DB 7; Length 249;
Best Local Similarity 90.0%; Pred. No. 1.4e-11;
Matches 27; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              |||||:||||||||||||||:|||| ||
Db          1 EVQLVQSGGGVVQPGRSLRLSCAASGFTFT 30
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RESULT 3
US-11-054-515-1628
; Sequence 1628, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1628
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1628

Query Match 91.4%; Score 138; DB 7; Length 253;
Best Local Similarity 90.0%; Pred. No. 1.4e-11;
Matches 27; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              |||||:||||||||||||||:|||| ||
Db          1 EVQLVQSGGGVVQPGRSLRLSCAASGFTFT 30
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RESULT 4
US-10-982-440-53
; Sequence 53, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
; APPLICANT: Oliner, John
; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; FILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; PRIOR FILING DATE: 2004-10-19
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 53
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-440-53

Query Match 90.7%; Score 137; DB 6; Length 122;
Best Local Similarity 90.0%; Pred. No. 9.1e-12;
Matches 27; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||||||||||||||||||:|||| |:
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30
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RESULT 5
US-10-982-440-1
; Sequence 1, Application US/10982440
; Publication No. US20060018909A1
; GENERAL INFORMATION:
; APPLICANT: Oliner, John
; APPLICANT: Graham, Kevin
; TITLE OF INVENTION: Angiopoietin-2 Specific Binding Agents
; FILE REFERENCE: 04-881-A
; CURRENT APPLICATION NUMBER: US/10/982,440
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: 60/620,161
; PRIOR FILING DATE: 2004-10-19
; NUMBER OF SEQ ID NOS: 215
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-440-1

Query Match 90.7%; Score 137; DB 6; Length 123;
Best Local Similarity 90.0%; Pred. No. 9.1e-12;

Matches 27; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              |||||||||||||||||||||:|||| |:
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30
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RESULT 6
US-11-040-159-14
; Sequence 14, Application US/11040159
; Publication No. US20050255552A1
; GENERAL INFORMATION:
; APPLICANT: Flynn, Peter
; APPLICANT: Luehrsen, Kenneth
; APPLICANT: Balint, Robert F.
; APPLICANT: Her, Jeng-Horng
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Yarranton, Geoffrey T.
; APPLICANT: KaloBios, Inc.
; TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
; TITLE OF INVENTION: Binding Determinants
; FILE REFERENCE: 021167-001730US
; CURRENT APPLICATION NUMBER: US/11/040,159
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US 60/537,364
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/546,216
; PRIOR FILING DATE: 2004-02-23
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:V-region of
; OTHER INFORMATION: anti-PcrV antibody F6 VH
US-11-040-159-14

Query Match 90.7%; Score 137; DB 7; Length 124;
Best Local Similarity 90.0%; Pred. No. 9.2e-12;
Matches 27; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              |||||||||||||||||||||:|||| |:
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30
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RESULT 7
US-11-040-159-16
; Sequence 16, Application US/11040159
; Publication No. US20050255552A1
; GENERAL INFORMATION:
; APPLICANT: Flynn, Peter
; APPLICANT: Luehrsen, Kenneth
; APPLICANT: Balint, Robert F.
; APPLICANT: Her, Jeng-Horng
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Yarranton, Geoffrey T.
; APPLICANT: KaloBios, Inc.
; TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
; TITLE OF INVENTION: Binding Determinants
; FILE REFERENCE: 021167-001730US
; CURRENT APPLICATION NUMBER: US/11/040,159
; CURRENT FILING DATE: 2005-01-20
; PRIOR APPLICATION NUMBER: US 60/537,364
; PRIOR FILING DATE: 2004-01-20
; PRIOR APPLICATION NUMBER: US 60/546,216
; PRIOR FILING DATE: 2004-02-23
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:V-region of
; OTHER INFORMATION: anti-PcrV antibody 1F1 VH
US-11-040-159-16

Query Match 90.7%; Score 137; DB 7; Length 124;
Best Local Similarity 90.0%; Pred. No. 9.2e-12;
Matches 27; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              |||||||||||||||||||||:|||| |:
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30
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RESULT 8
US-11-054-515-955
; Sequence 955, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 955
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-955

Query Match 90.7%; Score 137; DB 7; Length 251;
Best Local Similarity 90.0%; Pred. No. 1.9e-11;
Matches 27; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              |||||||||||||||||||||:|||| |:
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30
```

RESULT 9
US-11-054-515-988
; Sequence 988, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10

```
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 988
;   LENGTH: 252
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-988

  Query Match             90.7%;  Score 137;  DB 7;  Length 252;
  Best Local Similarity   90.0%;  Pred. No. 1.9e-11;
  Matches   27;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              |||||||||||||||||||||:|||| |:
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 10
US-11-054-515-1428
; Sequence 1428, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1428
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1428

  Query Match             90.7%;  Score 137;  DB 7;  Length 254;
  Best Local Similarity   90.0%;  Pred. No. 1.9e-11;
  Matches   27;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              |||||||||||||||||||||:|||| |:
Db          1 EVQLVESGGGVVQPGRSLRLSCAASGFTFS 30


RESULT 11
US-11-054-515-1302
; Sequence 1302, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1302
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1302

  Query Match             90.1%;  Score 136;  DB 7;  Length 254;
  Best Local Similarity   89.7%;  Pred. No. 2.6e-11;
  Matches   26;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VQLVESGGGVVQPGRSLRLSCSASGFDFT 30
              ||||:||||||||||||||:||||||:
Db          2 VQLVQSGGGVVQPGRSLRLSCAASGFDFS 30


RESULT 12
US-11-054-515-1796
; Sequence 1796, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
```

; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1796
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1796

Query Match 90.1%; Score 136; DB 7; Length 254;
Best Local Similarity 93.1%; Pred. No. 2.6e-11;
Matches 27; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCSASGFDF 29
||||||||||||||||||||||||:|||| |
Db 1 EVQLVESGGGVVQPGRSLRLSCAASGFTF 29

RESULT 13
US-11-080-587-6
; Sequence 6, Application US/11080587
; Publication No. US20060002942A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Calicheamicin Conjugates
; FILE REFERENCE: AM101462
; CURRENT APPLICATION NUMBER: US/11/080,587
; CURRENT FILING DATE: 2005-03-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Human/murine chimera
; FEATURE:
; OTHER INFORMATION: Human/Murine Chimera G193 Heavy Chain
US-11-080-587-6

Query Match 90.1%; Score 136; DB 7; Length 449;
Best Local Similarity 90.0%; Pred. No. 4.5e-11;
Matches 27; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
|||||||||||||||||||||||| ||| |:
Db 1 EVQLVESGGGVVQPGRSLRLSCSTSGFTFS 30

RESULT 14
US-10-648-816-10
; Sequence 10, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 10
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-10

Query Match 89.4%; Score 135; DB 6; Length 118;
Best Local Similarity 86.7%; Pred. No. 1.6e-11;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
|||||||||||:|||| ||||||:|||:|||
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFT 30

RESULT 15
US-10-648-816-12
; Sequence 12, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
; APPLICANT: Van Bruggen, Nicholas
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: P1717D1
; CURRENT APPLICATION NUMBER: US/10/648,816
; CURRENT FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: US/09/718,694
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 09/218,481
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 12
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-648-816-12

Query Match 89.4%; Score 135; DB 6; Length 118;
Best Local Similarity 86.7%; Pred. No. 1.6e-11;
Matches 26; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVQLVESGGGVVQPGRSLRLSCSASGFDFT 30
|||||||||||:|||| ||||||:|||:|||
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGYDFT 30

Search completed: March 25, 2006, 10:09:19
Job time : 10.8377 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:10 ; Search time 51.6021 Seconds
(without alignments)
119.206 Million cell updates/sec

Title: US-10-755-382-33
Perfect score: 81
Sequence: 1 WVRQAPGKGLEWVA 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	81	100.0	14	2	AAR97326	Aar97326 Humanised
2	81	100.0	14	5	AAO17610	Aao17610 Human FAP
3	81	100.0	14	7	ABO33890	Abo33890 Anti-GPI-
4	81	100.0	14	7	ADI20633	Adi20633 HFR2 prot
5	81	100.0	14	8	ADR38742	Adr38742 Mouse hea
6	81	100.0	14	8	ADR38754	Adr38754 Mouse hea
7	81	100.0	14	8	ADR38738	Adr38738 Mouse hea
8	81	100.0	14	8	ADR38762	Adr38762 Mouse hea
9	81	100.0	14	8	ADR38746	Adr38746 Mouse hea
10	81	100.0	14	8	ADR38766	Adr38766 Mouse hea
11	81	100.0	14	8	ADR38758	Adr38758 Mouse hea
12	81	100.0	14	8	ADR38750	Adr38750 Mouse hea
13	81	100.0	14	9	ADW96736	Adw96736 Anti-EGFR
14	81	100.0	14	9	ADW96723	Adw96723 Anti-EGFR
15	81	100.0	14	9	ADW80308	Adw80308 Human ant
16	81	100.0	14	9	ADW80295	Adw80295 Human ant
17	81	100.0	14	9	ADY31370	Ady31370 Human ant
18	81	100.0	14	9	ADY31373	Ady31373 Human ant
19	81	100.0	14	9	ADY31400	Ady31400 Human ant
20	81	100.0	14	9	ADZ35836	Adz35836 Anti-gluc
21	81	100.0	14	9	AEA21477	Aea21477 Human ant
22	81	100.0	17	9	ADY31505	Ady31505 Human ant
23	81	100.0	17	9	ADY31532	Ady31532 Human ant
24	81	100.0	17	9	ADY31502	Ady31502 Human ant
25	81	100.0	19	2	AAW94736	Aaw94736 Anti-Stap
26	81	100.0	44	8	ADU87725	Adu87725 Human hea
27	81	100.0	58	9	AEC20858	Aec20858 Human var
28	81	100.0	61	2	AAR76975	Aar76975 HSV-neutr
29	81	100.0	62	2	AAR76976	Aar76976 HSV-neutr
30	81	100.0	66	6	ABU56837	Abu56837 BoNT/A Hc
31	81	100.0	66	6	ABU56866	Abu56866 BoNT/A Hc
32	81	100.0	82	8	ADL35113	Adl35113 Humanised
33	81	100.0	82	8	ADL35115	Adl35115 Humanised
34	81	100.0	82	8	ADL35112	Adl35112 Murine an
35	81	100.0	82	8	ADL35114	Adl35114 Humanised
36	81	100.0	82	8	ADL35117	Adl35117 Humanised
37	81	100.0	82	8	ADL35116	Adl35116 Humanised
38	81	100.0	82	9	AEA21573	Aea21573 Human Ig
39	81	100.0	87	8	ADU87732	Adu87732 Amino aci
40	81	100.0	89	6	AAE35911	Aae35911 Human DP5
41	81	100.0	91	9	ADW97148	Adw97148 Human IL-
42	81	100.0	92	9	ADW97150	Adw97150 Human IL-
43	81	100.0	93	6	ABO27274	Abo27274 Human Hum
44	81	100.0	93	9	ADW97147	Adw97147 Human IL-
45	81	100.0	93	9	ADW97179	Adw97179 Human IL-

ALIGNMENTS

RESULT 1
AAR97326
ID AAR97326 standard; peptide; 14 AA.
XX
AC AAR97326;
XX
DT 15-OCT-1996 (first entry)
XX
DE Humanised monoclonal antibody heavy chain framework region.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Homo sapiens.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Claim 7; Page 39; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. This sequence corresponds to the second framework region of the
CC heavy chain of the humanised MAb. See AAR97313-97333

```
XX
SQ   Sequence 14 AA;

  Query Match             100.0%;  Score 81;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 2
AAO17610
ID   AAO17610 standard; peptide; 14 AA.
XX
AC   AAO17610;
XX
DT   08-AUG-2002  (first entry)
XX
DE   Human FAPalpha specific VL region from VH50 FR2 peptide.
XX
KW   Human; FAPalpha; fibroblast activating protein alpha; antibody; Ab;
KW   gene therapy; cancer; wound healing; inflammation; cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200168708-A2.
XX
PD   20-SEP-2001.
XX
PF   16-MAR-2001; 2001WO-EP004716.
XX
PR   17-MAR-2000; 2000DE-01013286.
PR   11-SEP-2000; 2000GB-00022216.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM PHARMA KG.
XX
PI   Park J,  Garin-Chesa P,  Pfizenmaier K,  Moosmayer D,  Mersmann M;
PI   Schmidt A;
XX
DR   WPI; 2002-041180/05.
DR   N-PSDB; AAL46555.
XX
PT   New human humanized antibody that specifically binds to fibroblasts
PT   activating protein alpha, useful for treating cancer or tumor, and for
PT   imaging tumors associated with activated stromal fibroblasts, e.g. lung
PT   or breast cancer.
XX
PS   Disclosure; Fig 6C; 109pp; English.
XX
CC   The present invention relates to a human or humanised antibody (Ab) which
CC   specifically binds to fibroblast activating protein alpha (FAPalpha). The
CC   antibodies are useful for preparing a composition for the treatment of
CC   cancer, and for imaging tumours associated with activated stromal
CC   fibroblasts, such as colorectal cancer, non-small-cell lung cancer,
CC   breast cancer, head and neck cancer, ovarian cancer, lung cancer, bladder
CC   cancer, pancreatic cancer and metastatic brain cancer, and diseases
CC   associated with the same, such as inflammation and wound healing. The
CC   present sequence is a peptide described in the exemplification of the
CC   invention
XX
SQ   Sequence 14 AA;

  Query Match             100.0%;  Score 81;  DB 5;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 3
ABO33890
ID   ABO33890 standard; peptide; 14 AA.
XX
AC   ABO33890;
XX
DT   18-SEP-2003  (first entry)
XX
DE   Anti-GPI-antibody heavy chain framework region #8.
XX
KW   Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide;
KW   anti-GPI-antibody; GPI; glucose-6-phosphate isomerase;
KW   autoimmune disease; rheumatoid arthritis; heavy chain variable region;
KW   VH; framework region.
XX
OS   Homo sapiens.
XX
PN   US2002146753-A1.
XX
PD   10-OCT-2002.
XX
PF   06-APR-2001; 2001US-00828708.
XX
PR   06-APR-2001; 2001US-00828708.
XX
PA   (DITZ/) DITZEL H.
PA   (BURT/) BURTON D R.
PA   (SCHA/) SCHALLER M.
XX
PI   Ditzel H,  Burton DR,  Schaller M;
XX
DR   WPI; 2003-521517/49.
XX
PT   Immunopolypeptide for diagnosis and treatment of human autoimmune
PT   disease, e.g., human rheumatoid arthritis, comprises a polypeptide that
PT   binds to human glucose-6-phosphate isomerase.
XX
PS   Claim 6; Fig 4B; 47pp; English.
XX
CC   The invention describes an immunopolypeptide comprising a polypeptide
CC   that binds to human glucose-6-phosphate isomerase (GPI). The methods and
CC   compositions are used for diagnosis and treatment of human autoimmune
CC   disease, e.g., human rheumatoid arthritis. This is the amino acid
CC   sequence of human anti-GPI-antibody heavy chain variable region framework
CC   region
XX
SQ   Sequence 14 AA;

  Query Match             100.0%;  Score 81;  DB 7;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 4
ADI20633
ID   ADI20633 standard; protein; 14 AA.
XX
AC   ADI20633;
XX
DT   22-APR-2004  (first entry)
XX
DE   HFR2 protein.
XX
KW   immunoglobulin molecule; heavy chain framework region; HFR1; HFR2; HFR3;
KW   HFR4; tumour imaging; protein chips assay; light chain framework region;
KW   LFR.
XX
OS   Synthetic.
XX
```

PN WO2003025124-A2.
XX
PD 27-MAR-2003.
XX
PF 13-SEP-2002; 2002WO-US029003.
XX
PR 14-SEP-2001; 2001US-0318904P.
XX
PA (FRAU-) FRAUNHOFER INST MOLEKULARBIOLOGIE & ANGE.
XX
PI Zhang MY, Schillberg S, Zimmermann S, Di Fiore S, Emans N;
PI Fischer R;
XX
DR WPI; 2003-371805/35.
DR N-PSDB; ADI20654, ADI20663, ADI20672.
XX
PT New immunoglobulin molecule, useful in therapeutic or diagnostic assays
PT comprising ELISA, phage display, tumor imaging or protein chips assay or
PT in screening assays for detecting molecules that bind to the
PT immunoglobulin molecule.
XX
PS Claim 7; SEQ ID NO 2; 198pp; English.
XX
CC The present invention relates to an immunoglobulin molecule comprising of
CC one or more heavy chain framework regions comprising HFR1, HFR2, HFR3 or
CC HFR4 and one or more light chain framework regions comprising LFR1, LFR2,
CC LFR3 or LFR4; and complementarity determining regions (CDRs) comprising
CC CDR-H1, CDR-H2, CDR-H3 and/or CDRL1, CDR-L2 or CDR-L3. The immunoglobulin
CC is useful in therapeutic or diagnostic assays comprising ELISA, phage
CC display, tumour imaging or protein chips assay. Further, the
CC immunoglobulin is useful in screening assays for detecting molecules that
CC bind to the immunoglobulin molecule. The present sequence represents a
CC chain framework region.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 81; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 1 WVRQAPGKGLEWVA 14

RESULT 5
ADR38742
ID ADR38742 standard; peptide; 14 AA.
XX
AC ADR38742;
XX
DT 02-DEC-2004 (first entry)
XX
DE Mouse heavy chain anti-BoNT-antibody framework 2 seqid 144.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KW framework 2.
XX
OS Mus sp.
XX
PN US2004175385-A1.
XX
PD 09-SEP-2004.
XX
PF 01-AUG-2003; 2003US-00632706.
XX
PR 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Marks JD, Amersdorfer P;
XX
DR WPI; 2004-652009/63.
XX
PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
XX
PS Example 4; SEQ ID NO 144; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BoNT-antibody framework region 2.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 81; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 1 WVRQAPGKGLEWVA 14

RESULT 6
ADR38754
ID ADR38754 standard; peptide; 14 AA.
XX
AC ADR38754;
XX
DT 02-DEC-2004 (first entry)
XX
DE Mouse heavy chain anti-BoNT-antibody framework 2 seqid 156.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KW framework 2.
XX
OS Mus sp.
XX
PN US2004175385-A1.
XX
PD 09-SEP-2004.
XX
PF 01-AUG-2003; 2003US-00632706.
XX
PR 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX

PA (REGC) UNIV CALIFORNIA.
XX
PI Marks JD, Amersdorfer P;
XX
DR WPI; 2004-652009/63.
XX
PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
XX
PS Example 4; SEQ ID NO 156; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BoNT-antibody framework region 2.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 81; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 1 WVRQAPGKGLEWVA 14

RESULT 7
ADR38738
ID ADR38738 standard; peptide; 14 AA.
XX
AC ADR38738;
XX
DT 02-DEC-2004 (first entry)
XX
DE Mouse heavy chain anti-BoNT-antibody framework 2 seqid 140.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KW framework 2.
XX
OS Mus sp.
XX
PN US2004175385-A1.
XX
PD 09-SEP-2004.
XX
PF 01-AUG-2003; 2003US-00632706.
XX
PR 31-AUG-1998; 98US-00144886.
XX
PR 01-AUG-2002; 2002US-0400721P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Marks JD, Amersdorfer P;
XX
DR WPI; 2004-652009/63.
XX
PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
XX
PS Example 4; SEQ ID NO 140; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BoNT-antibody framework region 2.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 81; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 1 WVRQAPGKGLEWVA 14

RESULT 8
ADR38762
ID ADR38762 standard; peptide; 14 AA.
XX
AC ADR38762;
XX
DT 02-DEC-2004 (first entry)
XX
DE Mouse heavy chain anti-BoNT-antibody framework 2 seqid 164.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KW framework 2.
XX
OS Mus sp.
XX
PN US2004175385-A1.
XX
PD 09-SEP-2004.
XX
PF 01-AUG-2003; 2003US-00632706.

XX
PR 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Marks JD, Amersdorfer P;
XX
DR WPI; 2004-652009/63.
XX
PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
XX
PS Example 4; SEQ ID NO 164; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BoNT-antibody framework region 2.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 81; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 1 WVRQAPGKGLEWVA 14

RESULT 9
ADR38746
ID ADR38746 standard; peptide; 14 AA.
XX
AC ADR38746;
XX
DT 02-DEC-2004 (first entry)
XX
DE Mouse heavy chain anti-BoNT-antibody framework 2 seqid 148.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KW framework 2.
XX
OS Mus sp.
XX
PN US2004175385-A1.
XX
PD 09-SEP-2004.
XX
PF 01-AUG-2003; 2003US-00632706.
XX
PR 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Marks JD, Amersdorfer P;
XX
DR WPI; 2004-652009/63.
XX
PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
XX
PS Example 4; SEQ ID NO 148; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BoNT-antibody framework region 2.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 81; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 1 WVRQAPGKGLEWVA 14

RESULT 10
ADR38766
ID ADR38766 standard; peptide; 14 AA.
XX
AC ADR38766;
XX
DT 02-DEC-2004 (first entry)
XX
DE Mouse heavy chain anti-BoNT-antibody framework 2 seqid 168.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KW framework 2.
XX
OS Mus sp.
XX
PN US2004175385-A1.

XX
PD 09-SEP-2004.
XX
PF 01-AUG-2003; 2003US-00632706.
XX
PR 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Marks JD, Amersdorfer P;
XX
DR WPI; 2004-652009/63.
XX
PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
XX
PS Example 4; SEQ ID NO 168; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BoNT-antibody framework region 2.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 81; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 1 WVRQAPGKGLEWVA 14

RESULT 11
ADR38758
ID ADR38758 standard; peptide; 14 AA.
XX
AC ADR38758;
XX
DT 02-DEC-2004 (first entry)
XX
DE Mouse heavy chain anti-BoNT-antibody framework 2 seqid 160.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KW framework 2.
XX
OS Mus sp.

XX
PN US2004175385-A1.
XX
PD 09-SEP-2004.
XX
PF 01-AUG-2003; 2003US-00632706.
XX
PR 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Marks JD, Amersdorfer P;
XX
DR WPI; 2004-652009/63.
XX
PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
XX
PS Example 4; SEQ ID NO 160; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BoNT-antibody framework region 2.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 81; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 1 WVRQAPGKGLEWVA 14

RESULT 12
ADR38750
ID ADR38750 standard; peptide; 14 AA.
XX
AC ADR38750;
XX
DT 02-DEC-2004 (first entry)
XX
DE Mouse heavy chain anti-BoNT-antibody framework 2 seqid 152.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; heavy chain;
KW framework 2.

XX
OS Mus sp.
XX
PN US2004175385-A1.
XX
PD 09-SEP-2004.
XX
PF 01-AUG-2003; 2003US-00632706.
XX
PR 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Marks JD, Amersdorfer P;
XX
DR WPI; 2004-652009/63.
XX
PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
XX
PS Example 4; SEQ ID NO 152; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse heavy chain anti-BoNT-antibody framework region 2.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 81; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 1 WVRQAPGKGLEWVA 14

RESULT 13
ADW96736
ID ADW96736 standard; peptide; 14 AA.
XX
AC ADW96736;
XX
DT 21-APR-2005 (first entry)
XX
DE Anti-EGFRvIII antibody 13.1.2 VH peptide #3.
XX
KW Monoclonal antibody; diagnosis; therapy; cancer; tumor; carcinoma;
KW glioma; neoplasm; cytostatic; epidermal growth factor receptor;
KW heavy chain variable region.
XX
OS Homo sapiens.
XX
PN WO2005012479-A2.
XX
PD 10-FEB-2005.
XX
PF 25-JUN-2004; 2004WO-US020564.
XX
PR 27-JUN-2003; 2003US-0483145P.
PR 26-NOV-2003; 2003US-0525570P.
PR 15-APR-2004; 2004US-0562453P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Weber R, Feng X, Foord O, Green L, Gudas J, Keyt B, Liu Y;
PI Rathanaswami P, Raya R, Yang XD, Corvalan J, Foltz I, Jia X;
PI Kang J, King CT, Klakamp SL, Su QJ;
XX
DR WPI; 2005-142884/15.
XX
PT New human monoclonal antibodies directed against type III deletion
PT mutants of epidermal growth factor receptor (EGFRvIII), useful for
PT diagnosing, preventing or treating diseases associated with EGFRvIII
PT expression, e.g. cancer.
XX
PS Example 17; SEQ ID NO 122; 207pp; English.
XX
CC The invention relates to an isolated human monoclonal antibody, or its
CC variant, directed against deletion mutants of epidermal growth factor
CC receptor, particularly to the type III deletion mutant (EGFRvIII). Also
CC included are a hybridoma cell line producing the above antibody, a
CC transformed cell comprising a gene encoding the antibody, inhibiting cell
CC proliferation associated with the expression of EGFRvIII, an isolated
CC polynucleotide molecule comprising a nucleotide sequence encoding a heavy
CC or light chain amino acid sequence (or its fragment), an article of
CC manufacture (comprising a container, a composition contained in the
CC container, and a package insert or label indicating that the composition
CC can be used to treat cancer characterized by the expression of EGFRvIII,
CC where the composition comprises the antibody cited above), an assay kit
CC for the detection of EGFRvIII in mammalian tissues or cells (to screen
CC for lung, colon, gastric, renal, prostate or ovarian carcinomas, the
CC EGFRvIII being an antigen expressed by epithelial cancers, the kit
CC comprising an antibody that binds the antigen protein and means for
CC indicating the reaction of the antibody with the antigen, if present), a
CC purified protein variant of EGFRvIII, selecting variants of antibodies to
CC EGFRvIII, making antibody variants to EGFRvIII and killing a targeted
CC cell. The composition and methods are useful for diagnosing, preventing
CC or treating diseases associated with the expression of EGFRvIII, such as
CC cancer, gliomas, tumors and carcinomas. The present sequence is a peptide
CC derived from a VH region of an anti-EGFRvIII antibody of the invention
CC used to determine the antibody structure.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 81; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 1 WVRQAPGKGLEWVA 14

RESULT 14
ADW96723
ID ADW96723 standard; peptide; 14 AA.
XX
AC ADW96723;
XX
DT 21-APR-2005 (first entry)
XX

```
DE   Anti-EGFRvIII antibody 131 VH peptide #3.
XX
KW   Monoclonal antibody; diagnosis; therapy; cancer; tumor; carcinoma;
KW   glioma; neoplasm; cytostatic; epidermal growth factor receptor;
KW   heavy chain variable region.
XX
OS   Homo sapiens.
XX
PN   WO2005012479-A2.
XX
PD   10-FEB-2005.
XX
PF   25-JUN-2004; 2004WO-US020564.
XX
PR   27-JUN-2003; 2003US-0483145P.
PR   26-NOV-2003; 2003US-0525570P.
PR   15-APR-2004; 2004US-0562453P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Weber R,  Feng X,  Foord O,  Green L,  Gudas J,  Keyt B,  Liu Y;
PI   Rathanaswami P,  Raya R,  Yang XD,  Corvalan J,  Foltz I,  Jia X;
PI   Kang J,  King CT,  Klakamp SL,  Su QJ;
XX
DR   WPI; 2005-142884/15.
XX
PT   New human monoclonal antibodies directed against type III deletion
PT   mutants of epidermal growth factor receptor (EGFRvIII), useful for
PT   diagnosing, preventing or treating diseases associated with EGFRvIII
PT   expression, e.g. cancer.
XX
PS   Example 16; SEQ ID NO 109; 207pp; English.
XX
CC   The invention relates to an isolated human monoclonal antibody, or its
CC   variant, directed against deletion mutants of epidermal growth factor
CC   receptor, particularly to the type III deletion mutant (EGFRvIII). Also
CC   included are a hybridoma cell line producing the above antibody, a
CC   transformed cell comprising a gene encoding the antibody, inhibiting cell
CC   proliferation associated with the expression of EGFRvIII, an isolated
CC   polynucleotide molecule comprising a nucleotide sequence encoding a heavy
CC   or light chain amino acid sequence (or its fragment), an article of
CC   manufacture (comprising a container, a composition contained in the
CC   container, and a package insert or label indicating that the composition
CC   can be used to treat cancer characterized by the expression of EGFRvIII,
CC   where the composition comprises the antibody cited above), an assay kit
CC   for the detection of EGFRvIII in mammalian tissues or cells (to screen
CC   for lung, colon, gastric, renal, prostate or ovarian carcinomas, the
CC   EGFRvIII being an antigen expressed by epithelial cancers, the kit
CC   comprising an antibody that binds the antigen protein and means for
CC   indicating the reaction of the antibody with the antigen, if present), a
CC   purified protein variant of EGFRvIII, selecting variants of antibodies to
CC   EGFRvIII, making antibody variants to EGFRvIII and killing a targeted
CC   cell. The composition and methods are useful for diagnosing, preventing
CC   or treating diseases associated with the expression of EGFRvIII, such as
CC   cancer, gliomas, tumors and carcinomas. The present sequence is a peptide
CC   derived from a VH region of an anti-EGFRvIII antibody of the invention
CC   used to determine the antibody structure.
XX
SQ   Sequence 14 AA;

  Query Match             100.0%;  Score 81;  DB 9;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 15
ADW80308
ID   ADW80308 standard; peptide; 14 AA.
XX
AC   ADW80308;
XX
DT   21-APR-2005  (first entry)
XX
DE   Human anti-EGFRvIII antibody 13.1.2 VH peptide - SEQ ID 122.
XX
KW   cell death; monoclonal antibody; toxin; cytostatic; cancer; neoplasm;
KW   lung tumor; colon tumor; stomach tumor; renal tumor; prostatic cancer;
KW   breast tumor; ovary tumor; epidermal growth factor receptor; EGFRvIII;
KW   heavy chain variable region.
XX
OS   Homo sapiens.
XX
PN   WO2005010151-A2.
XX
PD   03-FEB-2005.
XX
PF   25-JUN-2004; 2004WO-US020295.
XX
PR   27-JUN-2003; 2003US-0483145P.
PR   26-NOV-2003; 2003US-0525570P.
PR   15-APR-2004; 2004US-0562453P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Weber R,  Feng X,  Foord O,  Green L,  Gudas J,  Keyt B,  Liu Y;
PI   Rathanaswami P,  Raya R,  Yang XD,  Corvalan J,  Foltz I,  Jia X;
PI   Kang J,  King CT,  Klakamp SL,  Su QJ;
XX
DR   WPI; 2005-123139/13.
XX
PT   New isolated antibody that binds to epidermal growth factor receptor type
PT   III mutant EGFRvIII and being conjugated to therapeutic agent such as
PT   toxin, useful for inhibiting cell proliferation associated with
PT   expression of EGFRvIII.
XX
PS   Example 18; SEQ ID NO 122; 233pp; English.
XX
CC   The invention relates to a novel method for killing a target cell. The
CC   method comprises contacting the cell with an isolated antibody or its
CC   fragment that binds to epidermal growth factor receptor type III deletion
CC   mutant (EGFRvIII), the antibody being conjugated to a therapeutic agent,
CC   which is a toxin chosen from AEFP, MMAE, AURISTATIN E, DM-1 and ZAP, and
CC   where the antibody comprises a heavy chain amino acid sequence chosen
CC   from antibodies 13.1.2, 131, 170, 150, 095, 250. EGFR variants are caused
CC   by gene rearrangement accompanied by gene amplification. Eight major
CC   variants of EGFR are known. EGFRvIII, which is the most commonly
CC   occurring variant of EGFR in human cancers, comprises a 267 aa in-frame
CC   deletion in the extracellular domain. The method of the invention
CC   demonstrates cytostatic activity and may be useful for inhibiting cell
CC   proliferation associated with the expression of EGFRvIII or for
CC   inhibiting cell proliferation of cells expressing EGFRvIII. As such the
CC   method may be utilized, in vivo, on a mammal e.g. human, suffering from
CC   an epithelial cell cancer such as lung, colon, gastric, renal, prostate,
CC   breast, glioblastoma or ovarian carcinoma. The current sequence is that
CC   of a human anti-epidermal growth factor receptor type III variant
CC   (EGFRvIII) antibody 13.1.2 heavy chain variable region peptide of the
CC   invention.
XX
SQ   Sequence 14 AA;

  Query Match             100.0%;  Score 81;  DB 9;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


Search completed: March 25, 2006, 09:02:22
Job time : 52.7271 secs
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:02:50 ; Search time 8.06283 Seconds
(without alignments)
167.067 Million cell updates/sec

Title: US-10-755-382-33
Perfect score: 81
Sequence: 1 WVRQAPGKGLEWVA 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	81	100.0	94	2	PL0120	Ig heavy chain V-I
2	81	100.0	96	2	PH0873	Ig heavy chain V r
3	81	100.0	97	2	S44115	Ig heavy chain V r
4	81	100.0	97	2	PH0872	Ig heavy chain V r
5	81	100.0	98	2	PL0116	Ig heavy chain V-I
6	81	100.0	98	2	S29543	Ig heavy chain V r
7	81	100.0	98	2	PL0123	Ig heavy chain V-I
8	81	100.0	98	2	S29546	Ig heavy chain V r
9	81	100.0	99	2	S20765	Ig heavy chain V r
10	81	100.0	100	2	S26462	Ig heavy chain V r
11	81	100.0	101	2	B42575	Ig heavy chain V r
12	81	100.0	108	2	PH1642	Ig heavy chain V r
13	81	100.0	109	2	PH1646	Ig heavy chain V r
14	81	100.0	109	2	PH1644	Ig heavy chain V r
15	81	100.0	110	2	PH1655	Ig heavy chain V r
16	81	100.0	110	2	PH1092	Ig heavy chain V r
17	81	100.0	110	2	PH1091	Ig heavy chain V r
18	81	100.0	111	2	PH1643	Ig heavy chain V r
19	81	100.0	111	2	PH1645	Ig heavy chain V r
20	81	100.0	113	2	S57410	Ig heavy chain V-J
21	81	100.0	113	2	S57441	Ig heavy chain V-J
22	81	100.0	113	2	S38490	Ig heavy chain - h
23	81	100.0	114	2	PH1658	Ig heavy chain V r
24	81	100.0	114	2	PH1657	Ig heavy chain V r
25	81	100.0	114	2	S46390	Ig heavy chain V r
26	81	100.0	114	2	S46391	Ig heavy chain V r
27	81	100.0	114	2	S46392	Ig heavy chain V r
28	81	100.0	114	2	S36280	Ig heavy chain V r
29	81	100.0	115	2	S36284	Ig heavy chain V r
30	81	100.0	115	2	S57445	Ig heavy chain V-J
31	81	100.0	115	2	S36267	Ig heavy chain V r
32	81	100.0	116	1	M3HUGL	Ig heavy chain V-I
33	81	100.0	117	1	G1HUWS	Ig heavy chain V-I
34	81	100.0	117	2	S17079	Ig heavy chain V-g
35	81	100.0	117	2	S36270	Ig heavy chain V r
36	81	100.0	117	2	S78486	Ig heavy chain V r
37	81	100.0	118	2	S31677	Ig heavy chain V r
38	81	100.0	118	2	PH1660	Ig heavy chain V r
39	81	100.0	118	2	PH1662	Ig heavy chain V r
40	81	100.0	118	2	S31116	Ig heavy chain - h
41	81	100.0	119	1	G1HUNI	Ig heavy chain V-I
42	81	100.0	119	1	M3HULY	Ig heavy chain V-I
43	81	100.0	119	1	M3HUPM	Ig heavy chain V-I
44	81	100.0	119	2	S31111	Ig heavy chain - h
45	81	100.0	119	2	A27630	Ig heavy chain pre

ALIGNMENTS

RESULT 1
PL0120
Ig heavy chain V-III region (TD-Vo) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 31-Dec-2004
C;Accession: PL0120
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulir
A;Reference number: PL0116; MUID:88286083; PMID:2840480
A;Accession: PL0120
A;Molecule type: mRNA
A;Residues: 1-94 <BIR>
A;Cross-references: UNIPROT:Q8WUK1; UNIPROT:Q9UL93; UNIPARC:UPI0000176A2C
A;Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A;Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement f
C;Superfamily: immunoglobulin homology
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2

Query Match 100.0%; Score 81; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 36 WVRQAPGKGLEWVA 49

RESULT 2
PH0873
Ig heavy chain V region (anti-DNA, I-2a) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-1996
C;Accession: PH0873
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0873
A;Molecule type: DNA
A;Residues: 1-96 <MAN>
A;Cross-references: UNIPARC:UPI0000176C02
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-96/Domain: immunoglobulin homology <IMM>
F;30-35/Region: complementarity-determining 1
F;49-66/Region: complementarity-determining 2

Query Match 100.0%; Score 81; DB 2; Length 96;

```
  Best Local Similarity   100.0%;  Pred. No. 4.7e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         35 WVRQAPGKGLEWVA 48


RESULT 3
S44115
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44115
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
A;Accession: S44115
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <HAW>
A;Cross-references: UNIPARC:UPI000011662B; EMBL:Z31384; NID:g472969; PIDN:CAA83259.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             100.0%;  Score 81;  DB 2;  Length 97;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 4
PH0872
Ig heavy chain V region (anti-DNA, III-3R) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C;Accession: PH0872
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0872
A;Molecule type: DNA
A;Residues: 1-97 <MAN>
A;Cross-references: UNIPROT:Q9ULB6; UNIPARC:UPI0000176C04
A;Note: a "G" was inserted at the position of between 72nd and 73rd of the DNA sequence
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-97/Domain: immunoglobulin homology <IMM>
F;30-35/Region: complementarity-determining 1
F;49-66/Region: complementarity-determining 2

  Query Match             100.0%;  Score 81;  DB 2;  Length 97;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         35 WVRQAPGKGLEWVA 48


RESULT 5
PL0116
Ig heavy chain V-III region (AW-Vx) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PL0116; S26892
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A;Reference number: PL0116; MUID:88286083; PMID:2840480
A;Accession: PL0116
A;Molecule type: mRNA
A;Residues: 1-98 <BIR>
A;Cross-references: UNIPARC:UPI0000031F3A
A;Experimental source: B cells from patient AW with acute lymphoblastic leukemia, ALL
A;Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA rearrangement f
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26892
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI0000031F3A; EMBL:Z12349; NID:g32918; PIDN:CAA78219.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2

  Query Match             100.0%;  Score 81;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 6
S29543
Ig heavy chain V region (COS 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29543
R;Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Accession: S29543
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI000011649C; EMBL:Z17389; NID:g32835; PIDN:CAA78994.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 81;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 7
PL0123
Ig heavy chain V-III region (TD-Vr) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PL0123; S26897
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobuli
A;Reference number: PL0116; MUID:88286083; PMID:2840480
A;Accession: PL0123
A;Molecule type: mRNA
A;Residues: 1-98 <BIR>
A;Cross-references: UNIPARC:UPI0000116413
```

A;Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A;Note: the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement f
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26897
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI0000116413; EMBL:Z12354; NID:g32930; PIDN:CAA78224.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2

Query Match 100.0%; Score 81; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 36 WVRQAPGKGLEWVA 49

RESULT 8
S29546
Ig heavy chain V region (COS-8 / DP-46) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29546; S26888
R;Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Accession: S29546
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI000002DD16; EMBL:Z17394; NID:g32843; PIDN:CAA78997.1; PID
A;Note: designated COS-8
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TO2>
A;Cross-references: UNIPARC:UPI000002DD16; EMBL:Z12346; NID:g32912; PIDN:CAA78216.1; PID
A;Note: designated DP-46
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 36 WVRQAPGKGLEWVA 49

RESULT 9
S20765
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20765
R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A;Reference number: S20764
A;Accession: S20765
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <MOR>
A;Cross-references: UNIPARC:UPI00001163E7; EMBL:Z11943; NID:g33858; PIDN:CAA78000.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 81; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 4.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 12 WVRQAPGKGLEWVA 25

RESULT 10
S26462
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
C;Accession: S26462
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S26462
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-100 <KAV>
A;Cross-references: UNIPARC:UPI0000176E5E; EMBL:X59104; NID:g51920; PID:g51921
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. No. 4.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 28 WVRQAPGKGLEWVA 41

RESULT 11
B42575
Ig heavy chain V region (anti-angiotensin II) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: B42575
R;Garcia, K.C.; Desiderio, S.V.; Ronco, P.M.; Verroust, P.J.; Amzel, L.M.
Science 257, 528-531, 1992
A;Title: Recognition of angiotensin II: antibodies at different levels of an idiotypic n
A;Reference number: A42575; MUID:92342952; PMID:1636087
A;Accession: B42575
A;Molecule type: mRNA
A;Residues: 1-101 <GAR>
A;Cross-references: UNIPARC:UPI00001153E9; GB:S40679; NID:g252098; PIDN:AAB22669.1; PID:
A;Experimental source: BALB/c mice, myeloma cell line NS-1
A;Note: sequence extracted from NCBI backbone (NCBIN:109337, NCBIP:109338)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;7-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 28 WVRQAPGKGLEWVA 41

RESULT 12
PH1642
Ig heavy chain V region (clone 5A10) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 31-Dec-2004
C;Accession: PH1642
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylc
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1642
A;Molecule type: mRNA
A;Residues: 1-108 <HIL>
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176B78
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 5.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 28 WVRQAPGKGLEWVA 41

RESULT 13
PH1646
Ig heavy chain V region (clone 6H12) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 31-Dec-2004
C;Accession: PH1646
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylc
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1646
A;Molecule type: mRNA
A;Residues: 1-109 <HIL>
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176B7C
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 28 WVRQAPGKGLEWVA 41

RESULT 14
PH1644
Ig heavy chain V region (clone 5D11) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 31-Dec-2004
C;Accession: PH1644
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylc
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1644
A;Molecule type: mRNA
A;Residues: 1-109 <HIL>
A;Cross-references: UNIPROT:Q9UL93; UNIPARC:UPI0000176B7A
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 28 WVRQAPGKGLEWVA 41

RESULT 15
PH1655
Ig heavy chain V region (clone 2E8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1655
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1655
A;Molecule type: mRNA
A;Residues: 1-110 <HIL>
A;Cross-references: UNIPARC:UPI0000176BDC
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 5.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 28 WVRQAPGKGLEWVA 41

Search completed: March 25, 2006, 09:15:46
Job time : 9.06283 secs

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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:40 ; Search time 50.4293 Seconds
(without alignments)
195.866 Million cell updates/sec

Title: US-10-755-382-33
Perfect score: 81
Sequence: 1 WVRQAPGKGLEWVA 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	81	100.0	95	2	Q9ULB6_HUMAN	Q9ulb6 homo sapien
2	81	100.0	113	2	Q9UL90_HUMAN	Q9ul90 homo sapien
3	81	100.0	116	1	HV3T_HUMAN	P01781 homo sapien
4	81	100.0	116	2	Q9UL93_HUMAN	Q9ul93 homo sapien
5	81	100.0	117	1	HV3O_HUMAN	P01776 homo sapien
6	81	100.0	119	1	HV3I_HUMAN	P01770 homo sapien
7	81	100.0	119	1	HV3M_HUMAN	P01774 homo sapien
8	81	100.0	119	1	HV3N_HUMAN	P01775 homo sapien
9	81	100.0	121	1	HV3J_HUMAN	P01771 homo sapien
10	81	100.0	122	2	Q9UL84_HUMAN	Q9ul84 homo sapien
11	81	100.0	126	1	HV3K_HUMAN	P01772 homo sapien
12	81	100.0	142	1	HV01_RAT	P01805 rattus norv
13	81	100.0	240	2	Q65ZC9_HUMAN	Q65zc9 homo sapien
14	81	100.0	417	2	Q6N093_HUMAN	Q6n093 homo sapien
15	81	100.0	465	2	Q6P6C4_HUMAN	Q6p6c4 homo sapien
16	81	100.0	470	2	Q6PJA4_HUMAN	Q6pja4 homo sapien
17	81	100.0	471	2	Q66K04_MOUSE	Q66k04 mus musculu
18	81	100.0	473	2	Q6P055_HUMAN	Q6p055 homo sapien
19	81	100.0	478	2	Q6PI81_HUMAN	Q6pi81 homo sapien
20	81	100.0	483	2	Q6MZX9_HUMAN	Q6mzx9 homo sapien
21	81	100.0	487	2	Q6ZVX0_HUMAN	Q6zvx0 homo sapien
22	81	100.0	544	2	Q6PJ95_HUMAN	Q6pj95 homo sapien
23	81	100.0	613	2	Q8WUK1_HUMAN	Q8wuk1 homo sapien
24	80	98.8	96	2	Q4T5S4_TETNG	Q4t5s4 tetraodon n
25	80	98.8	97	2	Q4SZF9_TETNG	Q4szf9 tetraodon n
26	80	98.8	98	2	Q6B6V3_RABIT	Q6b6v3 oryctolagus
27	80	98.8	98	2	Q6B6W5_RABIT	Q6b6w5 oryctolagus
28	80	98.8	99	2	Q6B6S4_RABIT	Q6b6s4 oryctolagus
29	80	98.8	99	2	Q6B6S7_RABIT	Q6b6s7 oryctolagus
30	80	98.8	99	2	Q4T5M5_TETNG	Q4t5m5 tetraodon n
31	80	98.8	119	1	HV3L_HUMAN	P01773 homo sapien
32	80	98.8	124	2	Q9N0W4_RABIT	Q9n0w4 oryctolagus
33	80	98.8	124	2	Q9N0W6_RABIT	Q9n0w6 oryctolagus
34	80	98.8	479	2	Q5PQK9_RAT	Q5pqk9 rattus norv
35	80	98.8	480	2	Q6N094_HUMAN	Q6n094 homo sapien
36	78	96.3	104	2	Q9UL87_HUMAN	Q9ul87 homo sapien
37	78	96.3	112	2	Q9HCC1_HUMAN	Q9hcc1 homo sapien
38	78	96.3	112	2	Q9UGP3_HUMAN	Q9ugp3 homo sapien
39	78	96.3	116	1	HV3R_HUMAN	P01779 homo sapien
40	78	96.3	117	1	HV01_CAICR	P01813 caiman croc
41	78	96.3	117	1	HV03_CARAU	P19180 carassius a
42	78	96.3	117	1	HV3C_HUMAN	P01764 homo sapien
43	78	96.3	118	2	Q9UL91_HUMAN	Q9ul91 homo sapien
44	78	96.3	121	2	Q9UL71_HUMAN	Q9ul71 homo sapien
45	78	96.3	147	2	Q9Y509_HUMAN	Q9y509 homo sapien

ALIGNMENTS

RESULT 1
Q9ULB6_HUMAN
ID Q9ULB6_HUMAN PRELIMINARY; PRT; 95 AA.
AC Q9ULB6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Imunoglobulin heavy chain (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tange Y., Kayano H.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1660528;
RA Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA Diamond B.;
RT "Molecular characteristics of antibodies bearing an anti-DNA-
RT associated idiotype.";
RL J. Exp. Med. 174:1639-1652(1991).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=7679990;
RA Griffiths A.D., Malmqvist M., Marks J.D., Bye J.M., Embleton M.J.,
RA McCafferty J., Baier M., Holliger K.P., Gorick B.D.,
RA Hughes-Jones N.C.;
RT "Human anti-self antibodies with high specificity from phage display
RT libraries.";
RL EMBO J. 12:725-734(1993).
DR EMBL; AB035268; BAA87067.1; -; Genomic_DNA.
DR PIR; PH0872; PH0872.
DR PIR; S36280; S36280.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 95 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match 100.0%; Score 81; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.6e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 WVRQAPGKGLEWVA 14
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Db         35 WVRQAPGKGLEWVA 48
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RESULT 2
Q9UL90_HUMAN
ID   Q9UL90_HUMAN PRELIMINARY;      PRT;   113 AA.
AC   Q9UL90;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1730252;
RA   Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA   Schuurman R.K.;
RT   "Restricted utilization of germ-line VH3 genes and short diverse third
RT   complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT   immunoglobulin heavy chain rearrangements.";
RL   Eur. J. Immunol. 22:247-251(1992).
DR   EMBL; AF035024; AAD56260.1; -; mRNA.
DR   PIR; S78486; S78486.
DR   HSSP; P01772; 2FB4.
DR   SMR; Q9UL90; 1-113.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     113    113
SQ   SEQUENCE   113 AA;  12437 MW;  ED57FDD19086D07F CRC64;

  Query Match             100.0%;  Score 81;  DB 2;  Length 113;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 3
HV3T_HUMAN
ID   HV3T_HUMAN     STANDARD;      PRT;   116 AA.
AC   P01781;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region GAL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=75059123; PubMed=4803843;
RA   Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.;
RT   "The primary structure of a monoclonal IgM-immunoglobulin
RT   (macroglobulin Gal.), II: the amino acid sequence of the H-chain (mu-
RT   type), subgroup H III. Architecture of the complete IgM-molecule.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
RN   [2]
RP   SEQUENCE REVISION TO 28-33.
RA   Hilschmann N.;
RL   Submitted (JUN-1975) to the PIR data bank.
CC   -!- MISCELLANEOUS: This mu chain was isolated from a Waldenstrom's
CC       macroglobulin.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A02064; M3HUGL.
DR   HSSP; P01772; 2FB4.
DR   SMR; P01781; 1-116.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    112       Ig-like.
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12731 MW;  2C67CA9AAAAA1282 CRC64;

  Query Match             100.0%;  Score 81;  DB 1;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 4
Q9UL93_HUMAN
ID   Q9UL93_HUMAN PRELIMINARY;      PRT;   116 AA.
AC   Q9UL93;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA   Hillson J.L., Karr N.S., Oppliger I.R., Mannik M., Sasso E.H.;
RT   "The structural basis of germline-encoded VH3 immunoglobulin binding
RT   to staphylococcal protein A.";
RL   J. Exp. Med. 178:331-336(1993).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2840480;
RA   Bird J., Galili N., Link M., Stites D., Sklar J.;
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RT   "Continuing rearrangement but absence of somatic hypermutation in
RT   immunoglobulin genes of human B cell precursor leukemia.";
RL   J. Exp. Med. 168:229-245(1988).
DR   EMBL; AF035021; AAD56257.1; -; mRNA.
DR   PIR; PH1644; PH1644.
DR   PIR; PL0120; PL0120.
DR   HSSP; P01772; 2FB4.
DR   SMR; Q9UL93; 1-116.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12434 MW;  0DA0348154DD6061 CRC64;

  Query Match             100.0%;  Score 81;  DB 2;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         35 WVRQAPGKGLEWVA 48


RESULT 5
HV3O_HUMAN
ID   HV3O_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01776;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region WAS.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=74142702; PubMed=4522793;
RA   Capra J.D., Kehoe J.M.;
RT   "Variable region sequences of five human immunoglobulin heavy chains
RT   of the VH3 subgroup: definitive identification of four heavy chain
RT   hypervariable regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC       protein.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A02059; G1HUWS.
DR   HSSP; P01772; 2FB4.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    112       Ig-like.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13091 MW;  201DEF0E1E53D9BF CRC64;

  Query Match             100.0%;  Score 81;  DB 1;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 6
HV3I_HUMAN
ID   HV3I_HUMAN     STANDARD;      PRT;   119 AA.
AC   P01770;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region NIE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=77070269; PubMed=826475;
RA   Ponstingl H., Hilschmann N.;
RT   "The rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT   peptides of the H-chain, alignment of the tryptic peptides and
RT   discussion of the complete structure.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=77070267; PubMed=1002129;
RA   Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   IgG1 immunoglobulin (myeloma protein Nie), I: purification and
RT   characterization of the protein, the L- and H-chains, the cyanogen
RT   bromide cleavage products, and the disulfide bridges.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC       protein.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A91668; G1HUNI.
DR   HSSP; P01772; 2FB4.
DR   SMR; P01770; 1-119.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   DISULFID     22     96
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13243 MW;  C96935A6E55E165B CRC64;

  Query Match             100.0%;  Score 81;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
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Db         36 WVRQAPGKGLEWVA 49
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RESULT 7
HV3M_HUMAN
ID   HV3M_HUMAN     STANDARD;      PRT;   119 AA.
AC   P01774;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region POM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=75046755; PubMed=4139708;
RA   Capra J.D., Kehoe J.M.;
RT   "Structure of antibodies with shared idiotypy: the complete sequence
RT   of the heavy chain variable regions of two immunoglobulin M anti-gamma
RT   globulins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
CC   -!- MISCELLANEOUS: This chain was isolated from IgM with anti-gamma
CC       globulin activity.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A02057; M3HUPM.
DR   HSSP; P01772; 2FB4.
DR   SMR; P01774; 1-119.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    112       Ig-like.
FT   VARIANT      54     54       N -> D (probably due to deamidation
FT                                during isolation).
FT                                /FTId=VAR_003966.
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  12954 MW;  2E018AF4DCEB2610 CRC64;

  Query Match             100.0%;  Score 81;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 8
HV3N_HUMAN
ID   HV3N_HUMAN     STANDARD;      PRT;   119 AA.
AC   P01775;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region LAY.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=75046755; PubMed=4139708;
RA   Capra J.D., Kehoe J.M.;
RT   "Structure of antibodies with shared idiotypy: the complete sequence
RT   of the heavy chain variable regions of two immunoglobulin M anti-gamma
RT   globulins.";
RL   Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
CC   -!- MISCELLANEOUS: This chain was isolated from IgM with anti-gamma
CC       globulin activity.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A02058; M3HULY.
DR   HSSP; P01820; 1G7J.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    112       Ig-like.
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  12858 MW;  D6338098794DCF5E CRC64;

  Query Match             100.0%;  Score 81;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 9
HV3J_HUMAN
ID   HV3J_HUMAN     STANDARD;      PRT;   121 AA.
AC   P01771;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region HIL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=79124695; PubMed=420800;
RA   Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.;
RT   "Amino acid sequence of the VH region of human myeloma
RT   cryoimmunoglobulin IgG Hil.";
RL   Biochemistry 18:553-560(1979).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC       protein.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
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DR   PIR; A02054; G1HUHL.
DR   HSSP; P01772; 2FB4.
DR   SMR; P01771; 2-121.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13566 MW;  480FC53610EF5DAB CRC64;

  Query Match             100.0%;  Score 81;  DB 1;  Length 121;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 10
Q9UL84_HUMAN
ID   Q9UL84_HUMAN PRELIMINARY;      PRT;   122 AA.
AC   Q9UL84;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035030; AAD56266.1; -; mRNA.
DR   HSSP; P01772; 2FB4.
DR   SMR; Q9UL84; 1-122.
DR   Ensembl; ENSG00000130076; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13579 MW;  36054D41366545B8 CRC64;

  Query Match             100.0%;  Score 81;  DB 2;  Length 122;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
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Db         36 WVRQAPGKGLEWVA 49


RESULT 11
HV3K_HUMAN
ID   HV3K_HUMAN     STANDARD;      PRT;   126 AA.
AC   P01772;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region KOL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE, AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6884994;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=81072295; PubMed=7441755;
RA   Marquart M., Deisenhofer J., Huber R., Palm W.;
RT   "Crystallographic refinement and atomic models of the intact
RT   immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
RT   and 1.0-A resolution.";
RL   J. Mol. Biol. 141:369-391(1980).
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A02055; G1HUKL.
DR   PDB; 2FB4; X-ray; H=2-126.
DR   PDB; 2IG2; X-ray; H=2-126.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   DISULFID     22     96
FT   DISULFID    105    110
FT   NON_TER     126    126
FT   STRAND        3      7
FT   STRAND       11     12
FT   TURN         14     15
FT   STRAND       18     25
FT   HELIX        29     31
FT   STRAND       34     39
FT   TURN         41     42
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FT   TURN         74     77
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FT   HELIX        88     90
FT   STRAND       92     99
FT   STRAND      106    106
FT   TURN        107    108
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FT   STRAND      113    116
FT   STRAND      120    124
SQ   SEQUENCE   126 AA;  13718 MW;  E4D71B52B16F8776 CRC64;
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  Best Local Similarity   100.0%;  Pred. No. 3.4e-05;
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Qy          1 WVRQAPGKGLEWVA 14
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Db         36 WVRQAPGKGLEWVA 49


RESULT 12
HV01_RAT
ID   HV01_RAT       STANDARD;      PRT;   142 AA.
AC   P01805;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region IR2 precursor.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=83064537; PubMed=6292865;
RA   Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
RT   "Structure and evolution of the heavy chain from rat immunoglobulin
RT   E.";
RL   Nucleic Acids Res. 10:6041-6049(1982).
CC   -!- MISCELLANEOUS: The mRNA was isolated from an IgE-secreting
CC       immunocytoma that arises spontaneously in LOU/C/WsL rats.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A02075; EVRTR2.
DR   HSSP; P01789; 1MCP.
DR   SMR; P01805; 20-141.
DR   Ensembl; ENSRNOG00000031589; Rattus norvegicus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    142       Ig heavy chain V region IR2.
FT   DOMAIN       20    133       Ig-like.
FT   NON_TER     142    142
SQ   SEQUENCE   142 AA;  16024 MW;  DE29E6CFE745DF3B CRC64;

  Query Match             100.0%;  Score 81;  DB 1;  Length 142;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
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Db         55 WVRQAPGKGLEWVA 68


RESULT 13
Q65ZC9_HUMAN
ID   Q65ZC9_HUMAN PRELIMINARY;      PRT;   240 AA.
AC   Q65ZC9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Single-chain Fv (Fragment).
GN   Name=scFv;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C1q/7;
RX   MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA   Kontermann R.E., Wing M.G., Winter G.;
RT   "Complement recruitment using bispecific diabodies.";
RL   Nat. Biotechnol. 15:629-631(1997).
DR   EMBL; Y13056; CAA73499.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1      1
FT   NON_TER     240    240
SQ   SEQUENCE   240 AA;  25569 MW;  FDCFD3645F64B373 CRC64;

  Query Match             100.0%;  Score 81;  DB 2;  Length 240;
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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
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Db         36 WVRQAPGKGLEWVA 49


RESULT 14
Q6N093_HUMAN
ID   Q6N093_HUMAN PRELIMINARY;      PRT;   417 AA.
AC   Q6N093;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686I04196 (Fragment).
GN   Name=DKFZp686I04196;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Human esophagus tumor;
RG   The German Human cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640623; CAE45777.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   417 AA;  46061 MW;  C4518E844CFB883C CRC64;

  Query Match             100.0%;  Score 81;  DB 2;  Length 417;
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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 WVRQAPGKGLEWVA 14
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Db          8 WVRQAPGKGLEWVA 21


RESULT 15
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ID   Q6P6C4_HUMAN PRELIMINARY;      PRT;   465 AA.
AC   Q6P6C4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RA   Strausberg R.;
RL   Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC062335; AAH62335.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   SMR; Q6P6C4; 20-465.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   465 AA;  51325 MW;  FDDB9348ADC37E6D CRC64;

  Query Match           100.0%;  Score 81;  DB 2;  Length 465;
  Best Local Similarity  100.0%;  Pred. No. 0.00013;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         55 WVRQAPGKGLEWVA 68
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Job time : 51.4293 secs
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:14:16 ; Search time 12.7539 Seconds
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Title: US-10-755-382-33
Perfect score: 81
Sequence: 1 WVRQAPGKGLEWVA 14

Scoring table: BLOSUM62
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Searched: 572060 seqs, 82675679 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	81	100.0	14	1	US-08-318-157B-33	Sequence 33, Appl
2	81	100.0	14	2	US-09-253-794-33	Sequence 33, Appl
3	81	100.0	89	2	US-09-472-087-72	Sequence 72, Appl
4	81	100.0	95	2	US-09-534-717-653	Sequence 653, App
5	81	100.0	98	1	US-08-211-202-118	Sequence 118, App
6	81	100.0	98	1	US-07-942-245-37	Sequence 37, Appl
7	81	100.0	98	2	US-10-194-975-15	Sequence 15, Appl
8	81	100.0	98	2	US-10-194-975-23	Sequence 23, Appl
9	81	100.0	98	2	US-10-194-975-24	Sequence 24, Appl
10	81	100.0	98	2	US-10-194-975-25	Sequence 25, Appl
11	81	100.0	98	2	US-10-194-975-26	Sequence 26, Appl
12	81	100.0	98	2	US-09-534-717-624	Sequence 624, App
13	81	100.0	98	2	US-09-534-717-625	Sequence 625, App
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15	81	100.0	98	2	US-09-534-717-627	Sequence 627, App
16	81	100.0	98	2	US-09-534-717-628	Sequence 628, App
17	81	100.0	98	2	US-09-534-717-629	Sequence 629, App
18	81	100.0	98	2	US-09-534-717-630	Sequence 630, App
19	81	100.0	98	2	US-09-534-717-631	Sequence 631, App
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21	81	100.0	98	2	US-09-534-717-635	Sequence 635, App
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23	81	100.0	98	2	US-09-534-717-637	Sequence 637, App
24	81	100.0	98	2	US-09-534-717-640	Sequence 640, App
25	81	100.0	98	2	US-09-534-717-641	Sequence 641, App
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30	81	100.0	98	2	US-09-534-717-646	Sequence 646, App
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36	81	100.0	98	2	US-09-534-717-652	Sequence 652, App
37	81	100.0	98	2	US-09-534-717-654	Sequence 654, App
38	81	100.0	98	2	US-09-534-717-655	Sequence 655, App
39	81	100.0	98	2	US-09-534-717-664	Sequence 664, App
40	81	100.0	98	2	US-09-534-717-666	Sequence 666, App
41	81	100.0	98	2	US-09-534-717-667	Sequence 667, App
42	81	100.0	98	2	US-10-330-613A-61	Sequence 61, Appl
43	81	100.0	98	2	US-10-330-613A-62	Sequence 62, Appl
44	81	100.0	100	2	US-09-840-459-35	Sequence 35, Appl
45	81	100.0	100	2	US-09-497-625A-35	Sequence 35, Appl

ALIGNMENTS

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RESULT 1
US-08-318-157B-33
; Sequence 33, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  33:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-33

  Query Match           100.0%;  Score 81;  DB 1;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
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RESULT 2
US-09-253-794-33
; Sequence 33, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 33:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 14 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-253-794-33

  Query Match             100.0%;  Score 81;  DB 2;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-06;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 3
US-09-472-087-72
; Sequence 72, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
;   LENGTH: 89
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-472-087-72

  Query Match             100.0%;  Score 81;  DB 2;  Length 89;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         27 WVRQAPGKGLEWVA 40


RESULT 4
US-09-534-717-653
; Sequence 653, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
;  APPLICANT: Jochen, Salfeld et al.
;  TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
;  FILE REFERENCE: BBI-093CP
;  CURRENT APPLICATION NUMBER: US/09/534,717
;  CURRENT FILING DATE: 2000-03-24
;  EARLIER APPLICATION NUMBER: 60/126,603
;  EARLIER FILING DATE: March 25, 1999
;  NUMBER OF SEQ ID NOS: 675
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 653
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-534-717-653

  Query Match             100.0%;  Score 81;  DB 2;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 5
US-08-211-202-118
; Sequence 118, Application US/08211202
; Patent No. 5565332
;  GENERAL INFORMATION:
;    APPLICANT:  HOOGENBOOM, Hendricus Renerus Jacobus Matteus
;    APPLICANT:  BAIER, Michael
;    APPLICANT:  JESPERS, Laurent Stephane Anne Therese
;    APPLICANT:  WINTER, Gregory Paul
;    TITLE OF INVENTION:  Production of  chimeric antibodies - a
;    TITLE OF INVENTION:  combinatorial approach
;    NUMBER OF SEQUENCES:  144
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David W. Clough, Marshall O'Toole Gerstein Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/211,202
;      FILING DATE:  23-SEP-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9120252.3
;      FILING DATE:  23-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9120377.8
;      FILING DATE:  25-SEP-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206318.9
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9206372.6
;      FILING DATE:  24-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB92/00883
;      FILING DATE:  15-MAY-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  David W. Clough
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  28111/31960
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312-474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  118:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  98 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-211-202-118

  Query Match             100.0%;  Score 81;  DB 1;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 6
US-07-942-245-37
; Sequence 37, Application US/07942245
; Patent No. 5639641
;  GENERAL INFORMATION:
;    APPLICANT:  PEDERSEN, Jan T.
;    APPLICANT:  SEARLE,   Stephen M.J.
;    APPLICANT:  REES,     Anthony R.
;    APPLICANT:  ROGUSKA,  Michael A.
;    APPLICANT:  GUILD,    Braydon C.
;    TITLE OF INVENTION:  SURFACE RESIDUE VENEERING OF RODENT
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  522
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sughrue, Mion, Zinn, Macpeak & Seas
;      STREET:  2100 Pensylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States
;      ZIP:  20037-3202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  HP 9000/700 Workstation
;      OPERATING SYSTEM:  UNIX
;      SOFTWARE:  In house
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/942,245
;      FILING DATE:  09-SEP-1992
;      CLASSIFICATION:  530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;      TELEX:  6491103
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  98 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-942-245-37

  Query Match             100.0%;  Score 81;  DB 1;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 7
US-10-194-975-15
; Sequence 15, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: Super Humanized Antibodies
;  FILE REFERENCE: 501231.01
;  CURRENT APPLICATION NUMBER: US/10/194,975
;  CURRENT FILING DATE:  2002-10-10
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-194-975-15

  Query Match             100.0%;  Score 81;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 8
US-10-194-975-23
; Sequence 23, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: Super Humanized Antibodies
;  FILE REFERENCE: 501231.01
;  CURRENT APPLICATION NUMBER: US/10/194,975
;  CURRENT FILING DATE:  2002-10-10
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-194-975-23

  Query Match             100.0%;  Score 81;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-05;
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  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 9
US-10-194-975-24
; Sequence 24, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: Super Humanized Antibodies
;  FILE REFERENCE: 501231.01
;  CURRENT APPLICATION NUMBER: US/10/194,975
;  CURRENT FILING DATE:  2002-10-10
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-194-975-24

  Query Match             100.0%;  Score 81;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 10
US-10-194-975-25
; Sequence 25, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: Super Humanized Antibodies
;  FILE REFERENCE: 501231.01
;  CURRENT APPLICATION NUMBER: US/10/194,975
;  CURRENT FILING DATE:  2002-10-10
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-194-975-25

  Query Match             100.0%;  Score 81;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 11
US-10-194-975-26
; Sequence 26, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: Super Humanized Antibodies
;  FILE REFERENCE: 501231.01
;  CURRENT APPLICATION NUMBER: US/10/194,975
;  CURRENT FILING DATE:  2002-10-10
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-194-975-26

  Query Match             100.0%;  Score 81;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 12
US-09-534-717-624
; Sequence 624, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
;  APPLICANT: Jochen, Salfeld et al.
;  TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
;  FILE REFERENCE: BBI-093CP
;  CURRENT APPLICATION NUMBER: US/09/534,717
;  CURRENT FILING DATE: 2000-03-24
;  EARLIER APPLICATION NUMBER: 60/126,603
;  EARLIER FILING DATE: March 25, 1999
;  NUMBER OF SEQ ID NOS: 675
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 624
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-534-717-624

  Query Match             100.0%;  Score 81;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 13
US-09-534-717-625
; Sequence 625, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
;  APPLICANT: Jochen, Salfeld et al.
;  TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
;  FILE REFERENCE: BBI-093CP
;  CURRENT APPLICATION NUMBER: US/09/534,717
;  CURRENT FILING DATE: 2000-03-24
;  EARLIER APPLICATION NUMBER: 60/126,603
;  EARLIER FILING DATE: March 25, 1999
;  NUMBER OF SEQ ID NOS: 675
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 625
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-534-717-625

  Query Match             100.0%;  Score 81;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 14
US-09-534-717-626
; Sequence 626, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
;  APPLICANT: Jochen, Salfeld et al.
;  TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
;  FILE REFERENCE: BBI-093CP
;  CURRENT APPLICATION NUMBER: US/09/534,717
;  CURRENT FILING DATE: 2000-03-24
;  EARLIER APPLICATION NUMBER: 60/126,603
;  EARLIER FILING DATE: March 25, 1999
;  NUMBER OF SEQ ID NOS: 675
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 626
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-534-717-626

  Query Match            100.0%;  Score 81;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


RESULT 15
US-09-534-717-627
; Sequence 627, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
;  APPLICANT: Jochen, Salfeld et al.
;  TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
;  FILE REFERENCE: BBI-093CP
;  CURRENT APPLICATION NUMBER: US/09/534,717
;  CURRENT FILING DATE: 2000-03-24
;  EARLIER APPLICATION NUMBER: 60/126,603
;  EARLIER FILING DATE: March 25, 1999
;  NUMBER OF SEQ ID NOS: 675
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 627
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-534-717-627

  Query Match            100.0%;  Score 81;  DB 2;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49


Search completed: March 25, 2006, 09:18:46
Job time : 12.7539 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:55:36 ; Search time 41.7801 Seconds
(without alignments)
140.009 Million cell updates/sec

Title: US-10-755-382-33
Perfect score: 81
Sequence: 1 WVRQAPGKGLEWVA 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	81	100.0	14	3	US-09-253-794-33	Sequence 33, Appl
2	81	100.0	14	3	US-09-828-708-64	Sequence 64, Appl
3	81	100.0	14	4	US-10-632-706-140	Sequence 140, App
4	81	100.0	14	4	US-10-632-706-144	Sequence 144, App
5	81	100.0	14	4	US-10-632-706-148	Sequence 148, App
6	81	100.0	14	4	US-10-632-706-152	Sequence 152, App
7	81	100.0	14	4	US-10-632-706-156	Sequence 156, App
8	81	100.0	14	4	US-10-632-706-160	Sequence 160, App
9	81	100.0	14	4	US-10-632-706-164	Sequence 164, App
10	81	100.0	14	4	US-10-632-706-168	Sequence 168, App
11	81	100.0	14	5	US-10-788-625-6	Sequence 6, Appli
12	81	100.0	14	5	US-10-489-328-2	Sequence 2, Appli
13	81	100.0	14	5	US-10-923-068-202	Sequence 202, App
14	81	100.0	14	5	US-10-923-068-205	Sequence 205, App
15	81	100.0	14	5	US-10-923-068-232	Sequence 232, App
16	81	100.0	14	5	US-10-877-773-109	Sequence 109, App
17	81	100.0	14	5	US-10-877-773-122	Sequence 122, App
18	81	100.0	14	5	US-10-877-774-109	Sequence 109, App
19	81	100.0	14	5	US-10-877-774-122	Sequence 122, App
20	81	100.0	14	5	US-10-630-009-64	Sequence 64, Appl
21	81	100.0	14	5	US-10-755-382-33	Sequence 33, Appl
22	81	100.0	14	5	US-10-984-960A-41	Sequence 41, Appl
23	81	100.0	17	5	US-10-923-068-334	Sequence 334, App
24	81	100.0	17	5	US-10-923-068-337	Sequence 337, App
25	81	100.0	17	5	US-10-923-068-364	Sequence 364, App
26	81	100.0	44	5	US-10-842-011-39	Sequence 39, Appl
27	81	100.0	82	4	US-10-230-880-118	Sequence 118, App
28	81	100.0	82	4	US-10-230-880-119	Sequence 119, App
29	81	100.0	82	4	US-10-230-880-120	Sequence 120, App
30	81	100.0	82	4	US-10-230-880-121	Sequence 121, App
31	81	100.0	82	4	US-10-230-880-122	Sequence 122, App
32	81	100.0	82	4	US-10-230-880-123	Sequence 123, App
33	81	100.0	87	5	US-10-788-625-90	Sequence 90, Appl
34	81	100.0	87	5	US-10-842-011-45	Sequence 45, Appl
35	81	100.0	89	5	US-10-612-497-72	Sequence 72, Appl
36	81	100.0	89	5	US-10-776-649-72	Sequence 72, Appl
37	81	100.0	93	3	US-09-910-483-39	Sequence 39, Appl
38	81	100.0	93	3	US-09-910-483-45	Sequence 45, Appl
39	81	100.0	95	4	US-10-363-204-89	Sequence 89, Appl
40	81	100.0	95	4	US-10-363-204-91	Sequence 91, Appl
41	81	100.0	95	5	US-10-884-830-653	Sequence 653, App
42	81	100.0	98	3	US-09-948-939-15	Sequence 15, Appl
43	81	100.0	98	3	US-09-948-939-21	Sequence 21, Appl
44	81	100.0	98	4	US-10-194-975-15	Sequence 15, Appl
45	81	100.0	98	4	US-10-194-975-23	Sequence 23, Appl

ALIGNMENTS

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RESULT 1
US-09-253-794-33
; Sequence 33, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 33:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 14 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-253-794-33

  Query Match           100.0%;  Score 81;  DB 3;  Length 14;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 2
US-09-828-708-64
; Sequence 64, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
;  APPLICANT: Ditzel, H.
;  APPLICANT:  Burton, D.
;  APPLICANT:  Schaller, M.
;  TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
;  TITLE OF INVENTION:  autoimmune disease
;  FILE REFERENCE: 1361.005US1
;  CURRENT APPLICATION NUMBER: US/09/828,708
;  CURRENT FILING DATE:  2001-09-24
;  NUMBER OF SEQ ID NOS: 123
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 64
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-828-708-64

  Query Match             100.0%;  Score 81;  DB 3;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 3
US-10-632-706-140
; Sequence 140, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
;  APPLICANT: MARKS, JAMES D.
;  APPLICANT:  AMERSDORFER, PETER
;  TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
;  TITLE OF INVENTION:  NEUROTOXINS
;  FILE REFERENCE: 407T-895120US
;  CURRENT APPLICATION NUMBER: US/10/632,706
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: US 60/400,721
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: US 09/144,806
;  PRIOR FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 278
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 140
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: single chain antibody fragment
US-10-632-706-140

  Query Match             100.0%;  Score 81;  DB 4;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 4
US-10-632-706-144
; Sequence 144, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
;  APPLICANT: MARKS, JAMES D.
;  APPLICANT:  AMERSDORFER, PETER
;  TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
;  TITLE OF INVENTION:  NEUROTOXINS
;  FILE REFERENCE: 407T-895120US
;  CURRENT APPLICATION NUMBER: US/10/632,706
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: US 60/400,721
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: US 09/144,806
;  PRIOR FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 278
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 144
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: single chain antibody fragment
US-10-632-706-144

  Query Match             100.0%;  Score 81;  DB 4;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 5
US-10-632-706-148
; Sequence 148, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
;  APPLICANT: MARKS, JAMES D.
;  APPLICANT:  AMERSDORFER, PETER
;  TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
;  TITLE OF INVENTION:  NEUROTOXINS
;  FILE REFERENCE: 407T-895120US
;  CURRENT APPLICATION NUMBER: US/10/632,706
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: US 60/400,721
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: US 09/144,806
;  PRIOR FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 278
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 148
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: single chain antibody fragment
US-10-632-706-148

  Query Match             100.0%;  Score 81;  DB 4;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 6
US-10-632-706-152
; Sequence 152, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
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;  APPLICANT: MARKS, JAMES D.
;  APPLICANT:  AMERSDORFER, PETER
;  TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
;  TITLE OF INVENTION:  NEUROTOXINS
;  FILE REFERENCE: 407T-895120US
;  CURRENT APPLICATION NUMBER: US/10/632,706
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: US 60/400,721
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: US 09/144,806
;  PRIOR FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 278
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 152
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: single chain antibody fragment
US-10-632-706-152

  Query Match             100.0%;  Score 81;  DB 4;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 7
US-10-632-706-156
; Sequence 156, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
;  APPLICANT: MARKS, JAMES D.
;  APPLICANT:  AMERSDORFER, PETER
;  TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
;  TITLE OF INVENTION:  NEUROTOXINS
;  FILE REFERENCE: 407T-895120US
;  CURRENT APPLICATION NUMBER: US/10/632,706
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: US 60/400,721
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: US 09/144,806
;  PRIOR FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 278
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 156
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: single chain antibody fragment
US-10-632-706-156

  Query Match             100.0%;  Score 81;  DB 4;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 8
US-10-632-706-160
; Sequence 160, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
;  APPLICANT: MARKS, JAMES D.
;  APPLICANT:  AMERSDORFER, PETER
;  TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
;  TITLE OF INVENTION:  NEUROTOXINS
;  FILE REFERENCE: 407T-895120US
;  CURRENT APPLICATION NUMBER: US/10/632,706
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: US 60/400,721
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: US 09/144,806
;  PRIOR FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 278
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 160
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: single chain antibody fragment
US-10-632-706-160

  Query Match             100.0%;  Score 81;  DB 4;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 9
US-10-632-706-164
; Sequence 164, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
;  APPLICANT: MARKS, JAMES D.
;  APPLICANT:  AMERSDORFER, PETER
;  TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
;  TITLE OF INVENTION:  NEUROTOXINS
;  FILE REFERENCE: 407T-895120US
;  CURRENT APPLICATION NUMBER: US/10/632,706
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: US 60/400,721
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: US 09/144,806
;  PRIOR FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 278
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 164
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: single chain antibody fragment
US-10-632-706-164

  Query Match             100.0%;  Score 81;  DB 4;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 10
US-10-632-706-168
; Sequence 168, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
;  APPLICANT: MARKS, JAMES D.
;  APPLICANT:  AMERSDORFER, PETER
;  TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
;  TITLE OF INVENTION:  NEUROTOXINS
;  FILE REFERENCE: 407T-895120US
;  CURRENT APPLICATION NUMBER: US/10/632,706
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;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: US 60/400,721
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: US 09/144,806
;  PRIOR FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 278
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 168
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: single chain antibody fragment
US-10-632-706-168

  Query Match             100.0%;  Score 81;  DB 4;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 11
US-10-788-625-6
; Sequence 6, Application US/10788625
; Publication No. US20040260068A1
; GENERAL INFORMATION:
;  APPLICANT: Tsurushita, Naoya
;  APPLICANT:  Kumar, Shankar
;  APPLICANT:  Vasquez, Maximiliano
;  TITLE OF INVENTION: Humanized Chicken Antibodies
;  FILE REFERENCE: 05882.0044.NPUS02
;  CURRENT APPLICATION NUMBER: US/10/788,625
;  CURRENT FILING DATE:  2004-02-26
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-788-625-6

  Query Match             100.0%;  Score 81;  DB 5;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 12
US-10-489-328-2
; Sequence 2, Application US/10489328
; Publication No. US20050037420A1
; GENERAL INFORMATION:
;  APPLICANT: Fraunhofer -Gesselschaft zur Forderung der angewandten
;  APPLICANT:  Forschung e.V.
;  APPLICANT:  ZHANG, Mei Yun
;  APPLICANT:  SCHILLBERG, Stefan
;  APPLICANT:  ZIMMERMANN, Sabine
;  APPLICANT:  DI FIORE, Stefano
;  APPLICANT:  EMANS, Neil
;  APPLICANT:  FISCHER, Rainer
;  TITLE OF INVENTION: Immunoglobulin having Particular Framework Scaffold and Methods
;  TITLE OF INVENTION:  of Making and Using
;  FILE REFERENCE: FRAU-202.1US
;  CURRENT APPLICATION NUMBER: US/10/489,328
;  CURRENT FILING DATE:  2004-03-11
;  PRIOR APPLICATION NUMBER: PCT/US02/29003
;  PRIOR FILING DATE: 2002-09-13
;  PRIOR APPLICATION NUMBER: 60/318,904
;  PRIOR FILING DATE: 2001-09-14
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: This is a heavy chain framework region 2 (HFR2)
US-10-489-328-2

  Query Match             100.0%;  Score 81;  DB 5;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 13
US-10-923-068-202
; Sequence 202, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 202
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-202

  Query Match             100.0%;  Score 81;  DB 5;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 14
US-10-923-068-205
; Sequence 205, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 205
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-205

  Query Match             100.0%;  Score 81;  DB 5;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


RESULT 15
US-10-923-068-232
; Sequence 232, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 232
;   LENGTH: 14
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-232

  Query Match             100.0%;  Score 81;  DB 5;  Length 14;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-05;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db          1 WVRQAPGKGLEWVA 14


Search completed: March 25, 2006, 10:08:05
Job time : 41.7801 secs
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:58:56 ; Search time 5.05759 Seconds
(without alignments)
81.644 Million cell updates/sec

Title: US-10-755-382-33
Perfect score: 81
Sequence: 1 WVRQAPGKGLEWVA 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	81	100.0	44	6	US-10-982-357-39	Sequence 39, Appl
2	81	100.0	87	6	US-10-982-357-46	Sequence 46, Appl
3	81	100.0	89	7	US-11-128-900-72	Sequence 72, Appl
4	81	100.0	97	7	US-11-093-274-35	Sequence 35, Appl
5	81	100.0	98	7	US-11-054-669-15	Sequence 15, Appl
6	81	100.0	98	7	US-11-054-669-23	Sequence 23, Appl
7	81	100.0	98	7	US-11-054-669-24	Sequence 24, Appl
8	81	100.0	98	7	US-11-054-669-25	Sequence 25, Appl
9	81	100.0	98	7	US-11-054-669-26	Sequence 26, Appl
10	81	100.0	98	7	US-11-084-554-34	Sequence 34, Appl
11	81	100.0	98	7	US-11-084-554-35	Sequence 35, Appl
12	81	100.0	98	7	US-11-084-554-44	Sequence 44, Appl
13	81	100.0	98	7	US-11-093-274-31	Sequence 31, Appl
14	81	100.0	98	7	US-11-004-590-14	Sequence 14, Appl
15	81	100.0	98	7	US-11-004-590-24	Sequence 24, Appl
16	81	100.0	98	7	US-11-004-590-25	Sequence 25, Appl
17	81	100.0	98	7	US-11-004-590-26	Sequence 26, Appl
18	81	100.0	98	7	US-11-136-250-34	Sequence 34, Appl
19	81	100.0	98	7	US-11-136-250-35	Sequence 35, Appl
20	81	100.0	98	7	US-11-136-250-44	Sequence 44, Appl
21	81	100.0	115	6	US-10-952-535A-2	Sequence 2, Appli
22	81	100.0	116	7	US-11-093-274-20	Sequence 20, Appl
23	81	100.0	116	7	US-11-125-837-38	Sequence 38, Appl
24	81	100.0	116	7	US-11-127-677-51	Sequence 51, Appl
25	81	100.0	116	7	US-11-051-453-3	Sequence 3, Appli
26	81	100.0	117	6	US-10-771-257-9	Sequence 9, Appli
27	81	100.0	117	6	US-10-771-257-53	Sequence 53, Appl
28	81	100.0	117	6	US-10-771-257-60	Sequence 60, Appl
29	81	100.0	117	6	US-10-771-257-81	Sequence 81, Appl
30	81	100.0	117	6	US-10-771-257-82	Sequence 82, Appl
31	81	100.0	117	6	US-10-771-257-83	Sequence 83, Appl
32	81	100.0	117	6	US-10-771-257-85	Sequence 85, Appl
33	81	100.0	117	6	US-10-771-257-87	Sequence 87, Appl
34	81	100.0	117	6	US-10-771-257-89	Sequence 89, Appl
35	81	100.0	117	6	US-10-771-257-91	Sequence 91, Appl
36	81	100.0	117	6	US-10-771-257-92	Sequence 92, Appl
37	81	100.0	117	6	US-10-771-257-94	Sequence 94, Appl
38	81	100.0	117	6	US-10-771-257-96	Sequence 96, Appl
39	81	100.0	117	6	US-10-771-257-97	Sequence 97, Appl
40	81	100.0	117	6	US-10-981-356A-6	Sequence 6, Appli
41	81	100.0	117	7	US-11-075-184A-2	Sequence 2, Appli
42	81	100.0	117	7	US-11-075-184A-10	Sequence 10, Appl
43	81	100.0	117	7	US-11-075-184A-11	Sequence 11, Appl
44	81	100.0	117	7	US-11-093-274-19	Sequence 19, Appl
45	81	100.0	117	7	US-11-127-677-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-10-982-357-39
; Sequence 39, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/982,357
; CURRENT FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-357-39

Query Match 100.0%; Score 81; DB 6; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
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Db 31 WVRQAPGKGLEWVA 44

RESULT 2
US-10-982-357-46
; Sequence 46, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/982,357
; CURRENT FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-357-46

Query Match 100.0%; Score 81; DB 6; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         31 WVRQAPGKGLEWVA 44
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RESULT 3
US-11-128-900-72
; Sequence 72, Application US/11128900
; Publication No. US20050287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1 DIV3
; CURRENT APPLICATION NUMBER: US/11/128,900
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR APPLICATION NUMBER: US 09/472087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-72

Query Match 100.0%; Score 81; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 WVRQAPGKGLEWVA 14
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Db         27 WVRQAPGKGLEWVA 40
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RESULT 4
US-11-093-274-35
; Sequence 35, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-35

Query Match 100.0%; Score 81; DB 7; Length 97;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 WVRQAPGKGLEWVA 14
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Db         35 WVRQAPGKGLEWVA 48
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RESULT 5
US-11-054-669-15
; Sequence 15, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-15

Query Match 100.0%; Score 81; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49
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RESULT 6
US-11-054-669-23
; Sequence 23, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-23

Query Match 100.0%; Score 81; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 WVRQAPGKGLEWVA 14
              ||||||||||||||
Db         36 WVRQAPGKGLEWVA 49
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RESULT 7
US-11-054-669-24
; Sequence 24, Application US/11054669
; Publication No. US20050261480A1

; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-24

Query Match 100.0%; Score 81; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 36 WVRQAPGKGLEWVA 49

RESULT 8
US-11-054-669-25
; Sequence 25, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-25

Query Match 100.0%; Score 81; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 36 WVRQAPGKGLEWVA 49

RESULT 9
US-11-054-669-26
; Sequence 26, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
; FILE REFERENCE: 30219/US/3
; CURRENT APPLICATION NUMBER: US/11/054,669
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: US 10/194,975
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 26
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-669-26

Query Match 100.0%; Score 81; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 36 WVRQAPGKGLEWVA 49

RESULT 10
US-11-084-554-34
; Sequence 34, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-34

Query Match 100.0%; Score 81; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 36 WVRQAPGKGLEWVA 49

RESULT 11
US-11-084-554-35
; Sequence 35, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-084-554-35

Query Match 100.0%; Score 81; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 36 WVRQAPGKGLEWVA 49

RESULT 12
US-11-084-554-44
; Sequence 44, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A
; CURRENT APPLICATION NUMBER: US/11/084,554
; CURRENT FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-084-554-44

Query Match 100.0%; Score 81; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 36 WVRQAPGKGLEWVA 49

RESULT 13
US-11-093-274-31
; Sequence 31, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
; APPLICANT: Graziano, Robert
; APPLICANT: Cardarelli, Josephine M.
; APPLICANT: Kempe, Thomas
; APPLICANT: Cutter, Beth
; APPLICANT: Srinivasan, Mohan
; TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
; FILE REFERENCE: 04280/1201101-US1
; CURRENT APPLICATION NUMBER: US/11/093,274
; CURRENT FILING DATE: 2005-03-28
; PRIOR APPLICATION NUMBER: 60/557,741
; PRIOR FILING DATE: 2004-03-29
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-093-274-31

Query Match 100.0%; Score 81; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 36 WVRQAPGKGLEWVA 49

RESULT 14
US-11-004-590-14
; Sequence 14, Application US/11004590
; Publication No. US20060008883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-590-14

Query Match 100.0%; Score 81; DB 7; Length 98;
Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WVRQAPGKGLEWVA 14
||||||||||||||
Db 36 WVRQAPGKGLEWVA 49

RESULT 15
US-11-004-590-24
; Sequence 24, Application US/11004590
; Publication No. US20060008883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-590-24

Query Match 100.0%; Score 81; DB 7; Length 98;

Best Local Similarity 100.0%; Pred. No. 4.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 WVRQAPGKGLEWVA 14
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Db         36 WVRQAPGKGLEWVA 49
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Search completed: March 25, 2006, 10:09:20
Job time : 6.05759 secs

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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:10 ; Search time 117.948 Seconds
(without alignments)
119.206 Million cell updates/sec

Title: US-10-755-382-36
Perfect score: 167
Sequence: 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	167	100.0	32	2	AAR97329	Aar97329 Humanised
2	164	98.2	32	2	AAR97330	Aar97330 Humanised
3	164	98.2	118	6	ABR42755	Abr42755 Anti-CEA
4	164	98.2	119	8	ADM95101	Adm95101 Humanised
5	164	98.2	119	8	ADM98324	Adm98324 Humanised
6	164	98.2	138	6	ABG76489	Abg76489 Heavy cha
7	164	98.2	254	2	AAR94557	Aar94557 Humanised
8	164	98.2	256	6	ABR42757	Abr42757 Anti-CEA
9	164	98.2	257	6	ABR42758	Abr42758 Anti-CEA
10	164	98.2	261	6	ABR42289	Abr42289 Diabody 6
11	164	98.2	261	6	ABR42754	Abr42754 Anti-CEA
12	164	98.2	261	6	ABR83645	Abr83645 hMN14-scF
13	164	98.2	267	6	ABR42292	Abr42292 Bispecifi
14	164	98.2	267	6	ABR42299	Abr42299 Bispecifi
15	164	98.2	267	6	ABR42296	Abr42296 Bispecifi
16	164	98.2	267	6	ABR42294	Abr42294 Bispecifi
17	164	98.2	358	8	ADU26571	Adu26571 Chimeric
18	164	98.2	363	8	ADU26561	Adu26561 Chimeric
19	164	98.2	364	8	ADU26570	Adu26570 Chimeric
20	164	98.2	370	8	ADU26560	Adu26560 Chimeric
21	164	98.2	415	6	ABR83648	Abr83648 TS1 VH ch
22	164	98.2	443	6	ABG76488	Abg76488 Humanised
23	164	98.2	443	6	ABG74240	Abg74240 Chimaeric
24	164	98.2	468	7	ADE64201	Ade64201 MN14HCF p
25	164	98.2	468	7	ADF60815	Adf60815 hMN-14 he
26	164	98.2	669	9	ADY97271	Ady97271 Exemplary
27	163	97.6	117	2	AAR77305	Aar77305 Variable
28	163	97.6	119	2	AAR13092	Aar13092 Grafted h
29	163	97.6	119	2	AAR13098	Aar13098 Grafted h
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31	163	97.6	119	2	AAR67447	Aar67447 OKT3 huma
32	163	97.6	119	2	AAR82962	Aar82962 Humanised
33	163	97.6	119	2	AAW11919	Aaw11919 Humanised
34	163	97.6	119	2	AAR97336	Aar97336 Humanised
35	163	97.6	119	2	AAW73529	Aaw73529 Humanised
36	163	97.6	120	2	AAR54930	Aar54930 Fc recept
37	163	97.6	126	2	AAR28746	Aar28746 Heavy cha
38	163	97.6	126	2	AAW73527	Aaw73527 Humanised
39	163	97.6	126	9	ADX37204	Adx37204 Human ant
40	163	97.6	137	2	AAR22760	Aar22760 Reshaped
41	163	97.6	137	2	AAR22762	Aar22762 Reshaped
42	163	97.6	137	2	AAR22763	Aar22763 CD4VHKOL-
43	163	97.6	137	2	AAR22761	Aar22761 CD4VHKOL-
44	163	97.6	300	2	AAW11503	Aaw11503 Humanised
45	163	97.6	300	2	AAW73218	Aaw73218 H22-HRG f

ALIGNMENTS

RESULT 1
AAR97329
ID AAR97329 standard; peptide; 32 AA.
XX
AC AAR97329;
XX
DT 15-OCT-1996 (first entry)
XX
DE Humanised monoclonal antibody heavy chain framework region.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Homo sapiens.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Claim 7; Page 39; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. This sequence corresponds to the third framework region of the
CC heavy chain of the humanised MAb. See AAR97313-97333

```
XX
SQ   Sequence 32 AA;

  Query Match             100.0%;  Score 167;  DB 2;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-15;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32


RESULT 2
AAR97330
ID   AAR97330 standard; peptide; 32 AA.
XX
AC   AAR97330;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Humanised monoclonal antibody heavy chain framework region.
XX
KW   Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW   complementary determining region; anti-carcinoembryonic antigen; CEA;
KW   diagnosis; imaging; therapy; immune response.
XX
OS   Homo sapiens.
XX
PN   WO9611013-A1.
XX
PD   18-APR-1996.
XX
PF   28-SEP-1995;   95WO-US011964.
XX
PR   05-OCT-1994;   94US-00318157.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Hansen HJ,  Armour KL;
XX
DR   WPI; 1996-209653/21.
XX
PT   New humanised anti-CEA monoclonal antibody - having engrafted murine
PT   CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS   Claim 7; Page 40; 62pp; English.
XX
CC   New humanised monoclonal antibodies (MAbs) comprising the complementary
CC   determining regions (CDRs) of a parental murine class III anti-
CC   carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC   heterologous antibody which can be derived from any species including
CC   human, retain the anti-CEA binding specificity of the parental murine MAb
CC   but are less immunogenic in a human subject than the parental MAb. The
CC   humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC   -producing cancers and patients receiving the humanised antibodies and
CC   conjugates show improved therapeutic results, decreased immune responses
CC   and decreased immune-mediated adverse effects compared to the parent
CC   antibody. This sequence corresponds to the third framework region of the
CC   heavy chain of the humanised MAb. See AAR97313-97333
XX
SQ   Sequence 32 AA;

  Query Match             98.2%;  Score 164;  DB 2;  Length 32;
  Best Local Similarity   96.9%;  Pred. No. 7.1e-15;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32


RESULT 3
ABR42755
ID   ABR42755 standard; protein; 118 AA.
XX
AC   ABR42755;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14 VH region.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Disclosure; Fig 12; 62pp; English.
XX
CC   The present sequence is the protein sequence of the heavy chain variable
CC   region of anti-carcinoembryonic antigen (CEA) humanized monoclonal
CC   antibody hMN-14. scFv constructs comprising the hMN-14 VH and Vkappa
CC   regions are used in novel multivalent, monospecific binding proteins
CC   (diabody, triabody and tetrabody) of the invention (see also ABR42754,
CC   ABR42757 and ABR42758). Claimed binding proteins are specific for a
CC   tumour-associated antigen, and are used in the diagnosis and treatment of
CC   a tumour, carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma,
CC   lymphoma or myeloma, or a cancer selected from acute lymphoblastic
CC   leukaemia, acute myelogenous leukaemia, biliary, breast, cervical,
CC   chronic lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 118 AA;

  Query Match             98.2%;  Score 164;  DB 6;  Length 118;
  Best Local Similarity   96.9%;  Pred. No. 2.9e-14;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 4
ADM95101
ID   ADM95101 standard; protein; 119 AA.
XX
AC   ADM95101;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 MAb heavy chain variable region coding sequence.
```

XX
KW non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW complementarity determining region; pancreatic cancer; breast cancer;
KW ovarian cancer.
XX
OS Mus sp.
OS Homo sapiens.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-364813/34.
DR N-PSDB; ADM95099.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Claim 14; Fig 16B; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the humanised
CC murine MN-14 antibody heavy chain variable region.
XX
SQ Sequence 119 AA;

Query Match 98.2%; Score 164; DB 8; Length 119;
Best Local Similarity 96.9%; Pred. No. 3e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||:||||||||||||||||||||||||
Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98
```

RESULT 5
ADM98324
ID ADM98324 standard; protein; 119 AA.
XX
AC ADM98324;
XX
DT 15-JUL-2004 (first entry)
XX
DE Humanised murine MN-14 antibody heavy chain variable region protein.
XX
KW carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW antibody; MN-14; non-medullary thyroid carcinoma;
KW medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW hepatocellular carcinoma; breast cancer; lung cancer;
KW antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW apoptosis; humanised.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 33. .34
FT /note= "Encoded by TGGGATAGCAGTACGATTAACTATGCGATG"
FT Misc-difference 53. .62
FT /note= "Encoded by CCACCG"
XX
PN WO2004032857-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031801.
XX
PR 08-OCT-2002; 2002US-0416531P.
PR 11-OCT-2002; 2002WO-US032307.
PR 02-MAY-2003; 2003US-0467161P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-340797/31.
DR N-PSDB; ADM98323.
XX
PT Treating non-medullary or medullary thyroid carcinoma, involves
PT administering to subject, either concurrently or sequentially, anti-
PT carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS Disclosure; Fig 23b; 122pp; English.
XX
CC This invention relates to methods for treating cancers that express
CC carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC antibodies that can be used following administration of an agent that
CC will increase antibody effector functions or following administration of
CC an amount of interferon effective to upregulate CEA expression in tumour
CC cells. The present invention describes the anti-CEA antibody as a class
CC III humanised murine monoclonal antibody that retains specificity for CEA
CC binding and is preferably an MN-14 antibody or fragment thereof.
CC Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC composition useful for the treatment of non-medullary or medullary
CC thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC carcinoma, as well as breast or lung cancer. Furthermore, it can
CC stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC cell growth and angiogenesis. This polypeptide sequence is the humanised
CC murine MN-14 antibody heavy chain variable region protein of the
CC invention.
XX
SQ Sequence 119 AA;

Query Match 98.2%; Score 164; DB 8; Length 119;
Best Local Similarity 96.9%; Pred. No. 3e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||:||||||||||||||||||||||||
Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98
```

RESULT 6
ABG76489
ID ABG76489 standard; protein; 138 AA.
XX
AC ABG76489;
XX
DT 13-MAY-2003 (first entry)
XX
DE Heavy chain variable, VH, region of antibody hMN14.
XX
KW CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW human; zeta signalling chain; CD8alpha hinge; humanised antibody;
KW heavy chain variable region; VH.
XX

```
OS   Homo sapiens.
OS   Mus sp.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT   Protein         20. .138
FT                   /label= Mature_VH_of_hMN14
XX
PN   US2002165360-A1.
XX
PD   07-NOV-2002.
XX
PF   10-DEC-2001; 2001US-00006771.
XX
PR   30-NOV-2000; 2000US-0250087P.
PR   30-NOV-2000; 2000US-0250090P.
XX
PA   (JUNG/) JUNGHANS R P.
XX
PI   Junghans RP;
XX
DR   WPI; 2003-298705/29.
DR   N-PSDB; ABX13169.
XX
PT   New chimeric molecule from humanized antibody against carcinoembryonic
PT   antigen and having signaling molecules of T cells and other effector
PT   cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS   Disclosure; Page 9; 20pp; English.
XX
CC   The invention relates to a chimaeric molecule comprising the
CC   carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC   as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC   chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC   which the cysteine residues have been mutated, with the IgTCR molecule
CC   occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC   appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC   NK (not defined) or other effector cells are useful in treating patients
CC   with cancers expressing the CEA antigen, together with other or with
CC   heterologous constructs to engage additional stimulatory and functional
CC   properties of the effector cells to enhance the anti-tumour therapeutic
CC   efficacy. The cancer disorder includes colorectal, breast and lung
CC   cancers. The present sequence represents the heavy chain variable, VH,
CC   region of antibody hMN14. The VH protein is humanised (complementarity
CC   determining region-grafted) and has a leader peptide
XX
SQ   Sequence 138 AA;

  Query Match             98.2%;  Score 164;  DB 6;  Length 138;
  Best Local Similarity   96.9%;  Pred. No. 3.5e-14;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db         86 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 117


RESULT 7
AAR94557
ID   AAR94557 standard; protein; 254 AA.
XX
AC   AAR94557;
XX
DT   19-JUN-1996  (first entry)
XX
DE   Humanised antibody MN14 heavy chain.
XX
KW   Cancer; therapy; radiotherapy; radiolabelling; phosphorus;
KW   humanised antibody; complementarity determining region; CDR; targetting;
KW   protein kinase; Fab; F(ab')2; Escherichia coli; vector; MN14pBEV;
KW   carcinoembryonic antigen; CEA; MN14-Kemptide.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Sig_peptide
FT                   /note= "PelB signal peptide"
FT   Protein         23. .254
FT                   /label= Mat_protein
FT   Region          53. .57
FT                   /label= CDR-H1
FT   Region          72. .88
FT                   /label= CDR-H2
FT   Region          121. .130
FT                   /label= CDR-H3
FT   Domain          240. .254
FT                   /label= Hinge_domain
XX
PN   WO9608506-A1.
XX
PD   21-MAR-1996.
XX
PF   18-SEP-1995;   95WO-US011405.
XX
PR   16-SEP-1994;   94US-00308103.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Leung S,  Hansen HJ,  Griffiths GL;
XX
DR   WPI; 1996-179897/18.
DR   N-PSDB; AAT14493.
XX
PT   Phosphorus labelled antibodies for use in cancer therapy - comprise
PT   protein kinase peptide substrate sequence and specific targetting CDR,
PT   for radio-labelling diseased cells with a phosphorus isotope.
XX
PS   Example 1 (ix); Fig 5; 62pp; English.
XX
CC   The heavy chain and hinge region (AAR94557) and light chain (AAR94558) of
CC   humanised anti-CEA antibody MN14 are the products of an Fab'/F(ab')2
CC   dicistronic gene (AAT14493). They are derived from anti-CEA murine
CC   monoclonal antibody MN14 following cloning and humanisation of
CC   complementarity determining regions. The dicistronic gene was used to
CC   construct vector MN14pBEV. A protein kinase substrate (see AAR94550)
CC   encoding sequence was incorporated into the vector, and MN14-Kemptide
CC   fusion protein was secreted from E. coli BMH71-18 mutS. The fusion
CC   protein can be radiolabelled with 32P or 33P and used for targetted
CC   radiotherapy of tumours or infectious lesions
XX
SQ   Sequence 254 AA;

  Query Match             98.2%;  Score 164;  DB 2;  Length 254;
  Best Local Similarity   96.9%;  Pred. No. 6.7e-14;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db         89 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 120


RESULT 8
ABR42757
ID   ABR42757 standard; protein; 256 AA.
XX
AC   ABR42757;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-0.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-0;
```

```
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; triabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .256
FT                   /label= hMN-14-0
FT   Region          142. .250
FT                   /label= hMN-14Vkappa
FT   Region          251. .256
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
DR   N-PSDB; ACC58722.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 39; Fig 13; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-0, which is
CC   designed to form an hMN-14 triabody. The hMN-14-0 polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa without a peptide linker. The use of the zero linker enables the
CC   secreted polypeptide to form a triabody, forming 3 binding sites for CEA.
CC   The polypeptide also includes a pelB signal peptide, which precedes the
CC   VH moiety to facilitate synthesis of the polypeptide in the periplasmic
CC   space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific triabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 256 AA;

  Query Match             98.2%;  Score 164;  DB 6;  Length 256;
  Best Local Similarity   96.9%;  Pred. No. 6.8e-14;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 9
ABR42758
ID   ABR42758 standard; protein; 257 AA.
XX
AC   ABR42758;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-1G.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-1G;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; tetrabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .257
FT                   /label= hMN-14-0
FT   Region          142
FT                   /label= 1G_linker
FT   Region          143. .251
FT                   /label= hMN-14Vkappa
FT   Region          252. .257
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 48; Fig 14; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-1G, which is
CC   designed to form an hMN-14 tetrabody. The hMN-14-1G polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa via a single glycine residues. Use of the 1G linker enables some
CC   of the the secreted polypeptide to form a tetrabody with 4 binding sites
CC   for CEA. The polypeptide also includes a pelB signal peptide, which
CC   precedes the VH moiety to facilitate synthesis of the polypeptide in the
CC   periplasmic space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific tetrabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
```

```
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 257 AA;

  Query Match             98.2%;  Score 164;  DB 6;  Length 257;
  Best Local Similarity   96.9%;  Pred. No. 6.8e-14;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 10
ABR42289
ID   ABR42289 standard; protein; 261 AA.
XX
AC   ABR42289;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Diabody 679-scFv-L5 polypeptide (VH-I3Q/C101S mutant).
XX
KW   Diabody; antibody; 679-scFv-L5; histamine-succinyl-glycyl; HSG;
KW   affinity enhancement system; tumour; targeting; mutant; mutein.
XX
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB signal peptide"
FT   Misc-difference 3
FT                   /note= "wild-type Ile substituted by Gln"
FT   Protein         23. .268
FT                   /label= 679-scFv-L5
FT   Region          23. .142
FT                   /label= 679VH(I3Q/C101S)
FT   Misc-difference 101
FT                   /note= "wild-type Cys substituted by Ser"
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .260
FT                   /label= 679Vk
FT   Region          261. .268
FT                   /label= 6His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57803.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Disclosure; Fig 28; 87pp; English.
XX
CC   The present sequence is the protein sequence of a 679 mutant diabody in
CC   which antibody 679 VH has a Gln for Ile amino acid substitution at
CC   position 3 and a Ser for Gln amino acid substitution at position 101.
CC   Murine monoclonal antibody 679 binds with high affinity to molecules
CC   containing the moiety histamine-succinyl-glycyl (HSG). The present
CC   polypeptide comprises: 679 VH(I3Q) linked to 679 Vk via a peptide linker
CC   (enables the secreted polypeptide to dimerise into a diabody, forming 2
CC   sites for HSG); a pelB leader signal peptide (facilitates transport of
CC   the polypeptide into the periplasmic space of Escherichia coli); and 6
CC   His residues (allows purification by IMAC). The 679 diabody was expressed
CC   in E. coli at a level of 10 ug/l of culture, compared with 1 ug/l for the
CC   non-mutant polypeptide. The invention provides a bispecific diabody
CC   comprising an HSG binding site and a carcinoembryonic antigen (CEA)
CC   binding site. The HSG antigen binding site may comprise the VH and Vk
CC   polypeptides of 679 MAb. These diabodies are produced via recombinant DNA
CC   technology and create a novel affinity enhancement system that shows
CC   specific affinity for HSG and CEA. They pre-target CEA positive tumours
CC   for subsequent specific delivery of therapeutic radioisotopes carried by
CC   HSG-carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 261 AA;

  Query Match             98.2%;  Score 164;  DB 6;  Length 261;
  Best Local Similarity   96.9%;  Pred. No. 6.9e-14;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 11
ABR42754
ID   ABR42754 standard; protein; 261 AA.
XX
AC   ABR42754;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-scFv-L5.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-scFv-15;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .261
FT                   /label= hMN-14-scFv-L5
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .255
FT                   /label= hMN-14Vkappa
FT   Region          256. .261
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
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XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032718.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
PR 08-JAN-2002; 2002US-0345641P.
PR 22-AUG-2002; 2002US-0404919P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg DM;
XX
DR WPI; 2003-513460/48.
DR N-PSDB; ACC58721.
XX
PT New multivalent, monospecific binding protein comprising two or more
PT binding sites having affinity for the same single target antigen, where
PT each binding site is associated with scFv fragments, useful for
PT diagnosing or treating tumor.
XX
PS Claim 31; Fig 11; 62pp; English.
XX
CC The present sequence is the protein sequence of hMN-14-scFv-L5, which was
CC designed to form an hMN-14 diabody. The hMN-14-scFv-L5 polypeptide
CC comprises the C-terminal end of anti-carcinoembryonic antigen (CEA)
CC humanized monoclonal antibody hMN-14 VH linked to the N-terminal part of
CC hMN-14 Vkappa by a peptide linker that enables the secreted polypeptide
CC to dimerize into a diabody, forming 2 binding sites for CEA. The
CC polypeptide also includes a pelB signal peptide, which precedes the VH
CC moiety to facilitate synthesis of the polypeptide in the periplasmic
CC space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC purification. In the claimed monospecific diabody, each scFv comprises
CC the present sequence. The diabody is an example of claimed multivalent
CC binding proteins specific for a tumour-associated antigen. The binding
CC proteins are used in the diagnosis and treatment of a tumour, carcinoma,
CC melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma or myeloma,
CC or a cancer selected from acute lymphoblastic leukaemia, acute
CC myelogenous leukaemia, biliary, breast, cervical, chronic lymphocytic
CC leukaemia, chronic myelogenous leukaemia, colorectal, endometrial,
CC oesophageal, gastric, head and neck, Hodgkin's lymphoma, lung, medullary
CC thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic, prostate and
CC bladder
XX
SQ Sequence 261 AA;

Query Match 98.2%; Score 164; DB 6; Length 261;
Best Local Similarity 96.9%; Pred. No. 6.9e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
||||||||:|||||||||||||||||||||||
Db 90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121

RESULT 12
ABR83645
ID ABR83645 standard; protein; 261 AA.
XX
AC ABR83645;
XX
DT 16-OCT-2003 (first entry)
XX
DE hMN14-scFv-L5 amino acid sequence.
XX
KW Multispecific binding protein; multivalent; target antigen; cytostatic;
KW immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW immunotherapy; autoimmune disease; infectious disease;
KW cardiovascular disease; inflammatory disease.
XX
OS Escherichia coli.
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003057829-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US038985.
XX
PR 26-DEC-2001; 2001US-0342103P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg D;
XX
DR WPI; 2003-607997/57.
DR N-PSDB; ACF57430.
XX
PT Novel multivalent, multi-specific binding protein useful for treating
PT cancer, has first binding site having affinity towards hapten group and
PT second and third binding sites each having affinity towards target
PT antigen.
XX
PS Claim 11; Fig 6; 43pp; English.
XX
CC The present invention describes a multivalent, multi-specific binding
CC protein (I) comprising a first binding site having an affinity towards a
CC hapten group and a second and a third binding sites each having affinity
CC towards a target antigen, which may be the same or a different target
CC antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC useful for delivering a diagnostic agent, a therapeutic agent, or its
CC combination to a target, which involves administering (I) to a subject,
CC waiting for a sufficient amount of time for an amount of the non-binding
CC protein to clear the subject's blood stream, and administering to the
CC subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC agent, or its combination, that binds to a binding site of the binding
CC protein. (I) is also useful for detecting or treating a human disorder,
CC preferably cancer, autoimmune diseases, infectious diseases,
CC cardiovascular diseases and inflammatory diseases. The present sequence
CC represents a hMN14-scFv-L5 amino acid sequence, which is used in the
CC exemplification of the present invention
XX
SQ Sequence 261 AA;

Query Match 98.2%; Score 164; DB 6; Length 261;
Best Local Similarity 96.9%; Pred. No. 6.9e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
||||||||:|||||||||||||||||||||||
Db 90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121

RESULT 13
ABR42292
ID ABR42292 standard; protein; 267 AA.
XX
AC ABR42292;
XX
DT 11-AUG-2003 (first entry)
XX
DE Bispecific diabody polypeptide #2.
XX
KW Diabody; antibody; carcinoembryonic antigen; CEA;
KW histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW targeting.
XX
OS Homo sapiens.
OS Mus sp.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX

```
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .267
FT                   /label= BSI_polypeptide#1
FT   Region          24. .141
FT                   /label= hMN14_VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .259
FT                   /label= 679_Vk
FT   Region          262. .267
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57806.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 31; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of a
CC   novel bispecific diabody comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen. The bispecific diabody can be produced using
CC   recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC   a novel affinity enhancement system that shows specific affinity for HSG
CC   and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC   subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC   carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             98.2%;  Score 164;  DB 6;  Length 267;
  Best Local Similarity   96.9%;  Pred. No. 7.1e-14;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||:|||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 14
ABR42299
ID   ABR42299 standard; protein; 267 AA.
XX
AC   ABR42299;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS1.5H polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BS1.5H_polypeptide#2
FT   Region          24. .142
FT                   /label= hMN14_VH
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
FT                   /label= h679_Vk
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57813.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 38; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of novel
CC   bispecific diabody BS1.5H comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). A humanised version of its VH and Vk sequences
CC   have been used in BS1.5H. Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC   using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC   provides a novel affinity enhancement system that shows specific affinity
CC   for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC   tumours for subsequent specific delivery of therapeutic radioisotopes
CC   carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC   disease, cardiovascular diseases and inflammatory diseases can be
CC   detected or treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             98.2%;  Score 164;  DB 6;  Length 267;
  Best Local Similarity   96.9%;  Pred. No. 7.1e-14;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||:|||||||||||||||||||||||
```

```
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121

RESULT 15
ABR42296
ID   ABR42296 standard; protein; 267 AA.
XX
AC   ABR42296;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS2 polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .267
FT                   /label= BS2_polypeptide#2
FT   Region          24. .141
FT                   /label= hMN14-VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .259
FT                   /label= 679_Vk
FT   Region          262. .267
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57810.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 35; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of novel
CC   bispecific diabody BS2 comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC   using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC   provides a novel affinity enhancement system that shows specific affinity
CC   for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC   tumours for subsequent specific delivery of therapeutic radioisotopes
CC   carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC   disease, cardiovascular diseases and inflammatory diseases can be
CC   detected or treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             98.2%;  Score 164;  DB 6;  Length 267;
  Best Local Similarity   96.9%;  Pred. No. 7.1e-14;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


Search completed: March 25, 2006, 09:02:23
Job time : 119.073 secs
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:02:50 ; Search time 18.4293 Seconds
(without alignments)
167.067 Million cell updates/sec

Title: US-10-755-382-36
Perfect score: 167
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	163	97.6	126	1	G1HUKL	Ig heavy chain V-I
2	144	86.2	151	2	A60943	Ig heavy chain pre
3	143	85.6	70	2	S20770	Ig heavy chain V r
4	141	84.4	113	2	S24247	Ig heavy chain V r
5	140	83.8	63	2	S26796	Ig heavy chain V r
6	140	83.8	122	2	S69910	Ig V-D-J region (K
7	139	83.2	110	2	S69897	Ig heavy chain V r
8	139	83.2	118	2	S31116	Ig heavy chain - h
9	139	83.2	120	2	S31112	Ig heavy chain - h
10	139	83.2	121	2	S31113	Ig heavy chain - h
11	139	83.2	121	2	I55673	Ig heavy chain - h
12	139	83.2	138	2	B56701	Ig heavy chain V r
13	138	82.6	52	2	S21591	Ig heavy chain V r
14	138	82.6	76	2	S31592	Ig heavy chain V r
15	138	82.6	96	2	S20781	Ig heavy chain V r
16	138	82.6	97	2	S26935	Ig heavy chain V r
17	138	82.6	97	2	S46462	Ig heavy chain V r
18	138	82.6	98	2	S26889	Ig heavy chain V r
19	138	82.6	98	2	PL0116	Ig heavy chain V-I
20	138	82.6	98	2	S29543	Ig heavy chain V r
21	138	82.6	98	2	S29546	Ig heavy chain V r
22	138	82.6	99	2	S24259	Ig heavy chain V r
23	138	82.6	100	2	S24258	Ig heavy chain V r
24	138	82.6	101	2	S24257	Ig heavy chain V r
25	138	82.6	101	2	JT0511	Ig heavy chain V-I
26	138	82.6	102	2	S24260	Ig heavy chain V r
27	138	82.6	104	2	S24255	Ig heavy chain V r
28	138	82.6	105	2	S24249	Ig heavy chain V r
29	138	82.6	106	2	S24256	Ig heavy chain V r
30	138	82.6	108	2	PH1648	Ig heavy chain V r
31	138	82.6	108	2	PH1642	Ig heavy chain V r
32	138	82.6	109	2	PH1649	Ig heavy chain V r
33	138	82.6	109	2	PH1646	Ig heavy chain V r
34	138	82.6	109	2	PH1644	Ig heavy chain V r
35	138	82.6	111	2	PH1643	Ig heavy chain V r
36	138	82.6	111	2	PH1645	Ig heavy chain V r
37	138	82.6	112	2	PH1647	Ig heavy chain V r
38	138	82.6	114	2	S46390	Ig heavy chain V r
39	138	82.6	114	2	S46391	Ig heavy chain V r
40	138	82.6	114	2	S46392	Ig heavy chain V r
41	138	82.6	116	2	B28966	Ig heavy chain pre
42	138	82.6	117	1	H3HU26	Ig heavy chain pre
43	138	82.6	117	2	A45953	Ig heavy chain pre
44	138	82.6	117	2	A34964	Ig heavy chain pre
45	138	82.6	118	2	S31121	Ig heavy chain - h

ALIGNMENTS

RESULT 1
G1HUKL
Ig heavy chain V-III region (Kol) - human
C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C;Accession: A02055
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Accession: A02055
A;Molecule type: protein
A;Residues: 1-126 <SCH>
A;Cross-references: UNIPROT:P01772; UNIPARC:UPI000002D0C3
C;Genetics:
A;Gene: GDB:IGHV@
A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;15-98/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96,105-110/Disulfide bonds: #status experimental

Query Match 97.6%; Score 163; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 97
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RESULT 2
A60943
Ig heavy chain precursor V region (clone HN.14) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: A60943; A48165
R;Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat, E.A.;
J. Neuroimmunol. 30, 245, 1990
A;Title: Molecular cloning of a human immunoglobulin heavy chain variable (V-H) region w
A;Reference number: A60943; MUID:91036050; PMID:1699976
A;Accession: A60943
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-151 <DES>
A;Cross-references: UNIPARC:UPI0000176C11
R;Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat, E.A.;
J. Neuroimmunol. 26, 35-41, 1990
A;Title: Molecular cloning of a human immunoglobulin heavy chain variable (V-H) region w
A;Reference number: A48165; MUID:90094677; PMID:1688442

A;Accession: A48165
A;Molecule type: mRNA
A;Residues: 1-36,'M',38-62,'AR',67-151 <DE2>
A;Cross-references: UNIPARC:UPI0000176C12
A;Note: this sequence has been corrected in reference A60943
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 86.2%; Score 144; DB 2; Length 151;
Best Local Similarity 83.9%; Pred. No. 7.4e-12;
Matches 26; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
Db 86 RFTISRDNSKNTIYLQMNSLRPEDTAVYYCA 116

RESULT 3
S20770
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20770
R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A;Reference number: S20764
A;Accession: S20770
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-70 <MOR>
A;Cross-references: UNIPARC:UPI00001163F1; EMBL:Z11953; NID:g33869; PIDN:CAA78010.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 85.6%; Score 143; DB 2; Length 70;
Best Local Similarity 83.9%; Pred. No. 4.6e-12;
Matches 26; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
Db 10 RFTISRDNSKNTLYLQLNSLRPEDTAVYYCA 40

RESULT 4
S24247
Ig heavy chain V region (VH26-DLR2-JH3) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S24247
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B cel
A;Reference number: S24247
A;Accession: S24247
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <STE>
A;Cross-references: UNIPARC:UPI0000116084; EMBL:X67060; NID:g38377; PIDN:CAA47445.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 141; DB 2; Length 113;
Best Local Similarity 87.1%; Pred. No. 1.4e-11;
Matches 27; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
Db 66 RFTISRDNSKNTLYLQMNSLRAEDTAVYFCA 96

RESULT 5
S26796
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 30-Apr-1999 #text_change 20-Jun-2000
C;Accession: S26796
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami
A;Reference number: S26786; MUID:92111632; PMID:1730251
A;Accession: S26796
A;Molecule type: mRNA
A;Residues: 1-63 <MOR>
A;Cross-references: UNIPARC:UPI0000115FC9; EMBL:X61018; NID:g32785; PIDN:CAA43352.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 83.8%; Score 140; DB 2; Length 63;
Best Local Similarity 87.1%; Pred. No. 1e-11;
Matches 27; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
Db 13 RFTISRDNSKNTLFLQMNSLRVEDTAVYYCA 43

RESULT 6
S69910
Ig V-D-J region (KR) - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69910
R;Sahota, S.; Hamblin, T.; Oscier, D.G.; Stevenson, F.K.
Leukemia 8, 1285-1289, 1994
A;Title: Assessment of the role of clonogenic B lymphocytes in the pathogenesis of multi
A;Reference number: S69909; MUID:94335315; PMID:8057663
A;Accession: S69910
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-122 <SAH>
A;Cross-references: UNIPARC:UPI0000116642; EMBL:Z33400; NID:g871350; PIDN:CAA83851.1; PII
A;Note: the sequence of residues 108-122 and the corresponding nucleic acid sequence are
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 83.8%; Score 140; DB 2; Length 122;
Best Local Similarity 83.9%; Pred. No. 2e-11;
Matches 26; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
Db 67 RFTISRDNSKNTLYLEMDSLRAEDTAVYYCA 97

RESULT 7
S69897
Ig heavy chain V region (clone RFSJ5H), rheumatoid factor - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69897
R;Randen, I.; Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig, J
Eur. J. Immunol. 23, 1220-1225, 1993
A;Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune respo
A;Reference number: S69896; MUID:93272805; PMID:8500520
A;Accession: S69897
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-110 <RAN>
A;Cross-references: UNIPARC:UPI0000176D56; EMBL:Z34891
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 83.2%; Score 139; DB 2; Length 110;

```
  Best Local Similarity   81.2%;  Pred. No. 2.5e-11;
  Matches   26;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||:|||:||| ||| ||:||:
Db         67 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAT 98


RESULT 8
S31116
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C;Accession: S31116
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31116
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-118 <RAA>
A;Cross-references: UNIPROT:Q8WUK1; UNIPARC:UPI0000176E37; EMBL:X62966
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             83.2%;  Score 139;  DB 2;  Length 118;
  Best Local Similarity   81.2%;  Pred. No. 2.6e-11;
  Matches   26;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||:|||:||| ||| ||:||:
Db         67 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAT 98


RESULT 9
S31112
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31112
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31112
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-120 <RAA>
A;Cross-references: UNIPARC:UPI0000176C8C; EMBL:X62961
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             83.2%;  Score 139;  DB 2;  Length 120;
  Best Local Similarity   81.2%;  Pred. No. 2.7e-11;
  Matches   26;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||:|||:||| ||| ||:||:
Db         67 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAT 98


RESULT 10
S31113
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31113
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31113
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-121 <RAA>
A;Cross-references: UNIPARC:UPI0000176C89; EMBL:X62962
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             83.2%;  Score 139;  DB 2;  Length 121;
  Best Local Similarity   81.2%;  Pred. No. 2.7e-11;
  Matches   26;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||:|||:||| ||| ||:||:
Db         67 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAT 98


RESULT 11
I55673
Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I55673
R;Knight, G.B.; Agnello, V.; Bonagura, V.; Barnes, J.L.; Panka, D.J.; Zhang, Q.X.
J. Exp. Med. 178, 1903-1911, 1993
A;Title: Human rheumatoid factor cross-idiotypes. IV. Studies on WA XId-positive IgM wit
tinct from the 17.109 and G6 XIds.
A;Reference number: I55673; MUID:94065558; PMID:8245772
A;Accession: I55673
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-121 <RES>
A;Cross-references: UNIPARC:UPI0000117326; GB:M87268; NID:g186197; PIDN:AAC37536.1; PID
C;Genetics:
A;Gene: GDB:IGHM
A;Cross-references: GDB:120086; OMIM:147020
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             83.2%;  Score 139;  DB 2;  Length 121;
  Best Local Similarity   81.2%;  Pred. No. 2.7e-11;
  Matches   26;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||:|||:||| ||| ||:||:
Db         67 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAA 98


RESULT 12
B56701
Ig heavy chain V region precursor (HuA) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 23-Jul-1999
C;Accession: B56701
R;Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
J. Biol. Chem. 270, 12457-12465, 1995
A;Title: Human and mouse monoclonal antibodies to blood group A substance, which are nea
A;Reference number: A56701; MUID:95279371; PMID:7759488
A;Accession: B56701
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-138 <NIC>
A;Cross-references: UNIPARC:UPI00001139E2; GB:L41175; NID:g762821; PIDN:AAA64876.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-115/Domain: immunoglobulin homology <IMM>
```

Query Match 83.2%; Score 139; DB 2; Length 138;
Best Local Similarity 87.1%; Pred. No. 3.1e-11;
Matches 27; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
||||||||||||||:|||:||| ||| |||||
Db 84 RFTISRDNSKNTLYLQMNSLRLEDTAVYFCA 114

RESULT 13
S21591
Ig heavy chain V region (35D7) - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S21591
R;Kaartinen, M.
submitted to the EMBL Data Library, May 1992
A;Reference number: S21591
A;Accession: S21591
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-52 <KAA>
A;Cross-references: UNIPARC:UPI0000116056; EMBL:X66460; NID:g32789; PIDN:CAA47075.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 82.6%; Score 138; DB 2; Length 52;
Best Local Similarity 83.9%; Pred. No. 1.6e-11;
Matches 26; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
||||||||||||||:|||:||| ||| ||:||
Db 10 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 40

RESULT 14
S31592
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 23-Jul-1999
C;Accession: S31592
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31592
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-76 <CUI>
A;Cross-references: UNIPARC:UPI000011645E; EMBL:Z14179; NID:g31025; PIDN:CAA78548.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 82.6%; Score 138; DB 2; Length 76;
Best Local Similarity 83.9%; Pred. No. 2.3e-11;
Matches 26; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
||||||||||||||:|||:||| ||| ||:||
Db 23 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 53

RESULT 15
S20781
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20781
R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A;Reference number: S20764
A;Accession: S20781
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-96 <MOR>
A;Cross-references: UNIPARC:UPI00001163E9; EMBL:Z11945; NID:g33895; PIDN:CAA78002.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 82.6%; Score 138; DB 2; Length 96;
Best Local Similarity 83.9%; Pred. No. 2.9e-11;
Matches 26; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
||||||||||||||:|||:||| ||| ||:||
Db 42 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 72

Search completed: March 25, 2006, 09:15:46
Job time : 18.4293 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:40 ; Search time 115.267 Seconds
(without alignments)
195.866 Million cell updates/sec

Title: US-10-755-382-36
Perfect score: 167
Sequence: 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	163	97.6	126	1	HV3K_HUMAN	P01772 homo sapien
2	139	83.2	417	2	Q6N093_HUMAN	Q6n093 homo sapien
3	138	82.6	112	2	Q9UGP3_HUMAN	Q9ugp3 homo sapien
4	138	82.6	113	2	Q9UL90_HUMAN	Q9ul90 homo sapien
5	138	82.6	116	1	HV05_CARAU	P19181 carassius a
6	138	82.6	117	1	HV3C_HUMAN	P01764 homo sapien
7	138	82.6	240	2	Q65ZC9_HUMAN	Q65zc9 homo sapien
8	138	82.6	466	2	Q6IN78_HUMAN	Q6in78 homo sapien
9	138	82.6	613	2	Q8WUK1_HUMAN	Q8wuk1 homo sapien
10	135	80.8	116	2	Q9UL93_HUMAN	Q9ul93 homo sapien
11	135	80.8	147	2	Q9Y509_HUMAN	Q9y509 homo sapien
12	135	80.8	196	2	Q65ZL8_MOUSE	Q65zl8 mus musculu
13	134	80.2	466	2	Q6N096_HUMAN	Q6n096 homo sapien
14	133	79.6	118	2	Q9UL72_HUMAN	Q9ul72 homo sapien
15	133	79.6	465	2	Q5I0J0_RAT	Q5i0j0 rattus norv
16	133	79.6	473	2	Q91Z05_MOUSE	Q91z05 mus musculu
17	133	79.6	485	2	Q6PDB8_MOUSE	Q6pdb8 mus musculu
18	132	79.0	461	2	Q5M7V3_RAT	Q5m7v3 rattus norv
19	132	79.0	469	2	Q569F4_HUMAN	Q569f4 homo sapien
20	132	79.0	544	2	Q6PJ95_HUMAN	Q6pj95 homo sapien
21	131	78.4	112	2	Q9HCC1_HUMAN	Q9hcc1 homo sapien
22	131	78.4	118	2	Q9UL91_HUMAN	Q9ul91 homo sapien
23	131	78.4	119	1	HV3I_HUMAN	P01770 homo sapien
24	131	78.4	121	2	Q9UL71_HUMAN	Q9ul71 homo sapien
25	131	78.4	136	1	HV16_MOUSE	P01783 mus musculu
26	131	78.4	470	2	Q6PJA4_HUMAN	Q6pja4 homo sapien
27	131	78.4	478	2	Q6PI81_HUMAN	Q6pi81 homo sapien
28	131	78.4	483	2	Q566J7_MOUSE	Q566j7 mus musculu
29	131	78.4	606	2	Q6GMY2_HUMAN	Q6gmy2 homo sapien
30	130	77.8	122	1	HV3G_HUMAN	P01768 homo sapien
31	130	77.8	597	2	Q96BB9_HUMAN	Q96bb9 homo sapien
32	129	77.2	117	1	HV03_CARAU	P19180 carassius a
33	129	77.2	119	2	Q5F2I8_MOUSE	Q5f2i8 mus musculu
34	129	77.2	493	2	Q6GMX2_HUMAN	Q6gmx2 homo sapien
35	128	76.6	104	2	Q9UL87_HUMAN	Q9ul87 homo sapien
36	128	76.6	117	1	HV02_CANFA	P01785 canis famil
37	128	76.6	117	1	HV53_MOUSE	P18524 mus musculu
38	128	76.6	117	1	HV55_MOUSE	P18526 mus musculu
39	128	76.6	119	2	Q920E7_MOUSE	Q920e7 mus musculu
40	128	76.6	121	1	HV3J_HUMAN	P01771 homo sapien
41	128	76.6	255	2	Q6KB05_MOUSE	Q6kb05 mus musculu
42	128	76.6	465	2	Q6P6C4_HUMAN	Q6p6c4 homo sapien
43	128	76.6	473	2	Q6MZV7_HUMAN	Q6mzv7 homo sapien
44	128	76.6	479	2	Q6MZV6_HUMAN	Q6mzv6 homo sapien
45	128	76.6	573	2	Q8WU38_HUMAN	Q8wu38 homo sapien

ALIGNMENTS

RESULT 1
HV3K_HUMAN
ID HV3K_HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC ---
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ---
DR PIR; A02055; G1HUKL.
DR PDB; 2FB4; X-ray; H=2-126.
DR PDB; 2IG2; X-ray; H=2-126.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT DISULFID 22 96
FT DISULFID 105 110
FT NON_TER 126 126
FT STRAND 3 7

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FT   STRAND       11     12
FT   TURN         14     15
FT   STRAND       18     25
FT   HELIX        29     31
FT   STRAND       34     39
FT   TURN         41     42
FT   STRAND       45     51
FT   TURN         53     54
FT   STRAND       58     60
FT   HELIX        62     64
FT   STRAND       65     65
FT   TURN         66     67
FT   STRAND       68     73
FT   TURN         74     77
FT   STRAND       78     83
FT   HELIX        88     90
FT   STRAND       92     99
FT   STRAND      106    106
FT   TURN        107    108
FT   STRAND      109    109
FT   STRAND      113    116
FT   STRAND      120    124
SQ   SEQUENCE   126 AA;  13718 MW;  E4D71B52B16F8776 CRC64;

  Query Match             97.6%;  Score 163;  DB 1;  Length 126;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-15;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 97


RESULT 2
Q6N093_HUMAN
ID   Q6N093_HUMAN PRELIMINARY;      PRT;   417 AA.
AC   Q6N093;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686I04196 (Fragment).
GN   Name=DKFZp686I04196;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Human esophagus tumor;
RG   The German Human cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640623; CAE45777.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   417 AA;  46061 MW;  C4518E844CFB883C CRC64;

  Query Match             83.2%;  Score 139;  DB 2;  Length 417;
  Best Local Similarity   80.6%;  Pred. No. 2.8e-11;
  Matches   25;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              |||:||||| |||||:|:||||||| ||:||
Db         39 RFTVSRDNSANTLFLEMNSLRPEDTAVYYCA 69


RESULT 3
Q9UGP3_HUMAN
ID   Q9UGP3_HUMAN PRELIMINARY;      PRT;   112 AA.
AC   Q9UGP3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Immunoblobulin heavy chain (Fragment).
GN   Name=IgH;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Zafiropoulos A., Kandilogiannaki M., Dahlenborg C., Borrebaeck C.A.K.,
RA   Krambovitis E.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ132560; CAB65078.1; -; mRNA.
DR   HSSP; P01783; 1IGC.
DR   SMR; Q9UGP3; 1-105.
DR   Ensembl; ENSG00000188443; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  12226 MW;  0A1F17082C7A8CE3 CRC64;

  Query Match             82.6%;  Score 138;  DB 2;  Length 112;
  Best Local Similarity   83.9%;  Pred. No. 8.6e-12;
  Matches   26;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||:|||:||| ||| ||:||
Db         50 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 80


RESULT 4
Q9UL90_HUMAN
ID   Q9UL90_HUMAN PRELIMINARY;      PRT;   113 AA.
AC   Q9UL90;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1730252;
RA   Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
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RA   Schuurman R.K.;
RT   "Restricted utilization of germ-line VH3 genes and short diverse third
RT   complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT   immunoglobulin heavy chain rearrangements.";
RL   Eur. J. Immunol. 22:247-251(1992).
DR   EMBL; AF035024; AAD56260.1; -; mRNA.
DR   PIR; S78486; S78486.
DR   HSSP; P01772; 2FB4.
DR   SMR; Q9UL90; 1-113.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     113    113
SQ   SEQUENCE   113 AA;  12437 MW;  ED57FDD19086D07F CRC64;

  Query Match             82.6%;  Score 138;  DB 2;  Length 113;
  Best Local Similarity   83.9%;  Pred. No. 8.7e-12;
  Matches   26;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||:|||:||| ||| ||:||
Db         67 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 97


RESULT 5
HV05_CARAU
ID   HV05_CARAU     STANDARD;      PRT;   116 AA.
AC   P19181;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region 5A precursor.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Carassius.
OX   NCBI_TaxID=7957;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88144476; PubMed=3125551;
RA   Wilson M.R., Middleton D., Warr G.W.;
RT   "Immunoglobulin heavy chain variable region gene evolution: structure
RT   and family relationships of two genes and a pseudogene in a teleost
RT   fish.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   HSSP; P01783; 1IGC.
DR   SMR; P19181; 20-116.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    116       Ig heavy chain V region 5A.
FT   REGION       20     49       Framework-1.
FT   REGION       50     54       Complementarity-determining-1.
FT   REGION       55     68       Framework-2.
FT   REGION       69     84       Complementarity-determining-2.
FT   REGION       85    116       Framework-3.
FT   DISULFID     41    114       By similarity.
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12808 MW;  9C2279E2DF199B12 CRC64;

  Query Match             82.6%;  Score 138;  DB 1;  Length 116;
  Best Local Similarity   83.9%;  Pred. No. 8.9e-12;
  Matches   26;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||:|||:||| ||| ||:||
Db         85 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 115


RESULT 6
HV3C_HUMAN
ID   HV3C_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01764;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Ig heavy chain V-III region VH26 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=81101090; PubMed=6450418;
RA   Matthyssens G., Rabbitts T.H.;
RT   "Structure and multiplicity of genes for the human immunoglobulin
RT   heavy chain variable region.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 20-117.
RX   MEDLINE=93209281; PubMed=7681398;
RA   Mariette X., Tsapis A., Brouet J.C.;
RT   "Nucleotidic sequence analysis of the variable domains of four human
RT   monoclonal IgM with an antibody activity to myelin-associated
RT   glycoprotein.";
RL   Eur. J. Immunol. 23:846-851(1993).
RN   [3]
RP   3D-STRUCTURE MODELING OF 20-117.
RX   MEDLINE=86094276; PubMed=3866244;
RA   Toyonaga B., Yoshikai Y., Vadasz V., Chin B., Mak T.W.;
RT   "Organization and sequences of the diversity, joining, and constant
RT   region genes of the human T-cell receptor beta chain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:8624-8628(1985).
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; J00236; AAA53516.1; -; Unassigned_DNA.
DR   EMBL; M35415; AAA58735.1; -; Genomic_DNA.
DR   PIR; A02047; H3HU26.
DR   PDB; 1HOU; Model; H=20-117.
DR   HGNC; HGNC:5545; IGHV@.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       Ig heavy chain V-III region VH26.
FT   DOMAIN       20   >117       Ig-like.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12582 MW;  E826733F1A3CB0F1 CRC64;

  Query Match             82.6%;  Score 138;  DB 1;  Length 117;
  Best Local Similarity   83.9%;  Pred. No. 9e-12;
  Matches   26;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||||||||:|||:||| ||| ||:||
Db         86 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 116


RESULT 7
Q65ZC9_HUMAN
ID   Q65ZC9_HUMAN PRELIMINARY;      PRT;   240 AA.
AC   Q65ZC9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Single-chain Fv (Fragment).
GN   Name=scFv;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C1q/7;
RX   MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA   Kontermann R.E., Wing M.G., Winter G.;
RT   "Complement recruitment using bispecific diabodies.";
RL   Nat. Biotechnol. 15:629-631(1997).
DR   EMBL; Y13056; CAA73499.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1      1
FT   NON_TER     240    240
SQ   SEQUENCE   240 AA;  25569 MW;  FDCFD3645F64B373 CRC64;

  Query Match             82.6%;  Score 138;  DB 2;  Length 240;
  Best Local Similarity   83.9%;  Pred. No. 2e-11;
  Matches   26;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||||||||:|||:||| ||| ||:||
Db         67 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 97


RESULT 8
Q6IN78_HUMAN
ID   Q6IN78_HUMAN PRELIMINARY;      PRT;   466 AA.
AC   Q6IN78;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGHG1 protein.
GN   Name=IGHG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral Nervous System;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral Nervous System;
RG   NIH MGC Project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC072419; AAH72419.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   466 AA;  50854 MW;  53EB0BCEDE81076E CRC64;

  Query Match             82.6%;  Score 138;  DB 2;  Length 466;
  Best Local Similarity   83.9%;  Pred. No. 4.4e-11;
  Matches   26;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||||||||:|||:||| ||| ||:||
Db         85 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 115


RESULT 9
Q8WUK1_HUMAN
ID   Q8WUK1_HUMAN PRELIMINARY;      PRT;   613 AA.
AC   Q8WUK1;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
GN   Name=IGHM;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RG   NIH MGC Project;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2117273;
RA   Schroeder H.W. Jr, Wang J.Y.;
RT   "Preferential utilization of conserved immunoglobulin heavy chain
RT   variable gene segments during human fetal life.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1383695; DOI=10.1016/0161-5890(92)90173-U;
RA   Cuisinier A.M., Pumoux F., Fougereau M., Tonnelle C.;
RT   "IGM kappa/lambda EBV human B cell clone: an early step of
RT   differentiation of fetal B cells or a distinct B lineage?";
RL   Mol. Immunol. 29:1363-1373(1992).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1730252;
RA   Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA   Schuurman R.K.;
RT   "Restricted utilization of germ-line VH3 genes and short diverse third
RT   complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT   immunoglobulin heavy chain rearrangements.";
RL   Eur. J. Immunol. 22:247-251(1992).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1904154;
RA   Neale G.A., Kitchingman G.R.;
RT   "mRNA transcripts initiating within the human immunoglobulin mu heavy
RT   chain enhancer region contain a non-translatable exon and are
RT   extremely heterogeneous at the 5' end.";
RL   Nucleic Acids Res. 19:2427-2433(1991).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2840480; DOI=10.1084/jem.168.1.229;
RA   Bird J., Galili N., Link M., Stites D., Sklar J.;
RT   "Continuing rearrangement but absence of somatic hypermutation in
RT   immunoglobulin genes of human B cell precursor leukemia.";
RL   J. Exp. Med. 168:229-245(1988).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2538551; DOI=10.1084/jem.169.4.1391;
RA   Nickerson K.G., Berman J., Glickman E., Chess L., Alt F.W.;
RT   "Early human IgH gene assembly in Epstein-Barr virus-transformed fetal
RT   B cell lines. Preferential utilization of the most JH-proximal D
RT   segment (DQ52) and two unusual VH-related rearrangements.";
RL   J. Exp. Med. 169:1391-1403(1989).
RN   [9]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA   Hillson J.L., Karr N.S., Oppliger I.R., Mannik M., Sasso E.H.;
RT   "The structural basis of germline-encoded VH3 immunoglobulin binding
RT   to staphylococcal protein A.";
RL   J. Exp. Med. 178:331-336(1993).
DR   EMBL; BC020240; AAH20240.1; -; mRNA.
DR   PIR; F36005; F36005.
DR   PIR; G36005; G36005.
DR   PIR; PH1642; PH1642.
DR   PIR; PH1643; PH1643.
DR   PIR; PH1645; PH1645.
DR   PIR; PH1646; PH1646.
DR   PIR; PL0098; PL0098.
DR   PIR; PL0120; PL0120.
DR   PIR; S15590; S15590.
DR   PIR; S31116; S31116.
DR   PIR; S31119; S31119.
DR   PIR; S70442; S70442.
DR   HSSP; P01861; 1ADQ.
DR   SMR; Q8WUK1; 20-242.
DR   Ensembl; ENSG00000130076; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 5.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW   Immunoglobulin domain.
SQ   SEQUENCE   613 AA;  67296 MW;  60C7F5950671E315 CRC64;

  Query Match             82.6%;  Score 138;  DB 2;  Length 613;
  Best Local Similarity   83.9%;  Pred. No. 6e-11;
  Matches   26;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||:|||:||| ||| ||:||
Db         86 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 116


RESULT 10
Q9UL93_HUMAN
ID   Q9UL93_HUMAN PRELIMINARY;      PRT;   116 AA.
AC   Q9UL93;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA   Hillson J.L., Karr N.S., Oppliger I.R., Mannik M., Sasso E.H.;
RT   "The structural basis of germline-encoded VH3 immunoglobulin binding
RT   to staphylococcal protein A.";
RL   J. Exp. Med. 178:331-336(1993).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2840480;
RA   Bird J., Galili N., Link M., Stites D., Sklar J.;
RT   "Continuing rearrangement but absence of somatic hypermutation in
RT   immunoglobulin genes of human B cell precursor leukemia.";
RL   J. Exp. Med. 168:229-245(1988).
DR   EMBL; AF035021; AAD56257.1; -; mRNA.
DR   PIR; PH1644; PH1644.
DR   PIR; PL0120; PL0120.
DR   HSSP; P01772; 2FB4.
DR   SMR; Q9UL93; 1-116.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
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FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12434 MW;  0DA0348154DD6061 CRC64;

  Query Match             80.8%;  Score 135;  DB 2;  Length 116;
  Best Local Similarity   80.6%;  Pred. No. 2.4e-11;
  Matches   25;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||||||||:|||:||| ||| :|:||
Db         66 RFTISRDNSKNTLYLQMNSLRAEDTAMYYCA 96


RESULT 11
Q9Y509_HUMAN
ID   Q9Y509_HUMAN PRELIMINARY;      PRT;   147 AA.
AC   Q9Y509;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH3 protein (Fragment).
GN   Name=VH3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=96071149; PubMed=7475288;
RA   Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA   Lichtenstein A.K., Berenson J.R.;
RT   "A CD10-positive subset of malignant cells is identified in multiple
RT   myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL   Leukemia 9:1948-1953(1995).
DR   EMBL; S80860; AAD14339.1; -; mRNA.
DR   HSSP; P01842; 1AQK.
DR   Ensembl; ENSG00000130076; Homo sapiens.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0016066; P:cellular defense response (sensu Vertebrata); NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER     147    147
SQ   SEQUENCE   147 AA;  15768 MW;  8489FCAAA7BC925C CRC64;

  Query Match             80.8%;  Score 135;  DB 2;  Length 147;
  Best Local Similarity   83.9%;  Pred. No. 3.2e-11;
  Matches   26;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||||||||:||| ||| ||| ||:||
Db         67 RFTISRDNSKNTLYLQMTSLRVEDTAVYYCA 97


RESULT 12
Q65ZL8_MOUSE
ID   Q65ZL8_MOUSE PRELIMINARY;      PRT;   196 AA.
AC   Q65ZL8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   VH7183-DSP2-JH3-CH1 protein (Fragment).
GN   Name=VH7183-DSP2-JH3-CH1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BALB/c;
RX   MEDLINE=95362300; PubMed=7635518;
RA   Komori T., Sugiyama H.;
RT   "An aberrant splicing using a 3' cryptic splice site within the CH1
RT   exon induces truncated mu-chain production.";
RL   Immunology 85:166-170(1995).
DR   EMBL; S79401; AAB35023.2; -; mRNA.
DR   SMR; Q65ZL8; 20-195.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER     196    196
SQ   SEQUENCE   196 AA;  21429 MW;  12A381018944B268 CRC64;

  Query Match             80.8%;  Score 135;  DB 2;  Length 196;
  Best Local Similarity   78.1%;  Pred. No. 4.4e-11;
  Matches   25;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:||||:||| ||| ||| :|:|||
Db         86 RFTISRDNAKNTLYLQMSSLRSEDTAMYYCAS 117


RESULT 13
Q6N096_HUMAN
ID   Q6N096_HUMAN PRELIMINARY;      PRT;   466 AA.
AC   Q6N096;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686I15196.
GN   Name=DKFZp686I15196;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Esophagus tumor;
RG   The German cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640620; CAE45774.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   SMR; Q6N096; 20-466.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   466 AA;  50926 MW;  01E91B748D6D57C4 CRC64;

  Query Match             80.2%;  Score 134;  DB 2;  Length 466;
  Best Local Similarity   80.6%;  Pred. No. 1.6e-10;
  Matches   25;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||:|||||||: ||| ||| ||:||
Db         86 RFTISRDNAKNTLFLQLSSLRAEDTAVYYCA 116


RESULT 14
Q9UL72_HUMAN
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ID   Q9UL72_HUMAN PRELIMINARY;      PRT;   118 AA.
AC   Q9UL72;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   PROTEIN SEQUENCE.
RX   PubMed=1555592;
RA   Makiya R., Stigbrand T.;
RT   "Placental alkaline phosphatase has a binding site for the human
RT   immunoglobulin-G Fc portion.";
RL   Eur. J. Biochem. 205:341-345(1992).
DR   EMBL; AF035042; AAD56278.1; -; mRNA.
DR   PIR; S21205; S21205.
DR   HSSP; P01783; 1IGC.
DR   SMR; Q9UL72; 1-118.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER      1      1
FT   NON_TER    118    118
SQ   SEQUENCE   118 AA;  12872 MW;  B4D1A5944B2D5CCA CRC64;

  Query Match             79.6%;  Score 133;  DB 2;  Length 118;
  Best Local Similarity   80.6%;  Pred. No. 4.8e-11;
  Matches   25;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||||||:|||:||| |||  |:||
Db         66 RFTISRDNSKNTLYLQMNSLRAEDTAFYYCA 96


RESULT 15
Q5I0J0_RAT
ID   Q5I0J0_RAT  PRELIMINARY;      PRT;   465 AA.
AC   Q5I0J0;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical LOC299354.
GN   Name=LOC299354;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC       histocompatibility complex class I molecules (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; BC088271; AAH88271.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
KW   Hypothetical protein; Immunoglobulin domain; Repeat.
SQ   SEQUENCE   465 AA;  51699 MW;  97C4533A213A424F CRC64;

  Query Match             79.6%;  Score 133;  DB 2;  Length 465;
  Best Local Similarity   75.0%;  Pred. No. 2.3e-10;
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Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:||||:||||||| |||  |:| :
Db         86 RFTISRDNAKNTLYLQMDSLRSEDTATYYCTT 117


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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:14:16 ; Search time 29.1518 Seconds
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Title: US-10-755-382-36
Perfect score: 167
Sequence: 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	167	100.0	32	1	US-08-318-157B-36	Sequence 36, Appl
2	167	100.0	32	2	US-09-253-794-36	Sequence 36, Appl
3	167	100.0	119	1	US-08-318-157B-12	Sequence 12, Appl
4	167	100.0	119	1	US-08-318-157B-13	Sequence 13, Appl
5	167	100.0	119	1	US-08-318-157B-17	Sequence 17, Appl
6	167	100.0	119	2	US-09-253-794-12	Sequence 12, Appl
7	167	100.0	119	2	US-09-253-794-13	Sequence 13, Appl
8	167	100.0	119	2	US-09-253-794-17	Sequence 17, Appl
9	164	98.2	32	1	US-08-318-157B-37	Sequence 37, Appl
10	164	98.2	32	2	US-09-253-794-37	Sequence 37, Appl
11	164	98.2	119	1	US-08-318-157B-14	Sequence 14, Appl
12	164	98.2	119	2	US-09-253-794-14	Sequence 14, Appl
13	164	98.2	489	4	PCT-US95-11405-35	Sequence 35, Appl
14	163	97.6	117	1	US-08-652-558-3	Sequence 3, Appli
15	163	97.6	117	1	US-08-652-558-44	Sequence 44, Appl
16	163	97.6	119	1	US-08-303-569B-11	Sequence 11, Appl
17	163	97.6	119	1	US-08-303-569B-17	Sequence 17, Appl
18	163	97.6	119	1	US-08-859-649-20	Sequence 20, Appl
19	163	97.6	119	1	US-08-859-649-21	Sequence 21, Appl
20	163	97.6	119	1	US-08-859-649-31	Sequence 31, Appl
21	163	97.6	119	1	US-08-070-116A-12	Sequence 12, Appl
22	163	97.6	119	1	US-08-116-247-12	Sequence 12, Appl
23	163	97.6	119	1	US-08-116-247-18	Sequence 18, Appl
24	163	97.6	119	1	US-08-116-247-19	Sequence 19, Appl
25	163	97.6	119	2	US-08-207-861-20	Sequence 20, Appl
26	163	97.6	119	2	US-08-207-861-21	Sequence 21, Appl
27	163	97.6	119	2	US-08-207-861-31	Sequence 31, Appl
28	163	97.6	119	2	US-08-557-050-12	Sequence 12, Appl
29	163	97.6	119	2	US-08-859-648-20	Sequence 20, Appl
30	163	97.6	119	2	US-08-859-648-21	Sequence 21, Appl
31	163	97.6	119	2	US-08-859-648-31	Sequence 31, Appl
32	163	97.6	119	2	US-09-795-515-11	Sequence 11, Appl
33	163	97.6	119	2	US-09-795-515-17	Sequence 17, Appl
34	163	97.6	119	2	US-09-348-224-12	Sequence 12, Appl
35	163	97.6	119	2	US-09-348-224-18	Sequence 18, Appl
36	163	97.6	119	2	US-09-348-224-19	Sequence 19, Appl
37	163	97.6	119	4	PCT-US94-07659-6	Sequence 6, Appli
38	163	97.6	120	2	US-08-435-516-2	Sequence 2, Appli
39	163	97.6	122	2	US-09-155-106-17	Sequence 17, Appl
40	163	97.6	126	1	US-08-303-569B-10	Sequence 10, Appl
41	163	97.6	126	1	US-08-318-157B-7	Sequence 7, Appli
42	163	97.6	126	1	US-08-070-116A-11	Sequence 11, Appl
43	163	97.6	126	1	US-08-116-247-11	Sequence 11, Appl
44	163	97.6	126	2	US-08-557-050-11	Sequence 11, Appl
45	163	97.6	126	2	US-09-795-515-10	Sequence 10, Appl

ALIGNMENTS

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RESULT 1
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; Sequence 36, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-36

  Query Match           100.0%;  Score 167;  DB 1;  Length 32;
  Best Local Similarity  100.0%;  Pred. No. 4.2e-17;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
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```
RESULT 2
US-09-253-794-36
; Sequence 36, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 36:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 32 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-253-794-36

  Query Match             100.0%;  Score 167;  DB 2;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-17;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32


RESULT 3
US-08-318-157B-12
; Sequence 12, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-12

  Query Match             100.0%;  Score 167;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-16;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 4
US-08-318-157B-13
; Sequence 13, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-13

  Query Match             100.0%;  Score 167;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-16;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 5
US-08-318-157B-17
; Sequence 17, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-17

  Query Match             100.0%;  Score 167;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-16;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 6
US-09-253-794-12
; Sequence 12, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-253-794-12

  Query Match             100.0%;  Score 167;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-16;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 7
US-09-253-794-13
; Sequence 13, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
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;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-253-794-13

  Query Match             100.0%;  Score 167;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-16;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 8
US-09-253-794-17
; Sequence 17, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-253-794-17

  Query Match             100.0%;  Score 167;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-16;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 9
US-08-318-157B-37
; Sequence 37, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-37

  Query Match             98.2%;  Score 164;  DB 1;  Length 32;
  Best Local Similarity   96.9%;  Pred. No. 1.1e-16;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32


RESULT 10
US-09-253-794-37
; Sequence 37, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
```

```
;                 ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 37:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 32 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-253-794-37

  Query Match            98.2%;  Score 164;  DB 2;  Length 32;
  Best Local Similarity  96.9%;  Pred. No. 1.1e-16;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32


RESULT 11
US-08-318-157B-14
; Sequence 14, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  14:
;   SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-14

  Query Match            98.2%;  Score 164;  DB 1;  Length 119;
  Best Local Similarity  96.9%;  Pred. No. 5.2e-16;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 12
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
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;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

  Query Match             98.2%;  Score 164;  DB 2;  Length 119;
  Best Local Similarity   96.9%;  Pred. No. 5.2e-16;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:||||||||||||||||||||||
Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 13
PCT-US95-11405-35
; Sequence 35, Application PC/TUS9511405
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  PHOSPHOROUS-32 LABELING OF ANTIBODIES
;    TITLE OF INVENTION:  FOR CANCER THERAPY
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/11405
;      FILING DATE:  18-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/308,103
;      FILING DATE:  16-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/599/IMIN
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  489 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-11405-35

  Query Match             98.2%;  Score 164;  DB 4;  Length 489;
  Best Local Similarity   96.9%;  Pred. No. 2.7e-15;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:||||||||||||||||||||||
Db         89 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 120


RESULT 14
US-08-652-558-3
; Sequence 3, Application US/08652558
; Patent No. 5861155
;  GENERAL INFORMATION:
;    APPLICANT:  LIN, AUGUSTINE YEE-THARN
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER & WITCOFF
;      STREET:  75 STATE STREET, 23RD FLOOR
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette, 1.4 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,558
;      FILING DATE:  JUNE 6, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB94/00387
;      FILING DATE:  NOVEMBER 21, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YANKWICH, LEON R.
;      REGISTRATION NUMBER:  30,237
;      REFERENCE/DOCKET NUMBER:  95,497-L
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-345-9100
;      TELEFAX:  617-345-9111
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-558-3

  Query Match             97.6%;  Score 163;  DB 1;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-16;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
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Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 97


RESULT 15
US-08-652-558-44
; Sequence 44, Application US/08652558
; Patent No. 5861155
;  GENERAL INFORMATION:
;    APPLICANT:  LIN, AUGUSTINE YEE-THARN
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER & WITCOFF
;      STREET:  75 STATE STREET, 23RD FLOOR
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette, 1.4 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,558
;      FILING DATE:  JUNE 6, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB94/00387
;      FILING DATE:  NOVEMBER 21, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YANKWICH, LEON R.
;      REGISTRATION NUMBER:  30,237
;      REFERENCE/DOCKET NUMBER:  95,497-L
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-345-9100
; TELEFAX: 617-345-9111
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-652-558-44

Query Match 97.6%; Score 163; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.1e-16;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 97
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Search completed: March 25, 2006, 09:18:46
Job time : 29.1518 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:55:36 ; Search time 95.4974 Seconds
(without alignments)
140.009 Million cell updates/sec

Title: US-10-755-382-36
Perfect score: 167
Sequence: 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	167	100.0	32	3	US-09-253-794-36	Sequence 36, Appl
2	167	100.0	32	5	US-10-755-382-36	Sequence 36, Appl
3	167	100.0	119	3	US-09-253-794-12	Sequence 12, Appl
4	167	100.0	119	3	US-09-253-794-13	Sequence 13, Appl
5	167	100.0	119	3	US-09-253-794-17	Sequence 17, Appl
6	167	100.0	119	4	US-10-680-734-12	Sequence 12, Appl
7	167	100.0	119	4	US-10-680-734-13	Sequence 13, Appl
8	167	100.0	119	5	US-10-755-382-12	Sequence 12, Appl
9	167	100.0	119	5	US-10-755-382-13	Sequence 13, Appl
10	167	100.0	119	5	US-10-755-382-17	Sequence 17, Appl
11	164	98.2	32	3	US-09-253-794-37	Sequence 37, Appl
12	164	98.2	32	5	US-10-755-382-37	Sequence 37, Appl
13	164	98.2	118	4	US-10-270-073-3	Sequence 3, Appli
14	164	98.2	119	3	US-09-253-794-14	Sequence 14, Appl
15	164	98.2	119	4	US-10-680-734-14	Sequence 14, Appl
16	164	98.2	119	4	US-10-680-734-17	Sequence 17, Appl
17	164	98.2	119	5	US-10-755-382-14	Sequence 14, Appl
18	164	98.2	138	4	US-10-006-771A-4	Sequence 4, Appli
19	164	98.2	256	4	US-10-270-073-6	Sequence 6, Appli
20	164	98.2	257	4	US-10-270-073-8	Sequence 8, Appli
21	164	98.2	261	4	US-10-270-071-18	Sequence 18, Appl
22	164	98.2	261	4	US-10-270-073-2	Sequence 2, Appli
23	164	98.2	261	4	US-10-328-190-6	Sequence 6, Appli
24	164	98.2	267	4	US-10-270-071-22	Sequence 22, Appl
25	164	98.2	267	4	US-10-270-071-26	Sequence 26, Appl
26	164	98.2	267	4	US-10-270-071-30	Sequence 30, Appl
27	164	98.2	267	4	US-10-270-071-36	Sequence 36, Appl
28	164	98.2	358	5	US-10-829-388-12	Sequence 12, Appl
29	164	98.2	363	5	US-10-829-388-2	Sequence 2, Appli
30	164	98.2	364	5	US-10-829-388-11	Sequence 11, Appl
31	164	98.2	370	5	US-10-829-388-1	Sequence 1, Appli
32	164	98.2	415	4	US-10-328-190-12	Sequence 12, Appl
33	164	98.2	443	4	US-10-006-773-2	Sequence 2, Appli
34	164	98.2	443	4	US-10-006-771A-2	Sequence 2, Appli
35	164	98.2	468	4	US-10-377-109-2	Sequence 2, Appli
36	164	98.2	669	5	US-10-900-928-3	Sequence 3, Appli
37	163	97.6	119	3	US-09-795-515-11	Sequence 11, Appl
38	163	97.6	119	3	US-09-795-515-17	Sequence 17, Appl
39	163	97.6	119	4	US-10-267-286A-12	Sequence 12, Appl
40	163	97.6	119	4	US-10-704-352-11	Sequence 11, Appl
41	163	97.6	119	4	US-10-704-352-17	Sequence 17, Appl
42	163	97.6	119	4	US-10-704-071-11	Sequence 11, Appl
43	163	97.6	119	4	US-10-704-071-17	Sequence 17, Appl
44	163	97.6	119	4	US-10-680-734-27	Sequence 27, Appl
45	163	97.6	119	4	US-10-703-963-11	Sequence 11, Appl

ALIGNMENTS

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RESULT 1
US-09-253-794-36
; Sequence 36, Application US/09253794
; Patent No. US20020018750A1
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 36:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 32 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-253-794-36

  Query Match           100.0%;  Score 167;  DB 3;  Length 32;
  Best Local Similarity  100.0%;  Pred. No. 6.2e-15;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
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Db          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32


RESULT 2
US-10-755-382-36
; Sequence 36, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 36:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 32 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-755-382-36

  Query Match             100.0%;  Score 167;  DB 5;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 6.2e-15;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32


RESULT 3
US-09-253-794-12
; Sequence 12, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-253-794-12

  Query Match             100.0%;  Score 167;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 4
US-09-253-794-13
; Sequence 13, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
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;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-253-794-13

  Query Match             100.0%;  Score 167;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
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Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 5
US-09-253-794-17
; Sequence 17, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-253-794-17

  Query Match             100.0%;  Score 167;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 6
US-10-680-734-12
; Sequence 12, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-12

  Query Match             100.0%;  Score 167;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 7
US-10-680-734-13
; Sequence 13, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-13

  Query Match             100.0%;  Score 167;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
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  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 8
US-10-755-382-12
; Sequence 12, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-755-382-12

  Query Match             100.0%;  Score 167;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 9
US-10-755-382-13
; Sequence 13, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-755-382-13

  Query Match             100.0%;  Score 167;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 10
US-10-755-382-17
; Sequence 17, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
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;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-755-382-17

  Query Match             100.0%;  Score 167;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 11
US-09-253-794-37
; Sequence 37, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 37:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 32 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-253-794-37

  Query Match             98.2%;  Score 164;  DB 3;  Length 32;
  Best Local Similarity   96.9%;  Pred. No. 1.5e-14;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32


RESULT 12
US-10-755-382-37
; Sequence 37, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 37:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 32 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-755-382-37

  Query Match             98.2%;  Score 164;  DB 5;  Length 32;
  Best Local Similarity   96.9%;  Pred. No. 1.5e-14;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
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Db          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
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RESULT 13
US-10-270-073-3
; Sequence 3, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14VH deduced amino acid sequence
US-10-270-073-3

  Query Match             98.2%;  Score 164;  DB 4;  Length 118;
  Best Local Similarity   96.9%;  Pred. No. 6.3e-14;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 14
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

  Query Match             98.2%;  Score 164;  DB 3;  Length 119;
  Best Local Similarity   96.9%;  Pred. No. 6.3e-14;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 15
US-10-680-734-14
; Sequence 14, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-14

  Query Match             98.2%;  Score 164;  DB 4;  Length 119;
  Best Local Similarity   96.9%;  Pred. No. 6.3e-14;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98


Search completed: March 25, 2006, 10:08:05
Job time : 95.4974 secs
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:58:56 ; Search time 11.5602 Seconds
(without alignments)
81.644 Million cell updates/sec

Title: US-10-755-382-36
Perfect score: 167
Sequence: 1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	163	97.6	119	7	US-11-221-900-12	Sequence 12, Appl
2	163	97.6	126	7	US-11-221-900-11	Sequence 11, Appl
3	163	97.6	449	7	US-11-080-587-6	Sequence 6, Appli
4	158	94.6	236	7	US-11-221-900-2	Sequence 2, Appli
5	149	89.2	116	6	US-10-496-845A-4	Sequence 4, Appli
6	147	88.0	254	7	US-11-054-515-977	Sequence 977, App
7	144	86.2	142	6	US-10-993-543-132	Sequence 132, App
8	144	86.2	240	7	US-11-054-515-1886	Sequence 1886, Ap
9	144	86.2	240	7	US-11-054-515-2052	Sequence 2052, Ap
10	144	86.2	240	7	US-11-054-515-2059	Sequence 2059, Ap
11	144	86.2	240	7	US-11-054-515-2061	Sequence 2061, Ap
12	143	85.6	124	7	US-11-040-159-16	Sequence 16, Appl
13	143	85.6	126	7	US-11-064-174-25	Sequence 25, Appl
14	143	85.6	126	7	US-11-064-174-26	Sequence 26, Appl
15	143	85.6	153	7	US-11-267-310-5	Sequence 5, Appli
16	143	85.6	243	7	US-11-054-515-2057	Sequence 2057, Ap
17	142	85.0	120	6	US-10-925-366A-5	Sequence 5, Appli
18	142	85.0	120	6	US-10-925-366A-280	Sequence 280, App
19	142	85.0	121	7	US-11-049-536-522	Sequence 522, App
20	142	85.0	121	7	US-11-199-739-522	Sequence 522, App
21	142	85.0	122	7	US-11-102-621-1	Sequence 1, Appli
22	142	85.0	122	7	US-11-049-536-186	Sequence 186, App
23	142	85.0	122	7	US-11-199-739-186	Sequence 186, App
24	142	85.0	124	7	US-11-064-174-5	Sequence 5, Appli
25	142	85.0	124	7	US-11-064-174-6	Sequence 6, Appli
26	142	85.0	238	7	US-11-054-515-1931	Sequence 1931, Ap
27	142	85.0	240	7	US-11-054-515-1918	Sequence 1918, Ap
28	142	85.0	240	7	US-11-054-515-2047	Sequence 2047, Ap
29	142	85.0	243	7	US-11-054-515-995	Sequence 995, App
30	141	84.4	118	6	US-10-886-383-1	Sequence 1, Appli
31	141	84.4	121	6	US-10-771-257-20	Sequence 20, Appl
32	141	84.4	121	7	US-11-127-677-20	Sequence 20, Appl
33	141	84.4	124	7	US-11-064-174-2	Sequence 2, Appli
34	141	84.4	124	7	US-11-064-174-3	Sequence 3, Appli
35	141	84.4	124	7	US-11-064-174-4	Sequence 4, Appli
36	141	84.4	124	7	US-11-064-174-7	Sequence 7, Appli
37	141	84.4	167	7	US-11-128-900-74	Sequence 74, Appl
38	141	84.4	240	7	US-11-054-515-1930	Sequence 1930, Ap
39	141	84.4	251	7	US-11-054-515-1332	Sequence 1332, Ap
40	141	84.4	367	7	US-11-000-463-899	Sequence 899, App
41	141	84.4	463	7	US-11-128-900-1	Sequence 1, Appli
42	141	84.4	463	7	US-11-128-900-63	Sequence 63, Appl
43	141	84.4	463	7	US-11-128-900-64	Sequence 64, Appl
44	139	83.2	112	7	US-11-224-623-10	Sequence 10, Appl
45	139	83.2	118	7	US-11-049-536-606	Sequence 606, App

ALIGNMENTS

RESULT 1
US-11-221-900-12
; Sequence 12, Application US/11221900
; Publication No. US20060002933A1
; GENERAL INFORMATION:
; APPLICANT: BLUESTONE, JEFFREY A.
; APPLICANT: ZIVIN, ROBERT A.
; APPLICANT: JOLLIFFE, LINDA K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: TOLT:004USC1
; CURRENT APPLICATION NUMBER: US/11/221,900
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: US/10/267,286
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 08/557,050
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: PCT/US94/06198
; PRIOR FILING DATE: 1994-06-01
; PRIOR APPLICATION NUMBER: 08/070,116
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-221-900-12

Query Match 97.6%; Score 163; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 5.6e-15;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 97
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RESULT 2
US-11-221-900-11
; Sequence 11, Application US/11221900
; Publication No. US20060002933A1
; GENERAL INFORMATION:
; APPLICANT: BLUESTONE, JEFFREY A.

```
;  APPLICANT:  ZIVIN, ROBERT A.
;  APPLICANT:  JOLLIFFE, LINDA K.
;  TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
;  TITLE OF INVENTION:  IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: TOLT:004USC1
;  CURRENT APPLICATION NUMBER: US/11/221,900
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: US/10/267,286
;  PRIOR FILING DATE: 2003-01-28
;  PRIOR APPLICATION NUMBER: 08/557,050
;  PRIOR FILING DATE: 1998-10-09
;  PRIOR APPLICATION NUMBER: PCT/US94/06198
;  PRIOR FILING DATE: 1994-06-01
;  PRIOR APPLICATION NUMBER: 08/070,116
;  PRIOR FILING DATE: 1993-06-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-11-221-900-11

  Query Match             97.6%;  Score 163;  DB 7;  Length 126;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-15;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 97


RESULT 3
US-11-080-587-6
; Sequence 6, Application US/11080587
; Publication No. US20060002942A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  TITLE OF INVENTION: Calicheamicin Conjugates
;  FILE REFERENCE: AM101462
;  CURRENT APPLICATION NUMBER: US/11/080,587
;  CURRENT FILING DATE:  2005-03-15
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Human/murine chimera
;   FEATURE:
;   OTHER INFORMATION: Human/Murine Chimera G193 Heavy Chain
US-11-080-587-6

  Query Match             97.6%;  Score 163;  DB 7;  Length 449;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-14;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 97


RESULT 4
US-11-221-900-2
; Sequence 2, Application US/11221900
; Publication No. US20060002933A1
; GENERAL INFORMATION:
;  APPLICANT: BLUESTONE, JEFFREY A.
;  APPLICANT:  ZIVIN, ROBERT A.
;  APPLICANT:  JOLLIFFE, LINDA K.
;  TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
;  TITLE OF INVENTION:  IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: TOLT:004USC1
;  CURRENT APPLICATION NUMBER: US/11/221,900
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: US/10/267,286
;  PRIOR FILING DATE: 2003-01-28
;  PRIOR APPLICATION NUMBER: 08/557,050
;  PRIOR FILING DATE: 1998-10-09
;  PRIOR APPLICATION NUMBER: PCT/US94/06198
;  PRIOR FILING DATE: 1994-06-01
;  PRIOR APPLICATION NUMBER: 08/070,116
;  PRIOR FILING DATE: 1993-06-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-11-221-900-2

  Query Match             94.6%;  Score 158;  DB 7;  Length 236;
  Best Local Similarity   96.8%;  Pred. No. 5.1e-14;
  Matches   30;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||| ||||||||||||||||||
Db         86 RFTISRDNSKNTAFLQMDSLRPEDTGVYFCA 116


RESULT 5
US-10-496-845A-4
; Sequence 4, Application US/10496845A
; Publication No. US20060051292A1
; GENERAL INFORMATION:
;  APPLICANT: Mackenzie, Roger C
;  APPLICANT:  Zhang, Jianbing
;  TITLE OF INVENTION: Self-Assembly Molecules
;  FILE REFERENCE: 36361-0038
;  CURRENT APPLICATION NUMBER: US/10/496,845A
;  CURRENT FILING DATE:  2004-05-27
;  PRIOR APPLICATION NUMBER: US 60/334,098
;  PRIOR FILING DATE: 2001-11-30
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: llama
;   FEATURE:
;   OTHER INFORMATION: none
US-10-496-845A-4

  Query Match             89.2%;  Score 149;  DB 6;  Length 116;
  Best Local Similarity   81.2%;  Pred. No. 4e-13;
  Matches   26;  Conservative    6;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||::||||||:|||||||:||:
Db         67 RFTISRDNAKNTVYLQMDSLKPEDTGVYYCAA 98


RESULT 6
US-11-054-515-977
; Sequence 977, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
```

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;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 977
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-977

  Query Match             88.0%;  Score 147;  DB 7;  Length 254;
  Best Local Similarity   84.4%;  Pred. No. 1.6e-12;
  Matches   27;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||:|||:||||||| ||:||:
Db         67 RFTISRDNSKNTLYLQMNSLRPEDTAVYYCAT 98


RESULT 7
US-10-993-543-132
; Sequence 132, Application US/10993543
; Publication No. US20060036076A1
; GENERAL INFORMATION:
;  APPLICANT: Dransfield, Daniel T.
;  APPLICANT:  Rookey, Kristin
;  APPLICANT:  Ladner, Robert C.
;  TITLE OF INVENTION: Metalloproteinase-Binding Proteins
;  FILE REFERENCE: 10280-088001
;  CURRENT APPLICATION NUMBER: US/10/993,543
;  CURRENT FILING DATE:  2004-11-19
;  PRIOR APPLICATION NUMBER: US 60/523,745
;  PRIOR FILING DATE: 2003-11-19
;  NUMBER OF SEQ ID NOS: 299
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 132
;   LENGTH: 142
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-993-543-132

  Query Match             86.2%;  Score 144;  DB 6;  Length 142;
  Best Local Similarity   87.1%;  Pred. No. 2.3e-12;
  Matches   27;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||:|||:||| ||||||:||
Db         67 RFTISRDNSKNTLYLQMNSLRAEDTGVYYCA 97


RESULT 8
US-11-054-515-1886
; Sequence 1886, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1886
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1886

  Query Match             86.2%;  Score 144;  DB 7;  Length 240;
  Best Local Similarity   81.2%;  Pred. No. 3.9e-12;
  Matches   26;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||::|||::|||||| ||:|||
Db         67 RFTISRDNSKNTVYLQMNNLRPEDTAVYYCAS 98


RESULT 9
US-11-054-515-2052
; Sequence 2052, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
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;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2052
;    LENGTH: 240
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-11-054-515-2052

  Query Match             86.2%;  Score 144;  DB 7;  Length 240;
  Best Local Similarity   81.2%;  Pred. No. 3.9e-12;
  Matches   26;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||::|||::|||||| ||:|||
Db         67 RFTISRDNSKNTVYLQMNNLRPEDTAVYYCAS 98


RESULT 10
US-11-054-515-2059
; Sequence 2059, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2059
;    LENGTH: 240
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-11-054-515-2059

  Query Match             86.2%;  Score 144;  DB 7;  Length 240;
  Best Local Similarity   81.2%;  Pred. No. 3.9e-12;
  Matches   26;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||::|||::|||||| ||:|||
Db         67 RFTISRDNSKNTVYLQMNNLRPEDTAVYYCAS 98


RESULT 11
US-11-054-515-2061
; Sequence 2061, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2061
;    LENGTH: 240
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-11-054-515-2061

  Query Match             86.2%;  Score 144;  DB 7;  Length 240;
  Best Local Similarity   81.2%;  Pred. No. 3.9e-12;
  Matches   26;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||::|||::|||||| ||:|||
Db         67 RFTISRDNSKNTVYLQMNNLRPEDTAVYYCAS 98


RESULT 12
US-11-040-159-16
; Sequence 16, Application US/11040159
; Publication No. US20050255552A1
; GENERAL INFORMATION:
;  APPLICANT: Flynn, Peter
;  APPLICANT:  Luehrsen, Kenneth
;  APPLICANT:  Balint, Robert F.
;  APPLICANT:  Her, Jeng-Horng
;  APPLICANT:  Bebbington, Christopher R.
;  APPLICANT:  Yarranton, Geoffrey T.
;  APPLICANT:  KaloBios, Inc.
;  TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
;  TITLE OF INVENTION:  Binding Determinants
;  FILE REFERENCE: 021167-001730US
;  CURRENT APPLICATION NUMBER: US/11/040,159
;  CURRENT FILING DATE:  2005-01-20
;  PRIOR APPLICATION NUMBER: US 60/537,364
;  PRIOR FILING DATE: 2004-01-20
;  PRIOR APPLICATION NUMBER: US 60/546,216
;  PRIOR FILING DATE: 2004-02-23
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;    LENGTH: 124
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:V-region of
;    OTHER INFORMATION: anti-PcrV antibody 1F1 VH
US-11-040-159-16

  Query Match             85.6%;  Score 143;  DB 7;  Length 124;
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Best Local Similarity 83.9%; Pred. No. 2.7e-12;
Matches 26; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||:|:|:||||||| ||:||
Db         67 RFTISRDNSKNTLYLEMNSLRPEDTAVYYCA 97
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RESULT 13
US-11-064-174-25
; Sequence 25, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D30
US-11-064-174-25

Query Match 85.6%; Score 143; DB 7; Length 126;
Best Local Similarity 87.1%; Pred. No. 2.8e-12;
Matches 27; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||:||||||| ||| ||:||
Db         67 RFTISRDNSKNTLYLQMDSLRAEDTAVYYCA 97
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RESULT 14
US-11-064-174-26
; Sequence 26, Application US/11064174
; Publication No. US20050282252A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/11/064,174
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: US/09/240,274
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/081,380
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D31
US-11-064-174-26

Query Match 85.6%; Score 143; DB 7; Length 126;
Best Local Similarity 87.1%; Pred. No. 2.8e-12;
Matches 27; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 31
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Db         67 RFTISRDNSKNTLYLQMDSLRAEDTAVYYCA 97
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RESULT 15
US-11-267-310-5
; Sequence 5, Application US/11267310
; Publication No. US20060037107A1
; GENERAL INFORMATION:
; APPLICANT: Leo G.J. FRENKEN
; APPLICANT: Cornelis P.E. van der LOGT
; APPLICANT: Vin-Miin TEH
; APPLICANT: Martine E. VERHOEYEN
; APPLICANT: Joy E. WILKINSON
; APPLICANT: Stephen A. JOBLING
; TITLE OF INVENTION: Production of Antibodies
; FILE REFERENCE: PNK/060113/0275850 - T7060C
; CURRENT APPLICATION NUMBER: US/11/267,310
; CURRENT FILING DATE: 2005-11-07
; PRIOR APPLICATION NUMBER: US/09/737,476
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: EP 99310188.0
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: MS Word
; SEQ ID NO 5
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VHH with linker
US-11-267-310-5

Query Match 85.6%; Score 143; DB 7; Length 153;
Best Local Similarity 78.1%; Pred. No. 3.4e-12;
Matches 25; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||::|||||||:|||| ||:||:
Db         66 RFTISRDNAKNTVYLQMDSLKPEDTAVYYCAA 97
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Search completed: March 25, 2006, 10:09:20
Job time : 11.5602 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:10 ; Search time 117.948 Seconds
(without alignments)
119.206 Million cell updates/sec

Title: US-10-755-382-37
Perfect score: 167
Sequence: 1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	167	100.0	32	2	AAR97330	Aar97330 Humanised
2	167	100.0	118	6	ABR42755	Abr42755 Anti-CEA
3	167	100.0	119	8	ADM95101	Adm95101 Humanised
4	167	100.0	119	8	ADM98324	Adm98324 Humanised
5	167	100.0	138	6	ABG76489	Abg76489 Heavy cha
6	167	100.0	254	2	AAR94557	Aar94557 Humanised
7	167	100.0	256	6	ABR42757	Abr42757 Anti-CEA
8	167	100.0	257	6	ABR42758	Abr42758 Anti-CEA
9	167	100.0	261	6	ABR42289	Abr42289 Diabody 6
10	167	100.0	261	6	ABR42754	Abr42754 Anti-CEA
11	167	100.0	261	6	ABR83645	Abr83645 hMN14-scF
12	167	100.0	267	6	ABR42292	Abr42292 Bispecifi
13	167	100.0	267	6	ABR42299	Abr42299 Bispecifi
14	167	100.0	267	6	ABR42296	Abr42296 Bispecifi
15	167	100.0	267	6	ABR42294	Abr42294 Bispecifi
16	167	100.0	358	8	ADU26571	Adu26571 Chimeric
17	167	100.0	363	8	ADU26561	Adu26561 Chimeric
18	167	100.0	364	8	ADU26570	Adu26570 Chimeric
19	167	100.0	370	8	ADU26560	Adu26560 Chimeric
20	167	100.0	415	6	ABR83648	Abr83648 TS1 VH ch
21	167	100.0	443	6	ABG76488	Abg76488 Humanised
22	167	100.0	443	6	ABG74240	Abg74240 Chimaeric
23	167	100.0	468	7	ADE64201	Ade64201 MN14HCF p
24	167	100.0	468	7	ADF60815	Adf60815 hMN-14 he
25	167	100.0	669	9	ADY97271	Ady97271 Exemplary
26	164	98.2	32	2	AAR97329	Aar97329 Humanised
27	163	97.6	119	2	AAR82964	Aar82964 3S193HuVH
28	160	95.8	117	2	AAR77305	Aar77305 Variable
29	160	95.8	119	2	AAR13092	Aar13092 Grafted h
30	160	95.8	119	2	AAR13098	Aar13098 Grafted h
31	160	95.8	119	2	AAR13099	Aar13099 Grafted h
32	160	95.8	119	2	AAR67447	Aar67447 OKT3 huma
33	160	95.8	119	2	AAR82962	Aar82962 Humanised
34	160	95.8	119	2	AAW11919	Aaw11919 Humanised
35	160	95.8	119	2	AAR97336	Aar97336 Humanised
36	160	95.8	119	2	AAW73529	Aaw73529 Humanised
37	160	95.8	120	2	AAR54930	Aar54930 Fc recept
38	160	95.8	126	2	AAR28746	Aar28746 Heavy cha
39	160	95.8	126	2	AAW73527	Aaw73527 Humanised
40	160	95.8	126	9	ADX37204	Adx37204 Human ant
41	160	95.8	137	2	AAR22760	Aar22760 Reshaped
42	160	95.8	137	2	AAR22762	Aar22762 Reshaped
43	160	95.8	137	2	AAR22763	Aar22763 CD4VHKOL-
44	160	95.8	137	2	AAR22761	Aar22761 CD4VHKOL-
45	160	95.8	300	2	AAW11503	Aaw11503 Humanised

ALIGNMENTS

RESULT 1
AAR97330
ID AAR97330 standard; peptide; 32 AA.
XX
AC AAR97330;
XX
DT 15-OCT-1996 (first entry)
XX
DE Humanised monoclonal antibody heavy chain framework region.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Homo sapiens.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Claim 7; Page 40; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. This sequence corresponds to the third framework region of the
CC heavy chain of the humanised MAb. See AAR97313-97333

```
XX
SQ   Sequence 32 AA;

  Query Match             100.0%;  Score 167;  DB 2;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-15;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32


RESULT 2
ABR42755
ID   ABR42755 standard; protein; 118 AA.
XX
AC   ABR42755;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14 VH region.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Disclosure; Fig 12; 62pp; English.
XX
CC   The present sequence is the protein sequence of the heavy chain variable
CC   region of anti-carcinoembryonic antigen (CEA) humanized monoclonal
CC   antibody hMN-14. scFv constructs comprising the hMN-14 VH and Vkappa
CC   regions are used in novel multivalent, monospecific binding proteins
CC   (diabody, triabody and tetrabody) of the invention (see also ABR42754,
CC   ABR42757 and ABR42758). Claimed binding proteins are specific for a
CC   tumour-associated antigen, and are used in the diagnosis and treatment of
CC   a tumour, carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma,
CC   lymphoma or myeloma, or a cancer selected from acute lymphoblastic
CC   leukaemia, acute myelogenous leukaemia, biliary, breast, cervical,
CC   chronic lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 118 AA;

  Query Match             100.0%;  Score 167;  DB 6;  Length 118;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-15;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 3
ADM95101
ID   ADM95101 standard; protein; 119 AA.
XX
AC   ADM95101;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 MAb heavy chain variable region coding sequence.
XX
KW   non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW   complementarity determining region; pancreatic cancer; breast cancer;
KW   ovarian cancer.
XX
OS   Mus sp.
OS   Homo sapiens.
XX
PN   WO2004032962-A1.
XX
PD   22-APR-2004.
XX
PF   11-OCT-2002; 2002WO-US032307.
XX
PR   08-OCT-2002; 2002US-0416531P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-364813/34.
DR   N-PSDB; ADM95099.
XX
PT   Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT   comprises administering, either concurrently or sequentially, Class III
PT   anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT   therapeutic agent(s).
XX
PS   Claim 14; Fig 16B; 88pp; English.
XX
CC   The invention relates to a method of treating a non-medullary thyroid
CC   carcinoma or treating medullary thyroid carcinoma involves administering
CC   to a subject, either concurrently or sequentially, a Class III anti-CEA
CC   (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC   least one therapeutic agent. The antibody or its fragment comprises the
CC   complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC   antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC   medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC   ovarian cancer, in a subject. This sequence corresponds to the humanised
CC   murine MN-14 antibody heavy chain variable region.
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 167;  DB 8;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-15;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 4
ADM98324
ID   ADM98324 standard; protein; 119 AA.
XX
AC   ADM98324;
XX
DT   15-JUL-2004  (first entry)
```

```
XX
DE   Humanised murine MN-14 antibody heavy chain variable region protein.
XX
KW   carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW   antibody; MN-14; non-medullary thyroid carcinoma;
KW   medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW   hepatocellular carcinoma; breast cancer; lung cancer;
KW   antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW   apoptosis; humanised.
XX
OS   Mus sp.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 33. .34
FT                   /note= "Encoded by TGGGATAGCAGTACGATTAACTATGCGATG"
FT   Misc-difference 53. .62
FT                   /note= "Encoded by CCACCG"
XX
PN   WO2004032857-A2.
XX
PD   22-APR-2004.
XX
PF   08-OCT-2003; 2003WO-US031801.
XX
PR   08-OCT-2002; 2002US-0416531P.
PR   11-OCT-2002; 2002WO-US032307.
PR   02-MAY-2003; 2003US-0467161P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-340797/31.
DR   N-PSDB; ADM98323.
XX
PT   Treating non-medullary or medullary thyroid carcinoma, involves
PT   administering to subject, either concurrently or sequentially, anti-
PT   carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS   Disclosure; Fig 23b; 122pp; English.
XX
CC   This invention relates to methods for treating cancers that express
CC   carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC   therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC   antibodies that can be used following administration of an agent that
CC   will increase antibody effector functions or following administration of
CC   an amount of interferon effective to upregulate CEA expression in tumour
CC   cells. The present invention describes the anti-CEA antibody as a class
CC   III humanised murine monoclonal antibody that retains specificity for CEA
CC   binding and is preferably an MN-14 antibody or fragment thereof.
CC   Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC   composition useful for the treatment of non-medullary or medullary
CC   thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC   carcinoma, as well as breast or lung cancer. Furthermore, it can
CC   stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC   mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC   cell growth and angiogenesis. This polypeptide sequence is the humanised
CC   murine MN-14 antibody heavy chain variable region protein of the
CC   invention.
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 167;  DB 8;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-15;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 5
ABG76489
ID   ABG76489 standard; protein; 138 AA.
XX
AC   ABG76489;
XX
DT   13-MAY-2003  (first entry)
XX
DE   Heavy chain variable, VH, region of antibody hMN14.
XX
KW   CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW   colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW   human; zeta signalling chain; CD8alpha hinge; humanised antibody;
KW   heavy chain variable region; VH.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT   Protein         20. .138
FT                   /label= Mature_VH_of_hMN14
XX
PN   US2002165360-A1.
XX
PD   07-NOV-2002.
XX
PF   10-DEC-2001; 2001US-00006771.
XX
PR   30-NOV-2000; 2000US-0250087P.
PR   30-NOV-2000; 2000US-0250090P.
XX
PA   (JUNG/) JUNGHANS R P.
XX
PI   Junghans RP;
XX
DR   WPI; 2003-298705/29.
DR   N-PSDB; ABX13169.
XX
PT   New chimeric molecule from humanized antibody against carcinoembryonic
PT   antigen and having signaling molecules of T cells and other effector
PT   cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS   Disclosure; Page 9; 20pp; English.
XX
CC   The invention relates to a chimaeric molecule comprising the
CC   carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC   as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC   chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC   which the cysteine residues have been mutated, with the IgTCR molecule
CC   occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC   appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC   NK (not defined) or other effector cells are useful in treating patients
CC   with cancers expressing the CEA antigen, together with other or with
CC   heterologous constructs to engage additional stimulatory and functional
CC   properties of the effector cells to enhance the anti-tumour therapeutic
CC   efficacy. The cancer disorder includes colorectal, breast and lung
CC   cancers. The present sequence represents the heavy chain variable, VH,
CC   region of antibody hMN14. The VH protein is humanised (complementarity
CC   determining region-grafted) and has a leader peptide
XX
SQ   Sequence 138 AA;

  Query Match             100.0%;  Score 167;  DB 6;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-15;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         86 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 117
```

```
RESULT 6
AAR94557
ID   AAR94557 standard; protein; 254 AA.
XX
AC   AAR94557;
XX
DT   19-JUN-1996  (first entry)
XX
DE   Humanised antibody MN14 heavy chain.
XX
KW   Cancer; therapy; radiotherapy; radiolabelling; phosphorus;
KW   humanised antibody; complementarity determining region; CDR; targetting;
KW   protein kinase; Fab; F(ab')2; Escherichia coli; vector; MN14pBEV;
KW   carcinoembryonic antigen; CEA; MN14-Kemptide.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Sig_peptide
FT                   /note= "PelB signal peptide"
FT   Protein         23. .254
FT                   /label= Mat_protein
FT   Region          53. .57
FT                   /label= CDR-H1
FT   Region          72. .88
FT                   /label= CDR-H2
FT   Region          121. .130
FT                   /label= CDR-H3
FT   Domain          240. .254
FT                   /label= Hinge_domain
XX
PN   WO9608506-A1.
XX
PD   21-MAR-1996.
XX
PF   18-SEP-1995;   95WO-US011405.
XX
PR   16-SEP-1994;   94US-00308103.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Leung S,  Hansen HJ,  Griffiths GL;
XX
DR   WPI; 1996-179897/18.
DR   N-PSDB; AAT14493.
XX
PT   Phosphorus labelled antibodies for use in cancer therapy - comprise
PT   protein kinase peptide substrate sequence and specific targetting CDR,
PT   for radio-labelling diseased cells with a phosphorus isotope.
XX
PS   Example 1 (ix); Fig 5; 62pp; English.
XX
CC   The heavy chain and hinge region (AAR94557) and light chain (AAR94558) of
CC   humanised anti-CEA antibody MN14 are the products of an Fab'/F(ab')2
CC   dicistronic gene (AAT14493). They are derived from anti-CEA murine
CC   monoclonal antibody MN14 following cloning and humanisation of
CC   complementarity determining regions. The dicistronic gene was used to
CC   construct vector MN14pBEV. A protein kinase substrate (see AAR94550)
CC   encoding sequence was incorporated into the vector, and MN14-Kemptide
CC   fusion protein was secreted from E. coli BMH71-18 mutS. The fusion
CC   protein can be radiolabelled with 32P or 33P and used for targetted
CC   radiotherapy of tumours or infectious lesions
XX
SQ   Sequence 254 AA;

  Query Match           100.0%;  Score 167;  DB 2;  Length 254;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         89 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 120


RESULT 7
ABR42757
ID   ABR42757 standard; protein; 256 AA.
XX
AC   ABR42757;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-0.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-0;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; triabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .256
FT                   /label= hMN-14-0
FT   Region          142. .250
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FT   Region          251. .256
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
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PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
DR   N-PSDB; ACC58722.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 39; Fig 13; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-0, which is
CC   designed to form an hMN-14 triabody. The hMN-14-0 polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa without a peptide linker. The use of the zero linker enables the
CC   secreted polypeptide to form a triabody, forming 3 binding sites for CEA.
CC   The polypeptide also includes a pelB signal peptide, which precedes the
CC   VH moiety to facilitate synthesis of the polypeptide in the periplasmic
CC   space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific triabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
```

```
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 256 AA;

  Query Match             100.0%;  Score 167;  DB 6;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 8
ABR42758
ID   ABR42758 standard; protein; 257 AA.
XX
AC   ABR42758;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-1G.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-1G;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; tetrabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .257
FT                   /label= hMN-14-0
FT   Region          142
FT                   /label= 1G_linker
FT   Region          143. .251
FT                   /label= hMN-14Vkappa
FT   Region          252. .257
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 48; Fig 14; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-1G, which is
CC   designed to form an hMN-14 tetrabody. The hMN-14-1G polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa via a single glycine residues. Use of the 1G linker enables some
CC   of the the secreted polypeptide to form a tetrabody with 4 binding sites
CC   for CEA. The polypeptide also includes a pelB signal peptide, which
CC   precedes the VH moiety to facilitate synthesis of the polypeptide in the
CC   periplasmic space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific tetrabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 257 AA;

  Query Match             100.0%;  Score 167;  DB 6;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 9
ABR42289
ID   ABR42289 standard; protein; 261 AA.
XX
AC   ABR42289;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Diabody 679-scFv-L5 polypeptide (VH-I3Q/C101S mutant).
XX
KW   Diabody; antibody; 679-scFv-L5; histamine-succinyl-glycyl; HSG;
KW   affinity enhancement system; tumour; targeting; mutant; mutein.
XX
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB signal peptide"
FT   Misc-difference 3
FT                   /note= "wild-type Ile substituted by Gln"
FT   Protein         23. .268
FT                   /label= 679-scFv-L5
FT   Region          23. .142
FT                   /label= 679VH(I3Q/C101S)
FT   Misc-difference 101
FT                   /note= "wild-type Cys substituted by Ser"
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .260
FT                   /label= 679Vk
FT   Region          261. .268
FT                   /label= 6His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
```

```
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57803.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Disclosure; Fig 28; 87pp; English.
XX
CC   The present sequence is the protein sequence of a 679 mutant diabody in
CC   which antibody 679 VH has a Gln for Ile amino acid substitution at
CC   position 3 and a Ser for Gln amino acid substitution at position 101.
CC   Murine monoclonal antibody 679 binds with high affinity to molecules
CC   containing the moiety histamine-succinyl-glycyl (HSG). The present
CC   polypeptide comprises: 679 VH(I3Q) linked to 679 Vk via a peptide linker
CC   (enables the secreted polypeptide to dimerise into a diabody, forming 2
CC   sites for HSG); a pelB leader signal peptide (facilitates transport of
CC   the polypeptide into the periplasmic space of Escherichia coli); and 6
CC   His residues (allows purification by IMAC). The 679 diabody was expressed
CC   in E. coli at a level of 10 ug/l of culture, compared with 1 ug/l for the
CC   non-mutant polypeptide. The invention provides a bispecific diabody
CC   comprising an HSG binding site and a carcinoembryonic antigen (CEA)
CC   binding site. The HSG antigen binding site may comprise the VH and Vk
CC   polypeptides of 679 MAb. These diabodies are produced via recombinant DNA
CC   technology and create a novel affinity enhancement system that shows
CC   specific affinity for HSG and CEA. They pre-target CEA positive tumours
CC   for subsequent specific delivery of therapeutic radioisotopes carried by
CC   HSG-carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 261 AA;

  Query Match             100.0%;  Score 167;  DB 6;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 10
ABR42754
ID   ABR42754 standard; protein; 261 AA.
XX
AC   ABR42754;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-scFv-L5.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-scFv-15;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .261
FT                   /label= hMN-14-scFv-L5
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .255
FT                   /label= hMN-14Vkappa
FT   Region          256. .261
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
DR   N-PSDB; ACC58721.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 31; Fig 11; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-scFv-L5, which was
CC   designed to form an hMN-14 diabody. The hMN-14-scFv-L5 polypeptide
CC   comprises the C-terminal end of anti-carcinoembryonic antigen (CEA)
CC   humanized monoclonal antibody hMN-14 VH linked to the N-terminal part of
CC   hMN-14 Vkappa by a peptide linker that enables the secreted polypeptide
CC   to dimerize into a diabody, forming 2 binding sites for CEA. The
CC   polypeptide also includes a pelB signal peptide, which precedes the VH
CC   moiety to facilitate synthesis of the polypeptide in the periplasmic
CC   space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. In the claimed monospecific diabody, each scFv comprises
CC   the present sequence. The diabody is an example of claimed multivalent
CC   binding proteins specific for a tumour-associated antigen. The binding
CC   proteins are used in the diagnosis and treatment of a tumour, carcinoma,
CC   melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma or myeloma,
CC   or a cancer selected from acute lymphoblastic leukaemia, acute
CC   myelogenous leukaemia, biliary, breast, cervical, chronic lymphocytic
CC   leukaemia, chronic myelogenous leukaemia, colorectal, endometrial,
CC   oesophageal, gastric, head and neck, Hodgkin's lymphoma, lung, medullary
CC   thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic, prostate and
CC   bladder
XX
SQ   Sequence 261 AA;

  Query Match             100.0%;  Score 167;  DB 6;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 11
ABR83645
ID   ABR83645 standard; protein; 261 AA.
```

XX
AC ABR83645;
XX
DT 16-OCT-2003 (first entry)
XX
DE hMN14-scFv-L5 amino acid sequence.
XX
KW Multispecific binding protein; multivalent; target antigen; cytostatic;
KW immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW immunotherapy; autoimmune disease; infectious disease;
KW cardiovascular disease; inflammatory disease.
XX
OS Escherichia coli.
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003057829-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US038985.
XX
PR 26-DEC-2001; 2001US-0342103P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg D;
XX
DR WPI; 2003-607997/57.
DR N-PSDB; ACF57430.
XX
PT Novel multivalent, multi-specific binding protein useful for treating
PT cancer, has first binding site having affinity towards hapten group and
PT second and third binding sites each having affinity towards target
PT antigen.
XX
PS Claim 11; Fig 6; 43pp; English.
XX
CC The present invention describes a multivalent, multi-specific binding
CC protein (I) comprising a first binding site having an affinity towards a
CC hapten group and a second and a third binding sites each having affinity
CC towards a target antigen, which may be the same or a different target
CC antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC useful for delivering a diagnostic agent, a therapeutic agent, or its
CC combination to a target, which involves administering (I) to a subject,
CC waiting for a sufficient amount of time for an amount of the non-binding
CC protein to clear the subject's blood stream, and administering to the
CC subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC agent, or its combination, that binds to a binding site of the binding
CC protein. (I) is also useful for detecting or treating a human disorder,
CC preferably cancer, autoimmune diseases, infectious diseases,
CC cardiovascular diseases and inflammatory diseases. The present sequence
CC represents a hMN14-scFv-L5 amino acid sequence, which is used in the
CC exemplification of the present invention
XX
SQ Sequence 261 AA;

Query Match 100.0%; Score 167; DB 6; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.5e-14;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
||||||||||||||||||||||||||||||||
Db 90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121

RESULT 12
ABR42292
ID ABR42292 standard; protein; 267 AA.
XX
AC ABR42292;
XX
DT 11-AUG-2003 (first entry)
XX
DE Bispecific diabody polypeptide #2.
XX
KW Diabody; antibody; carcinoembryonic antigen; CEA;
KW histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW targeting.
XX
OS Homo sapiens.
OS Mus sp.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1. .22
FT /label= Signal_peptide
FT /note= "pelB leader peptide"
FT Protein 23. .267
FT /label= BSI_polypeptide#1
FT Region 24. .141
FT /label= hMN14_VH
FT Region 142. .146
FT /label= Linker
FT Region 147. .259
FT /label= 679_Vk
FT Region 262. .267
FT /label= His_tag
XX
PN WO2003033653-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032717.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (IBCP-) IBC PHARM.
XX
PI Chang CK, Rossi E;
XX
DR WPI; 2003-393513/37.
DR N-PSDB; ACC57806.
XX
PT New kit comprising a multivalent, multi-specific binding protein and a
PT carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT for treating cancer, and cardiovascular, immune, inflammatory, or
PT infectious diseases.
XX
PS Claim 14; Fig 31; 87pp; English.
XX
CC The present sequence is the protein sequence for polypeptide #2 of a
CC novel bispecific diabody comprising the VH region of monoclonal antibody
CC hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC binds with high affinity to molecules containing the moiety histamine-
CC succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC carcinoembryonic antigen. The bispecific diabody can be produced using
CC recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC a novel affinity enhancement system that shows specific affinity for HSG
CC and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC cardiovascular diseases and inflammatory diseases can be detected or
CC treated using the methods of the invention
XX
SQ Sequence 267 AA;

Query Match 100.0%; Score 167; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.6e-14;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 13
ABR42299
ID   ABR42299 standard; protein; 267 AA.
XX
AC   ABR42299;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS1.5H polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BS1.5H_polypeptide#2
FT   Region          24. .142
FT                   /label= hMN14_VH
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
FT                   /label= h679_Vk
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57813.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 38; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of novel
CC   bispecific diabody BS1.5H comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). A humanised version of its VH and Vk sequences
CC   have been used in BS1.5H. Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC   using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC   provides a novel affinity enhancement system that shows specific affinity
CC   for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC   tumours for subsequent specific delivery of therapeutic radioisotopes
CC   carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC   disease, cardiovascular diseases and inflammatory diseases can be
CC   detected or treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             100.0%;  Score 167;  DB 6;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 14
ABR42296
ID   ABR42296 standard; protein; 267 AA.
XX
AC   ABR42296;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS2 polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .267
FT                   /label= BS2_polypeptide#2
FT   Region          24. .141
FT                   /label= hMN14-VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .259
FT                   /label= 679_Vk
FT   Region          262. .267
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57810.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
```

```
XX
PS   Claim 14; Fig 35; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of novel
CC   bispecific diabody BS2 comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC   using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC   provides a novel affinity enhancement system that shows specific affinity
CC   for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC   tumours for subsequent specific delivery of therapeutic radioisotopes
CC   carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC   disease, cardiovascular diseases and inflammatory diseases can be
CC   detected or treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             100.0%;  Score 167;  DB 6;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 15
ABR42294
ID   ABR42294 standard; protein; 267 AA.
XX
AC   ABR42294;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS1.5 polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .267
FT                   /label= BS1.5_polypeptide#2
FT   Region          24. .141
FT                   /label= hMN14_VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .259
FT                   /label= 679_Vk(I3Q)
FT   Region          261. .267
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57808.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 33; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of a
CC   novel bispecific diabody comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen. The bispecific diabody can be produced using
CC   recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC   a novel affinity enhancement system that shows specific affinity for HSG
CC   and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC   subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC   carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             100.0%;  Score 167;  DB 6;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


Search completed: March 25, 2006, 09:02:23
Job time : 118.073 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:02:50 ; Search time 18.4293 Seconds
(without alignments)
167.067 Million cell updates/sec

Title: US-10-755-382-37
Perfect score: 167
Sequence: 1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	160	95.8	126	1	G1HUKL	Ig heavy chain V-I
2	141	84.4	151	2	A60943	Ig heavy chain pre
3	140	83.8	58	2	S31683	Ig heavy chain V r
4	140	83.8	70	2	S20770	Ig heavy chain V r
5	138	82.6	98	2	PL0121	Ig heavy chain V-I
6	138	82.6	98	2	S29545	Ig heavy chain V r
7	138	82.6	98	2	S26896	Ig heavy chain V r
8	138	82.6	111	2	PH1007	Ig heavy chain V r
9	138	82.6	113	2	S24247	Ig heavy chain V r
10	138	82.6	113	2	S38490	Ig heavy chain - h
11	138	82.6	114	2	S31120	Ig heavy chain - h
12	138	82.6	114	2	S36280	Ig heavy chain V r
13	138	82.6	123	2	PC4281	anti-SS-A/Ro 60K p
14	137	82.0	63	2	S26796	Ig heavy chain V r
15	137	82.0	98	2	PH0874	Ig heavy chain V r
16	137	82.0	119	2	PH1533	Ig H chain V regio
17	137	82.0	122	2	S69910	Ig V-D-J region (K
18	136	81.4	102	2	PH1017	Ig heavy chain V r
19	136	81.4	108	2	PH1015	Ig heavy chain V r
20	136	81.4	110	2	S69897	Ig heavy chain V r
21	136	81.4	118	2	S31116	Ig heavy chain - h
22	136	81.4	120	2	S31112	Ig heavy chain - h
23	136	81.4	121	2	S31113	Ig heavy chain - h
24	136	81.4	121	2	I55673	Ig heavy chain - h
25	136	81.4	138	2	B56701	Ig heavy chain V r
26	136	81.4	140	2	S22657	Ig heavy chain pre
27	135	80.8	52	2	S21591	Ig heavy chain V r
28	135	80.8	76	2	S31592	Ig heavy chain V r
29	135	80.8	96	2	S20781	Ig heavy chain V r
30	135	80.8	97	2	S26935	Ig heavy chain V r
31	135	80.8	97	2	S46462	Ig heavy chain V r
32	135	80.8	98	2	S26889	Ig heavy chain V r
33	135	80.8	98	2	PL0116	Ig heavy chain V-I
34	135	80.8	98	2	S29543	Ig heavy chain V r
35	135	80.8	98	2	S29546	Ig heavy chain V r
36	135	80.8	99	2	S24259	Ig heavy chain V r
37	135	80.8	100	2	S24258	Ig heavy chain V r
38	135	80.8	101	2	S24257	Ig heavy chain V r
39	135	80.8	101	2	JT0511	Ig heavy chain V-I
40	135	80.8	102	2	S24260	Ig heavy chain V r
41	135	80.8	104	2	S24255	Ig heavy chain V r
42	135	80.8	105	2	S24249	Ig heavy chain V r
43	135	80.8	106	2	S24256	Ig heavy chain V r
44	135	80.8	108	2	PH1648	Ig heavy chain V r
45	135	80.8	108	2	PH1642	Ig heavy chain V r

ALIGNMENTS

RESULT 1
G1HUKL
Ig heavy chain V-III region (Kol) - human
C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C;Accession: A02055
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOI
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Accession: A02055
A;Molecule type: protein
A;Residues: 1-126 <SCH>
A;Cross-references: UNIPROT:P01772; UNIPARC:UPI000002D0C3
C;Genetics:
A;Gene: GDB:IGHV@
A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;15-98/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96,105-110/Disulfide bonds: #status experimental

Query Match 95.8%; Score 160; DB 1; Length 126;
Best Local Similarity 96.8%; Pred. No. 3.5e-14;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||:||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 97
```

RESULT 2
A60943
Ig heavy chain precursor V region (clone HN.14) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: A60943; A48165
R;Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat, E.A.;
J. Neuroimmunol. 30, 245, 1990
A;Title: Molecular cloning of a human immunoglobulin heavy chain variable (V-H) region w
A;Reference number: A60943; MUID:91036050; PMID:1699976
A;Accession: A60943
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-151 <DES>
A;Cross-references: UNIPARC:UPI0000176C11
R;Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat, E.A.;
J. Neuroimmunol. 26, 35-41, 1990
A;Title: Molecular cloning of a human immunoglobulin heavy chain variable (V-H) region w
A;Reference number: A48165; MUID:90094677; PMID:1688442

A;Accession: A48165
A;Molecule type: mRNA
A;Residues: 1-36,'M',38-62,'AR',67-151 <DE2>
A;Cross-references: UNIPARC:UPI0000176C12
A;Note: this sequence has been corrected in reference A60943
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 84.4%; Score 141; DB 2; Length 151;
Best Local Similarity 80.6%; Pred. No. 1.4e-11;
Matches 25; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
Db 86 RFTISRDNSKNTIYLQMNSLRPEDTAVYYCA 116

RESULT 3
S31683
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31683
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31683
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-58 <CUI>
A;Cross-references: UNIPARC:UPI0000116460; EMBL:Z14181; NID:g31029; PIDN:CAA78550.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 83.8%; Score 140; DB 2; Length 58;
Best Local Similarity 83.9%; Pred. No. 7.3e-12;
Matches 26; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
Db 7 RFTISRDNAKNSLYLQMNSLRAEDTGVYYCA 37

RESULT 4
S20770
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S20770
R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A;Reference number: S20764
A;Accession: S20770
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-70 <MOR>
A;Cross-references: UNIPARC:UPI00001163F1; EMBL:Z11953; NID:g33869; PIDN:CAA78010.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 83.8%; Score 140; DB 2; Length 70;
Best Local Similarity 80.6%; Pred. No. 8.8e-12;
Matches 25; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
Db 10 RFTISRDNSKNTLYLQLNSLRPEDTAVYYCA 40

RESULT 5
PL0121
Ig heavy chain V-III region (TD-Vp) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Aug-1996
C;Accession: PL0121
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A;Reference number: PL0116; MUID:88286083; PMID:2840480
A;Accession: PL0121
A;Molecule type: mRNA
A;Residues: 1-98 <BIR>
A;Cross-references: UNIPARC:UPI0000176B97
A;Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A;Note: the sequence shows the V region (TD-Vp) from one of five DNA rearrangements from
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2

Query Match 82.6%; Score 138; DB 2; Length 98;
Best Local Similarity 83.9%; Pred. No. 2.3e-11;
Matches 26; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
Db 67 RFTISRDNAKNTLYLQMNSLRAEDTAVYYCA 97

RESULT 6
S29545
Ig heavy chain V region (COS 6) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29545
R;Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Accession: S29545
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI0000116412; EMBL:Z17392; NID:g32840; PIDN:CAA78996.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 82.6%; Score 138; DB 2; Length 98;
Best Local Similarity 83.9%; Pred. No. 2.3e-11;
Matches 26; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
Db 67 RFTISRDNAKNTLYLQMNSLRAEDTAVYYCA 97

RESULT 7
S26896
Ig heavy chain V region (DP-53) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C;Accession: S26896
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26896
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI0000176E66; EMBL:Z12353
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

```
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             82.6%;  Score 138;  DB 2;  Length 98;
  Best Local Similarity   83.9%;  Pred. No. 2.3e-11;
  Matches   26;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||:|||:||| ||| ||:||
Db         67 RFTISRDNAKNTLYLQMNSLRAEDTAVYYCA 97


RESULT 8
PH1007
Ig heavy chain V region (clone 163-c1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1007
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1007
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-111 <TIL>
A;Cross-references: UNIPARC:UPI0000176D17
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             82.6%;  Score 138;  DB 2;  Length 111;
  Best Local Similarity   81.2%;  Pred. No. 2.6e-11;
  Matches   26;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||:||| ||| ||| :|:|||
Db         67 RFTISRDNAKNTLYLQMSSLRSEDTAMYYCAS 98


RESULT 9
S24247
Ig heavy chain V region (VH26-DLR2-JH3) - human
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S24247
R;Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A;Description: A single VH gene predominates in the rearranged and expressed human B cel
A;Reference number: S24247
A;Accession: S24247
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <STE>
A;Cross-references: UNIPARC:UPI0000116084; EMBL:X67060; NID:g38377; PIDN:CAA47445.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

  Query Match             82.6%;  Score 138;  DB 2;  Length 113;
  Best Local Similarity   83.9%;  Pred. No. 2.6e-11;
  Matches   26;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||:||||:|||:||| ||| |||||
Db         66 RFTISRDNSKNTLYLQMNSLRAEDTAVYFCA 96


RESULT 10
S38490
Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38490
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe,
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a
A;Reference number: S38488
A;Accession: S38490
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <MAR>
A;Cross-references: UNIPARC:UPI0000116549; EMBL:Z23030; NID:g414027; PIDN:CAA80565.1; P
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             82.6%;  Score 138;  DB 2;  Length 113;
  Best Local Similarity   81.2%;  Pred. No. 2.6e-11;
  Matches   26;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||:|:|||:||| ||| ||:|||
Db         67 RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAS 98


RESULT 11
S31120
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31120
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurmar
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31120
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 1-114 <RAA>
A;Cross-references: UNIPARC:UPI0000176DC9; EMBL:X62972
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             82.6%;  Score 138;  DB 2;  Length 114;
  Best Local Similarity   81.2%;  Pred. No. 2.7e-11;
  Matches   26;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||:|:|||:||| ||| ||:|||
Db         67 RFTISRDNAKNSLYLQMNSLRAEDTAVYYCAS 98


RESULT 12
S36280
Ig heavy chain V region (clone alpha-FOG1-A3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: S36280
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36280
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-114 <GRI>
A;Cross-references: UNIPROT:Q9ULB6; UNIPARC:UPI0000176D1E; EMBL:Z18822
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             82.6%;  Score 138;  DB 2;  Length 114;
  Best Local Similarity   83.9%;  Pred. No. 2.7e-11;
```

```
  Matches   26;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||||||||:|||:||| ||| ||:||
Db         67 RFTISRDNAKNTLYLQMNSLRDEDTAVYYCA 97


RESULT 13
PC4281
anti-SS-A/Ro 60K peptide heavy chain E-56 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 21-Jan-2000
C;Accession: PC4281
R;Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.
Biochem. Biophys. Res. Commun. 232, 101-106, 1997
A;Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltratin
A;Reference number: PC4279; MUID:97236289; PMID:9125110
A;Accession: PC4281
A;Molecule type: protein
A;Residues: 1-123 <SUZ>
A;Cross-references: UNIPARC:UPI0000176E91
C;Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjoeg
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             82.6%;  Score 138;  DB 2;  Length 123;
  Best Local Similarity   80.6%;  Pred. No. 2.9e-11;
  Matches   25;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||||||:|:||| ||||||| :|:||
Db         67 RFTISRDNAKNSLYLQMSSLRPEDTALYYCA 97


RESULT 14
S26796
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 30-Apr-1999 #text_change 20-Jun-2000
C;Accession: S26796
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami
A;Reference number: S26786; MUID:92111632; PMID:1730251
A;Accession: S26796
A;Molecule type: mRNA
A;Residues: 1-63 <MOR>
A;Cross-references: UNIPARC:UPI0000115FC9; EMBL:X61018; NID:g32785; PIDN:CAA43352.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             82.0%;  Score 137;  DB 2;  Length 63;
  Best Local Similarity   83.9%;  Pred. No. 2e-11;
  Matches   26;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||:||||||||:||| ||| ||:||
Db         13 RFTISRDNSKNTLFLQMNSLRVEDTAVYYCA 43


RESULT 15
PH0874
Ig heavy chain V region (anti-DNA, 1X7RG1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-1996
C;Accession: PH0874
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0874
A;Molecule type: DNA
A;Residues: 1-98 <MAN>
A;Cross-references: UNIPARC:UPI0000176BFB
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-36/Region: complementarity-determining 1
F;50-67/Region: complementarity-determining 2

  Query Match             82.0%;  Score 137;  DB 2;  Length 98;
  Best Local Similarity   83.9%;  Pred. No. 3.1e-11;
  Matches   26;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||||:|:|||:||| ||| |||||
Db         67 RFTISRDNAKNSLYLQMNSLRAEDTAVYFCA 97


Search completed: March 25, 2006, 09:15:46
Job time : 18.4293 secs
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:40 ; Search time 115.267 Seconds
(without alignments)
195.866 Million cell updates/sec

Title: US-10-755-382-37
Perfect score: 167
Sequence: 1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	160	95.8	126	1	HV3K_HUMAN	P01772 homo sapien
2	138	82.6	196	2	Q65ZL8_MOUSE	Q65zl8 mus musculu
3	137	82.0	466	2	Q6N096_HUMAN	Q6n096 homo sapien
4	136	81.4	417	2	Q6N093_HUMAN	Q6n093 homo sapien
5	136	81.4	465	2	Q5I0J0_RAT	Q5i0j0 rattus norv
6	136	81.4	473	2	Q91Z05_MOUSE	Q91z05 mus musculu
7	136	81.4	485	2	Q6PDB8_MOUSE	Q6pdb8 mus musculu
8	135	80.8	112	2	Q9UGP3_HUMAN	Q9ugp3 homo sapien
9	135	80.8	113	2	Q9UL90_HUMAN	Q9ul90 homo sapien
10	135	80.8	116	1	HV05_CARAU	P19181 carassius a
11	135	80.8	117	1	HV3C_HUMAN	P01764 homo sapien
12	135	80.8	240	2	Q65ZC9_HUMAN	Q65zc9 homo sapien
13	135	80.8	461	2	Q5M7V3_RAT	Q5m7v3 rattus norv
14	135	80.8	466	2	Q6IN78_HUMAN	Q6in78 homo sapien
15	135	80.8	613	2	Q8WUK1_HUMAN	Q8wuk1 homo sapien
16	134	80.2	112	2	Q9HCC1_HUMAN	Q9hcc1 homo sapien
17	134	80.2	118	2	Q9UL91_HUMAN	Q9ul91 homo sapien
18	134	80.2	470	2	Q6PJA4_HUMAN	Q6pja4 homo sapien
19	134	80.2	478	2	Q6PI81_HUMAN	Q6pi81 homo sapien
20	134	80.2	483	2	Q566J7_MOUSE	Q566j7 mus musculu
21	134	80.2	606	2	Q6GMY2_HUMAN	Q6gmy2 homo sapien
22	132	79.0	116	2	Q9UL93_HUMAN	Q9ul93 homo sapien
23	132	79.0	117	1	HV03_CARAU	P19180 carassius a
24	132	79.0	119	2	Q5F2I8_MOUSE	Q5f2i8 mus musculu
25	132	79.0	147	2	Q9Y509_HUMAN	Q9y509 homo sapien
26	132	79.0	493	2	Q6GMX2_HUMAN	Q6gmx2 homo sapien
27	131	78.4	104	2	Q9UL87_HUMAN	Q9ul87 homo sapien
28	131	78.4	117	1	HV02_CANFA	P01785 canis famil
29	131	78.4	117	1	HV53_MOUSE	P18524 mus musculu
30	131	78.4	117	1	HV55_MOUSE	P18526 mus musculu
31	131	78.4	119	2	Q920E7_MOUSE	Q920e7 mus musculu
32	131	78.4	136	1	HV16_MOUSE	P01783 mus musculu
33	131	78.4	255	2	Q6KB05_MOUSE	Q6kb05 mus musculu
34	131	78.4	465	2	Q6P6C4_HUMAN	Q6p6c4 homo sapien
35	131	78.4	473	2	Q6MZV7_HUMAN	Q6mzv7 homo sapien
36	131	78.4	479	2	Q6MZV6_HUMAN	Q6mzv6 homo sapien
37	131	78.4	573	2	Q8WU38_HUMAN	Q8wu38 homo sapien
38	130	77.8	95	2	Q9ULB6_HUMAN	Q9ulb6 homo sapien
39	130	77.8	116	1	HV3T_HUMAN	P01781 homo sapien
40	130	77.8	118	2	Q9UL72_HUMAN	Q9ul72 homo sapien
41	130	77.8	479	2	Q5BK12_RAT	Q5bk12 rattus norv
42	130	77.8	494	2	Q96K68_HUMAN	Q96k68 homo sapien
43	130	77.8	499	2	Q8N5K4_HUMAN	Q8n5k4 homo sapien
44	129	77.2	464	2	Q6MZU6_HUMAN	Q6mzu6 homo sapien
45	129	77.2	469	2	Q569F4_HUMAN	Q569f4 homo sapien

ALIGNMENTS

```
RESULT 1
HV3K_HUMAN
ID   HV3K_HUMAN     STANDARD;      PRT;   126 AA.
AC   P01772;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-III region KOL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE, AND DISULFIDE BONDS.
RX   MEDLINE=83289131; PubMed=6884994;
RA   Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT   "Three-dimensional structure determination of antibodies. Primary
RT   structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=81072295; PubMed=7441755;
RA   Marquart M., Deisenhofer J., Huber R., Palm W.;
RT   "Crystallographic refinement and atomic models of the intact
RT   immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
RT   and 1.0-A resolution.";
RL   J. Mol. Biol. 141:369-391(1980).
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A02055; G1HUKL.
DR   PDB; 2FB4; X-ray; H=2-126.
DR   PDB; 2IG2; X-ray; H=2-126.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    112       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   DISULFID     22     96
FT   DISULFID    105    110
FT   NON_TER     126    126
FT   STRAND        3      7
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FT   STRAND       11     12
FT   TURN         14     15
FT   STRAND       18     25
FT   HELIX        29     31
FT   STRAND       34     39
FT   TURN         41     42
FT   STRAND       45     51
FT   TURN         53     54
FT   STRAND       58     60
FT   HELIX        62     64
FT   STRAND       65     65
FT   TURN         66     67
FT   STRAND       68     73
FT   TURN         74     77
FT   STRAND       78     83
FT   HELIX        88     90
FT   STRAND       92     99
FT   STRAND      106    106
FT   TURN        107    108
FT   STRAND      109    109
FT   STRAND      113    116
FT   STRAND      120    124
SQ   SEQUENCE   126 AA;  13718 MW;  E4D71B52B16F8776 CRC64;

  Query Match             95.8%;  Score 160;  DB 1;  Length 126;
  Best Local Similarity   96.8%;  Pred. No. 6.2e-15;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||:||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 97


RESULT 2
Q65ZL8_MOUSE
ID   Q65ZL8_MOUSE PRELIMINARY;      PRT;   196 AA.
AC   Q65ZL8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   VH7183-DSP2-JH3-CH1 protein (Fragment).
GN   Name=VH7183-DSP2-JH3-CH1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BALB/c;
RX   MEDLINE=95362300; PubMed=7635518;
RA   Komori T., Sugiyama H.;
RT   "An aberrant splicing using a 3' cryptic splice site within the CH1
RT   exon induces truncated mu-chain production.";
RL   Immunology 85:166-170(1995).
DR   EMBL; S79401; AAB35023.2; -; mRNA.
DR   SMR; Q65ZL8; 20-195.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER     196    196
SQ   SEQUENCE   196 AA;  21429 MW;  12A381018944B268 CRC64;

  Query Match             82.6%;  Score 138;  DB 2;  Length 196;
  Best Local Similarity   81.2%;  Pred. No. 1.5e-11;
  Matches   26;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||:||| ||| ||| :|:|||
Db         86 RFTISRDNAKNTLYLQMSSLRSEDTAMYYCAS 117


RESULT 3
Q6N096_HUMAN
ID   Q6N096_HUMAN PRELIMINARY;      PRT;   466 AA.
AC   Q6N096;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686I15196.
GN   Name=DKFZp686I15196;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Esophagus tumor;
RG   The German cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640620; CAE45774.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   SMR; Q6N096; 20-466.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   466 AA;  50926 MW;  01E91B748D6D57C4 CRC64;

  Query Match             82.0%;  Score 137;  DB 2;  Length 466;
  Best Local Similarity   83.9%;  Pred. No. 5.7e-11;
  Matches   26;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||||: ||| ||| ||:||
Db         86 RFTISRDNAKNTLFLQLSSLRAEDTAVYYCA 116


RESULT 4
Q6N093_HUMAN
ID   Q6N093_HUMAN PRELIMINARY;      PRT;   417 AA.
AC   Q6N093;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686I04196 (Fragment).
GN   Name=DKFZp686I04196;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Human esophagus tumor;
RG   The German Human cDNA Consortium;
RA   Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640623; CAE45777.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
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DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   417 AA;  46061 MW;  C4518E844CFB883C CRC64;

  Query Match             81.4%;  Score 136;  DB 2;  Length 417;
  Best Local Similarity   77.4%;  Pred. No. 7e-11;
  Matches   24;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              |||:||||: |||||:|:||||||| ||:||
Db         39 RFTVSRDNSANTLFLEMNSLRPEDTAVYYCA 69


RESULT 5
Q5I0J0_RAT
ID   Q5I0J0_RAT  PRELIMINARY;      PRT;   465 AA.
AC   Q5I0J0;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical LOC299354.
GN   Name=LOC299354;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC       histocompatibility complex class I molecules (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; BC088271; AAH88271.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
KW   Hypothetical protein; Immunoglobulin domain; Repeat.
SQ   SEQUENCE   465 AA;  51699 MW;  97C4533A213A424F CRC64;

  Query Match             81.4%;  Score 136;  DB 2;  Length 465;
  Best Local Similarity   78.1%;  Pred. No. 7.9e-11;
  Matches   25;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||:||||||| |||  |:| :
Db         86 RFTISRDNAKNTLYLQMDSLRSEDTATYYCTT 117


RESULT 6
Q91Z05_MOUSE
ID   Q91Z05_MOUSE PRELIMINARY;      PRT;   473 AA.
AC   Q91Z05;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Immunoglobulin heavy chain (Gamma polypeptide).
GN   Name=Ighg; Synonyms=AU044919;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RA   Director MGC Project;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=7498516; DOI=10.1016/0014-5793(95)01224-3;
RA   Takagi M., Kohda K., Hamuro T., Harada A., Yamaguchi H., Kamachi M.,
RA   Imanaka T.;
RT   "Thermostable peroxidase activity with a recombinant antibody L chain-
RT   porphyrin Fe(III) complex.";
RL   FEBS Lett. 375:273-276(1995).
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DR   EMBL; BC010327; AAH10327.1; -; mRNA.
DR   PIR; S68213; S68213.
DR   HSSP; P01783; 1IGC.
DR   SMR; Q91Z05; 20-469.
DR   MGI; MGI:2144967; AU044919.
DR   MGI; MGI:2144967; Ighg.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   473 AA;  51946 MW;  CF625F008932AF12 CRC64;

  Query Match             81.4%;  Score 136;  DB 2;  Length 473;
  Best Local Similarity   83.9%;  Pred. No. 8.1e-11;
  Matches   26;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||||||| ||| ||| :|:||
Db         86 RFTISRDNAKNTLFLQMTSLRSEDTAMYYCA 116


RESULT 7
Q6PDB8_MOUSE
ID   Q6PDB8_MOUSE PRELIMINARY;      PRT;   485 AA.
AC   Q6PDB8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   LOC544903 protein.
GN   Name=LOC544903;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RG   NIH MGC Project;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC058814; AAH58814.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   SMR; Q6PDB8; 20-242.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   485 AA;  52473 MW;  81236FF3AD821056 CRC64;

  Query Match             81.4%;  Score 136;  DB 2;  Length 485;
  Best Local Similarity   83.9%;  Pred. No. 8.3e-11;
  Matches   26;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||||||||||| ||| ||| :|:||
Db         86 RFTISRDNAKNTLFLQMTSLRSEDTAMYYCA 116


RESULT 8
Q9UGP3_HUMAN
ID   Q9UGP3_HUMAN PRELIMINARY;      PRT;   112 AA.
AC   Q9UGP3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Immunoblobulin heavy chain (Fragment).
GN   Name=IgH;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Zafiropoulos A., Kandilogiannaki M., Dahlenborg C., Borrebaeck C.A.K.,
RA   Krambovitis E.;
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ132560; CAB65078.1; -; mRNA.
DR   HSSP; P01783; 1IGC.
DR   SMR; Q9UGP3; 1-105.
DR   Ensembl; ENSG00000188443; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  12226 MW;  0A1F17082C7A8CE3 CRC64;

  Query Match             80.8%;  Score 135;  DB 2;  Length 112;
  Best Local Similarity   80.6%;  Pred. No. 2.2e-11;
  Matches   25;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||:||||:|||:||| ||| ||:||
Db         50 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 80


RESULT 9
Q9UL90_HUMAN
ID   Q9UL90_HUMAN PRELIMINARY;      PRT;   113 AA.
AC   Q9UL90;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1730252;
RA   Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA   Schuurman R.K.;
RT   "Restricted utilization of germ-line VH3 genes and short diverse third
RT   complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT   immunoglobulin heavy chain rearrangements.";
RL   Eur. J. Immunol. 22:247-251(1992).
DR   EMBL; AF035024; AAD56260.1; -; mRNA.
DR   PIR; S78486; S78486.
DR   HSSP; P01772; 2FB4.
DR   SMR; Q9UL90; 1-113.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     113    113
SQ   SEQUENCE   113 AA;  12437 MW;  ED57FDD19086D07F CRC64;

  Query Match             80.8%;  Score 135;  DB 2;  Length 113;
  Best Local Similarity   80.6%;  Pred. No. 2.2e-11;
  Matches   25;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||:||||:|||:||| ||| ||:||
Db         67 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 97


RESULT 10
HV05_CARAU
ID   HV05_CARAU     STANDARD;      PRT;   116 AA.
AC   P19181;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region 5A precursor.
OS   Carassius auratus (Goldfish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Carassius.
OX   NCBI_TaxID=7957;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88144476; PubMed=3125551;
RA   Wilson M.R., Middleton D., Warr G.W.;
RT   "Immunoglobulin heavy chain variable region gene evolution: structure
RT   and family relationships of two genes and a pseudogene in a teleost
RT   fish.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   HSSP; P01783; 1IGC.
DR   SMR; P19181; 20-116.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    116       Ig heavy chain V region 5A.
FT   REGION       20     49       Framework-1.
FT   REGION       50     54       Complementarity-determining-1.
FT   REGION       55     68       Framework-2.
FT   REGION       69     84       Complementarity-determining-2.
FT   REGION       85    116       Framework-3.
FT   DISULFID     41    114       By similarity.
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12808 MW;  9C2279E2DF199B12 CRC64;

  Query Match             80.8%;  Score 135;  DB 1;  Length 116;
  Best Local Similarity   80.6%;  Pred. No. 2.3e-11;
  Matches   25;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||:||||:|||:||| ||| ||:||
Db         85 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 115


RESULT 11
HV3C_HUMAN
ID   HV3C_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01764;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Ig heavy chain V-III region VH26 precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=81101090; PubMed=6450418;
RA   Matthyssens G., Rabbitts T.H.;
RT   "Structure and multiplicity of genes for the human immunoglobulin
RT   heavy chain variable region.";
RL   Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 20-117.
RX   MEDLINE=93209281; PubMed=7681398;
RA   Mariette X., Tsapis A., Brouet J.C.;
RT   "Nucleotidic sequence analysis of the variable domains of four human
RT   monoclonal IgM with an antibody activity to myelin-associated
RT   glycoprotein.";
RL   Eur. J. Immunol. 23:846-851(1993).
RN   [3]
RP   3D-STRUCTURE MODELING OF 20-117.
RX   MEDLINE=86094276; PubMed=3866244;
RA   Toyonaga B., Yoshikai Y., Vadasz V., Chin B., Mak T.W.;
RT   "Organization and sequences of the diversity, joining, and constant
RT   region genes of the human T-cell receptor beta chain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:8624-8628(1985).
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; J00236; AAA53516.1; -; Unassigned_DNA.
DR   EMBL; M35415; AAA58735.1; -; Genomic_DNA.
DR   PIR; A02047; H3HU26.
DR   PDB; 1HOU; Model; H=20-117.
DR   HGNC; HGNC:5545; IGHV@.
DR   GO; GO:0005576; C:extracellular region; NAS.
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DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       Ig heavy chain V-III region VH26.
FT   DOMAIN       20   >117       Ig-like.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12582 MW;  E826733F1A3CB0F1 CRC64;

  Query Match             80.8%;  Score 135;  DB 1;  Length 117;
  Best Local Similarity   80.6%;  Pred. No. 2.3e-11;
  Matches   25;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||:||||:|||:||| ||| ||:||
Db         86 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 116


RESULT 12
Q65ZC9_HUMAN
ID   Q65ZC9_HUMAN PRELIMINARY;      PRT;   240 AA.
AC   Q65ZC9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Single-chain Fv (Fragment).
GN   Name=scFv;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C1q/7;
RX   MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA   Kontermann R.E., Wing M.G., Winter G.;
RT   "Complement recruitment using bispecific diabodies.";
RL   Nat. Biotechnol. 15:629-631(1997).
DR   EMBL; Y13056; CAA73499.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1      1
FT   NON_TER     240    240
SQ   SEQUENCE   240 AA;  25569 MW;  FDCFD3645F64B373 CRC64;

  Query Match             80.8%;  Score 135;  DB 2;  Length 240;
  Best Local Similarity   80.6%;  Pred. No. 5.2e-11;
  Matches   25;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||:||||:|||:||| ||| ||:||
Db         67 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCA 97


RESULT 13
Q5M7V3_RAT
ID   Q5M7V3_RAT  PRELIMINARY;      PRT;   461 AA.
AC   Q5M7V3;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   LOC367586 protein.
GN   Name=LOC367586;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RG   NIH MGC Project;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC       histocompatibility complex class I molecules (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; BC088423; AAH88423.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 3.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
KW   Immunoglobulin domain; Repeat.
SQ   SEQUENCE   461 AA;  50949 MW;  25EA4ECE6FE0F5A9 CRC64;

  Query Match             80.8%;  Score 135;  DB 2;  Length 461;
  Best Local Similarity   78.1%;  Pred. No. 1.1e-10;
  Matches   25;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||:||:||||||| |||  |:||:
Db         86 RFTISRDNAKSTLYLQMDSLRSEDTATYYCAT 117


RESULT 14
Q6IN78_HUMAN
ID   Q6IN78_HUMAN PRELIMINARY;      PRT;   466 AA.
AC   Q6IN78;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGHG1 protein.
GN   Name=IGHG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
```

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RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral Nervous System;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral Nervous System;
RG   NIH MGC Project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC072419; AAH72419.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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  Query Match             80.8%;  Score 135;  DB 2;  Length 466;
  Best Local Similarity   80.6%;  Pred. No. 1.1e-10;
  Matches   25;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

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RESULT 15
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DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGHM protein.
GN   Name=IGHM;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RG   NIH MGC Project;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2117273;
RA   Schroeder H.W. Jr, Wang J.Y.;
RT   "Preferential utilization of conserved immunoglobulin heavy chain
RT   variable gene segments during human fetal life.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:6146-6150(1990).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1383695; DOI=10.1016/0161-5890(92)90173-U;
RA   Cuisinier A.M., Fumoux F., Fougereau M., Tonnelle C.;
RT   "IGM kappa/lambda EBV human B cell clone: an early step of
RT   differentiation of fetal B cells or a distinct B lineage?";
RL   Mol. Immunol. 29:1363-1373(1992).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1730252;
RA   Raaphorst F.M., Timmers E., Kenter M.J., Van Tol M.J., Vossen J.M.,
RA   Schuurman R.K.;
RT   "Restricted utilization of germ-line VH3 genes and short diverse third
RT   complementarity-determining regions (CDR3) in human fetal B lymphocyte
RT   immunoglobulin heavy chain rearrangements.";
RL   Eur. J. Immunol. 22:247-251(1992).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1904154;
RA   Neale G.A., Kitchingman G.R.;
RT   "mRNA transcripts initiating within the human immunoglobulin mu heavy
RT   chain enhancer region contain a non-translatable exon and are
RT   extremely heterogeneous at the 5' end.";
RL   Nucleic Acids Res. 19:2427-2433(1991).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2840480; DOI=10.1084/jem.168.1.229;
RA   Bird J., Galili N., Link M., Stites D., Sklar J.;
RT   "Continuing rearrangement but absence of somatic hypermutation in
RT   immunoglobulin genes of human B cell precursor leukemia.";
RL   J. Exp. Med. 168:229-245(1988).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2538551; DOI=10.1084/jem.169.4.1391;
RA   Nickerson K.G., Berman J., Glickman E., Chess L., Alt F.W.;
RT   "Early human IgH gene assembly in Epstein-Barr virus-transformed fetal
RT   B cell lines. Preferential utilization of the most JH-proximal D
RT   segment (DQ52) and two unusual VH-related rearrangements.";
RL   J. Exp. Med. 169:1391-1403(1989).
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RX   MEDLINE=93301610; PubMed=8315388; DOI=10.1084/jem.178.1.331;
RA   Hillson J.L., Karr N.S., Oppliger I.R., Mannik M., Sasso E.H.;
RT   "The structural basis of germline-encoded VH3 immunoglobulin binding
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RT   to staphylococcal protein A.";
RL   J. Exp. Med. 178:331-336(1993).
DR   EMBL; BC020240; AAH20240.1; -; mRNA.
DR   PIR; F36005; F36005.
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DR   PIR; PH1642; PH1642.
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DR   SMR; Q8WUK1; 20-242.
DR   Ensembl; ENSG00000130076; Homo sapiens.
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DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 4.
DR   SMART; SM00406; IGv; 1.
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SQ   SEQUENCE   613 AA;  67296 MW;  60C7F5950671E315 CRC64;

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  Best Local Similarity   80.6%;  Pred. No. 1.5e-10;
  Matches   25;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

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Job time : 116.267 secs
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:14:16 ; Search time 29.1518 Seconds
(without alignments)
90.753 Million cell updates/sec

Title: US-10-755-382-37
Perfect score: 167
Sequence: 1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	167	100.0	32	1	US-08-318-157B-37	Sequence 37, Appl
2	167	100.0	32	2	US-09-253-794-37	Sequence 37, Appl
3	167	100.0	119	1	US-08-318-157B-14	Sequence 14, Appl
4	167	100.0	119	2	US-09-253-794-14	Sequence 14, Appl
5	167	100.0	489	4	PCT-US95-11405-35	Sequence 35, Appl
6	164	98.2	32	1	US-08-318-157B-36	Sequence 36, Appl
7	164	98.2	32	2	US-09-253-794-36	Sequence 36, Appl
8	164	98.2	119	1	US-08-318-157B-12	Sequence 12, Appl
9	164	98.2	119	1	US-08-318-157B-13	Sequence 13, Appl
10	164	98.2	119	1	US-08-318-157B-15	Sequence 15, Appl
11	164	98.2	119	1	US-08-318-157B-17	Sequence 17, Appl
12	164	98.2	119	2	US-09-253-794-12	Sequence 12, Appl
13	164	98.2	119	2	US-09-253-794-13	Sequence 13, Appl
14	164	98.2	119	2	US-09-253-794-15	Sequence 15, Appl
15	164	98.2	119	2	US-09-253-794-17	Sequence 17, Appl
16	163	97.6	119	1	US-08-859-649-22	Sequence 22, Appl
17	163	97.6	119	2	US-08-207-861-22	Sequence 22, Appl
18	163	97.6	119	2	US-08-859-648-22	Sequence 22, Appl
19	160	95.8	117	1	US-08-652-558-3	Sequence 3, Appli
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21	160	95.8	119	1	US-08-303-569B-11	Sequence 11, Appl
22	160	95.8	119	1	US-08-303-569B-17	Sequence 17, Appl
23	160	95.8	119	1	US-08-859-649-20	Sequence 20, Appl
24	160	95.8	119	1	US-08-859-649-21	Sequence 21, Appl
25	160	95.8	119	1	US-08-859-649-31	Sequence 31, Appl
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28	160	95.8	119	1	US-08-116-247-18	Sequence 18, Appl
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38	160	95.8	119	2	US-09-795-515-17	Sequence 17, Appl
39	160	95.8	119	2	US-09-348-224-12	Sequence 12, Appl
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41	160	95.8	119	2	US-09-348-224-19	Sequence 19, Appl
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43	160	95.8	120	2	US-08-435-516-2	Sequence 2, Appli
44	160	95.8	122	2	US-09-155-106-17	Sequence 17, Appl
45	160	95.8	126	1	US-08-303-569B-10	Sequence 10, Appl

ALIGNMENTS

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RESULT 1
US-08-318-157B-37
; Sequence 37, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-37

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  Best Local Similarity   100.0%;  Pred. No. 5.2e-17;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
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RESULT 2
US-09-253-794-37
; Sequence 37, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 37:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 32 amino acids
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;             TOPOLOGY: linear
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  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
US-08-318-157B-14
; Sequence 14, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
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;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-14

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RESULT 4
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; Sequence 14, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;
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;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
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US-09-253-794-14

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Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 5
PCT-US95-11405-35
; Sequence 35, Application PC/TUS9511405
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  PHOSPHOROUS-32 LABELING OF ANTIBODIES
;    TITLE OF INVENTION:  FOR CANCER THERAPY
;    NUMBER OF SEQUENCES:  38
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/11405
;      FILING DATE:  18-SEP-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/308,103
;      FILING DATE:  16-SEP-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/599/IMIN
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  489 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-11405-35

  Query Match             100.0%;  Score 167;  DB 4;  Length 489;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-15;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         89 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 120


RESULT 6
US-08-318-157B-36
; Sequence 36, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  36:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-36

  Query Match             98.2%;  Score 164;  DB 1;  Length 32;
  Best Local Similarity   96.9%;  Pred. No. 1.4e-16;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32


RESULT 7
US-09-253-794-36
; Sequence 36, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
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;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 36:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 32 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-253-794-36

  Query Match             98.2%;  Score 164;  DB 2;  Length 32;
  Best Local Similarity   96.9%;  Pred. No. 1.4e-16;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db          1 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 32


RESULT 8
US-08-318-157B-12
; Sequence 12, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-12

  Query Match             98.2%;  Score 164;  DB 1;  Length 119;
  Best Local Similarity   96.9%;  Pred. No. 6.3e-16;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 9
US-08-318-157B-13
; Sequence 13, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-13

  Query Match             98.2%;  Score 164;  DB 1;  Length 119;
  Best Local Similarity   96.9%;  Pred. No. 6.3e-16;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 10
US-08-318-157B-15
; Sequence 15, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
```

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;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-15

  Query Match             98.2%;  Score 164;  DB 1;  Length 119;
  Best Local Similarity   96.9%;  Pred. No. 6.3e-16;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||:||||||||||||||||||
Db         67 RFTISRDNAKNTLYLQMDSLRPEDTGVYFCAS 98


RESULT 11
US-08-318-157B-17
; Sequence 17, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-17

  Query Match             98.2%;  Score 164;  DB 1;  Length 119;
  Best Local Similarity   96.9%;  Pred. No. 6.3e-16;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 12
US-09-253-794-12
; Sequence 12, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 12:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-253-794-12

  Query Match             98.2%;  Score 164;  DB 2;  Length 119;
  Best Local Similarity   96.9%;  Pred. No. 6.3e-16;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
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                ||||||||:||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 13
US-09-253-794-13
; Sequence 13, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-253-794-13

  Query Match             98.2%;  Score 164;  DB 2;  Length 119;
  Best Local Similarity   96.9%;  Pred. No. 6.3e-16;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
                ||||||||:||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 14
US-09-253-794-15
; Sequence 15, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-253-794-15

  Query Match             98.2%;  Score 164;  DB 2;  Length 119;
  Best Local Similarity   96.9%;  Pred. No. 6.3e-16;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
                ||||||||||||:||||||||||||||||||
Db         67 RFTISRDNAKNTLYLQMDSLRPEDTGVYFCAS 98


RESULT 15
US-09-253-794-17
; Sequence 17, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
```

```
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-253-794-17

  Query Match             98.2%;  Score 164;  DB 2;  Length 119;
  Best Local Similarity   96.9%;  Pred. No. 6.3e-16;
  Matches   31;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:||||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCAS 98


Search completed: March 25, 2006, 09:18:47
Job time : 30.1518 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:55:36 ; Search time 95.4974 Seconds
(without alignments)
140.009 Million cell updates/sec

Title: US-10-755-382-37
Perfect score: 167
Sequence: 1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	167	100.0	32	3	US-09-253-794-37	Sequence 37, Appl
2	167	100.0	32	5	US-10-755-382-37	Sequence 37, Appl
3	167	100.0	118	4	US-10-270-073-3	Sequence 3, Appli
4	167	100.0	119	3	US-09-253-794-14	Sequence 14, Appl
5	167	100.0	119	4	US-10-680-734-14	Sequence 14, Appl
6	167	100.0	119	4	US-10-680-734-17	Sequence 17, Appl
7	167	100.0	119	5	US-10-755-382-14	Sequence 14, Appl
8	167	100.0	138	4	US-10-006-771A-4	Sequence 4, Appli
9	167	100.0	256	4	US-10-270-073-6	Sequence 6, Appli
10	167	100.0	257	4	US-10-270-073-8	Sequence 8, Appli
11	167	100.0	261	4	US-10-270-071-18	Sequence 18, Appl
12	167	100.0	261	4	US-10-270-073-2	Sequence 2, Appli
13	167	100.0	261	4	US-10-328-190-6	Sequence 6, Appli
14	167	100.0	267	4	US-10-270-071-22	Sequence 22, Appl
15	167	100.0	267	4	US-10-270-071-26	Sequence 26, Appl
16	167	100.0	267	4	US-10-270-071-30	Sequence 30, Appl
17	167	100.0	267	4	US-10-270-071-36	Sequence 36, Appl
18	167	100.0	358	5	US-10-829-388-12	Sequence 12, Appl
19	167	100.0	363	5	US-10-829-388-2	Sequence 2, Appli
20	167	100.0	364	5	US-10-829-388-11	Sequence 11, Appl
21	167	100.0	370	5	US-10-829-388-1	Sequence 1, Appli
22	167	100.0	415	4	US-10-328-190-12	Sequence 12, Appl
23	167	100.0	443	4	US-10-006-773-2	Sequence 2, Appli
24	167	100.0	443	4	US-10-006-771A-2	Sequence 2, Appli
25	167	100.0	468	4	US-10-377-109-2	Sequence 2, Appli
26	167	100.0	669	5	US-10-900-928-3	Sequence 3, Appli
27	164	98.2	32	3	US-09-253-794-36	Sequence 36, Appl
28	164	98.2	32	5	US-10-755-382-36	Sequence 36, Appl
29	164	98.2	119	3	US-09-253-794-12	Sequence 12, Appl
30	164	98.2	119	3	US-09-253-794-13	Sequence 13, Appl
31	164	98.2	119	3	US-09-253-794-15	Sequence 15, Appl
32	164	98.2	119	3	US-09-253-794-17	Sequence 17, Appl
33	164	98.2	119	4	US-10-680-734-12	Sequence 12, Appl
34	164	98.2	119	4	US-10-680-734-13	Sequence 13, Appl
35	164	98.2	119	4	US-10-680-734-15	Sequence 15, Appl
36	164	98.2	119	5	US-10-755-382-12	Sequence 12, Appl
37	164	98.2	119	5	US-10-755-382-13	Sequence 13, Appl
38	164	98.2	119	5	US-10-755-382-15	Sequence 15, Appl
39	164	98.2	119	5	US-10-755-382-17	Sequence 17, Appl
40	160	95.8	119	3	US-09-795-515-11	Sequence 11, Appl
41	160	95.8	119	3	US-09-795-515-17	Sequence 17, Appl
42	160	95.8	119	4	US-10-267-286A-12	Sequence 12, Appl
43	160	95.8	119	4	US-10-704-352-11	Sequence 11, Appl
44	160	95.8	119	4	US-10-704-352-17	Sequence 17, Appl
45	160	95.8	119	4	US-10-704-071-11	Sequence 11, Appl

ALIGNMENTS

```
RESULT 1
US-09-253-794-37
; Sequence 37, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 37:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 32 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-253-794-37

  Query Match           100.0%;  Score 167;  DB 3;  Length 32;
  Best Local Similarity  100.0%;  Pred. No. 6.9e-15;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32


RESULT 2
US-10-755-382-37
; Sequence 37, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 37:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 32 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-755-382-37

  Query Match             100.0%;  Score 167;  DB 5;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 6.9e-15;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32


RESULT 3
US-10-270-073-3
; Sequence 3, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14VH deduced amino acid sequence
US-10-270-073-3

  Query Match             100.0%;  Score 167;  DB 4;  Length 118;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 4
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
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;            TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

  Query Match             100.0%;  Score 167;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 5
US-10-680-734-14
; Sequence 14, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-14

  Query Match             100.0%;  Score 167;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
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Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 6
US-10-680-734-17
; Sequence 17, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-17

  Query Match             100.0%;  Score 167;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 7
US-10-755-382-14
; Sequence 14, Application US/10755382
; Publication No. US20050089538A1
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/755,382
;            FILING DATE: 13-Jan-2004
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-755-382-14

  Query Match             100.0%;  Score 167;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         67 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 98


RESULT 8
US-10-006-771A-4
; Sequence 4, Application US/10006771A
; Publication No. US20020165360A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
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;  TITLE OF INVENTION: Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen
;  FILE REFERENCE: 002
;  CURRENT APPLICATION NUMBER: US/10/006,771A
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: 60/250,090
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 138
;   TYPE: PRT
;   ORGANISM: Homo sapiens and Mus sp.
US-10-006-771A-4

  Query Match            100.0%;  Score 167;  DB 4;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         86 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 117


RESULT 9
US-10-270-073-6
; Sequence 6, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14-0 amino acid sequence
US-10-270-073-6

  Query Match            100.0%;  Score 167;  DB 4;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
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Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 10
US-10-270-073-8
; Sequence 8, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 257
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14-1G amino acid sequence
US-10-270-073-8

  Query Match            100.0%;  Score 167;  DB 4;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 11
US-10-270-071-18
; Sequence 18, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of hMN14VK
US-10-270-071-18

  Query Match            100.0%;  Score 167;  DB 4;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 12
US-10-270-073-2
; Sequence 2, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
```

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;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14scFv-L5 amino acid sequence
US-10-270-073-2

  Query Match             100.0%;  Score 167;  DB 4;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 13
US-10-328-190-6
; Sequence 6, Application US/10328190
; Publication No. US20030162709A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID M.
;  TITLE OF INVENTION: METHODS OF GENERATING MULTISPECIFIC, MULTIVALENT AGENTS
;  TITLE OF INVENTION:  FROM VH AND VL DOMAINS
;  FILE REFERENCE: 042418/0115
;  CURRENT APPLICATION NUMBER: US/10/328,190
;  CURRENT FILING DATE:  2003-04-03
;  PRIOR APPLICATION NUMBER: 60/342,103
;  PRIOR FILING DATE: 2001-12-26
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: hMN14-scFv-L5
;   OTHER INFORMATION: protein sequence
US-10-328-190-6

  Query Match             100.0%;  Score 167;  DB 4;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 14
US-10-270-071-22
; Sequence 22, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 267
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of polypeptide 2 of BS1
US-10-270-071-22

  Query Match             100.0%;  Score 167;  DB 4;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


RESULT 15
US-10-270-071-26
; Sequence 26, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
;   LENGTH: 267
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of polypeptide 2 of BS1.5
US-10-270-071-26

  Query Match             100.0%;  Score 167;  DB 4;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 6.7e-14;
  Matches   32;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||||||||||||||||||||||||||
Db         90 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 121


Search completed: March 25, 2006, 10:08:06
Job time : 96.4974 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:58:56 ; Search time 11.5602 Seconds
(without alignments)
81.644 Million cell updates/sec

Title: US-10-755-382-37
Perfect score: 167
Sequence: 1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	160	95.8	119	7	US-11-221-900-12	Sequence 12, Appl
2	160	95.8	126	7	US-11-221-900-11	Sequence 11, Appl
3	160	95.8	449	7	US-11-080-587-6	Sequence 6, Appli
4	155	92.8	236	7	US-11-221-900-2	Sequence 2, Appli
5	152	91.0	116	6	US-10-496-845A-4	Sequence 4, Appli
6	146	87.4	153	7	US-11-267-310-5	Sequence 5, Appli
7	144	86.2	254	7	US-11-054-515-977	Sequence 977, App
8	142	85.0	112	7	US-11-224-623-10	Sequence 10, Appl
9	142	85.0	442	7	US-11-224-623-12	Sequence 12, Appl
10	141	84.4	142	6	US-10-993-543-132	Sequence 132, App
11	141	84.4	240	7	US-11-054-515-1886	Sequence 1886, Ap
12	141	84.4	240	7	US-11-054-515-2052	Sequence 2052, Ap
13	141	84.4	240	7	US-11-054-515-2059	Sequence 2059, Ap
14	141	84.4	240	7	US-11-054-515-2061	Sequence 2061, Ap
15	140	83.8	124	7	US-11-040-159-16	Sequence 16, Appl
16	140	83.8	126	7	US-11-064-174-25	Sequence 25, Appl
17	140	83.8	126	7	US-11-064-174-26	Sequence 26, Appl
18	140	83.8	149	7	US-11-267-310-67	Sequence 67, Appl
19	140	83.8	152	7	US-11-267-310-7	Sequence 7, Appli
20	140	83.8	243	7	US-11-054-515-2057	Sequence 2057, Ap
21	139	83.2	120	6	US-10-925-366A-5	Sequence 5, Appli
22	139	83.2	120	6	US-10-925-366A-280	Sequence 280, App
23	139	83.2	121	7	US-11-049-536-522	Sequence 522, App
24	139	83.2	121	7	US-11-199-739-522	Sequence 522, App
25	139	83.2	122	7	US-11-102-621-1	Sequence 1, Appli
26	139	83.2	122	7	US-11-049-536-186	Sequence 186, App
27	139	83.2	122	7	US-11-199-739-186	Sequence 186, App
28	139	83.2	124	7	US-11-064-174-5	Sequence 5, Appli
29	139	83.2	124	7	US-11-064-174-6	Sequence 6, Appli
30	139	83.2	238	7	US-11-054-515-1931	Sequence 1931, Ap
31	139	83.2	240	7	US-11-054-515-1918	Sequence 1918, Ap
32	139	83.2	240	7	US-11-054-515-2047	Sequence 2047, Ap
33	139	83.2	243	7	US-11-054-515-995	Sequence 995, App
34	138	82.6	98	7	US-11-054-669-33	Sequence 33, Appl
35	138	82.6	98	7	US-11-084-554-47	Sequence 47, Appl
36	138	82.6	98	7	US-11-004-590-37	Sequence 37, Appl
37	138	82.6	98	7	US-11-136-250-47	Sequence 47, Appl
38	138	82.6	116	7	US-11-125-837-38	Sequence 38, Appl
39	138	82.6	118	6	US-10-886-383-1	Sequence 1, Appli
40	138	82.6	120	7	US-11-125-837-26	Sequence 26, Appl
41	138	82.6	121	6	US-10-771-257-20	Sequence 20, Appl
42	138	82.6	121	7	US-11-127-677-20	Sequence 20, Appl
43	138	82.6	124	7	US-11-064-174-2	Sequence 2, Appli
44	138	82.6	124	7	US-11-064-174-3	Sequence 3, Appli
45	138	82.6	124	7	US-11-064-174-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-11-221-900-12
; Sequence 12, Application US/11221900
; Publication No. US20060002933A1
; GENERAL INFORMATION:
; APPLICANT: BLUESTONE, JEFFREY A.
; APPLICANT: ZIVIN, ROBERT A.
; APPLICANT: JOLLIFFE, LINDA K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: TOLT:004USC1
; CURRENT APPLICATION NUMBER: US/11/221,900
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: US/10/267,286
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 08/557,050
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: PCT/US94/06198
; PRIOR FILING DATE: 1994-06-01
; PRIOR APPLICATION NUMBER: 08/070,116
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-221-900-12

Query Match 95.8%; Score 160; DB 7; Length 119;
Best Local Similarity 96.8%; Pred. No. 1.4e-14;
Matches 30; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||:|||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 97
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RESULT 2
US-11-221-900-11
; Sequence 11, Application US/11221900
; Publication No. US20060002933A1
; GENERAL INFORMATION:
; APPLICANT: BLUESTONE, JEFFREY A.

```
;  APPLICANT:  ZIVIN, ROBERT A.
;  APPLICANT:  JOLLIFFE, LINDA K.
;  TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
;  TITLE OF INVENTION:  IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: TOLT:004USC1
;  CURRENT APPLICATION NUMBER: US/11/221,900
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: US/10/267,286
;  PRIOR FILING DATE: 2003-01-28
;  PRIOR APPLICATION NUMBER: 08/557,050
;  PRIOR FILING DATE: 1998-10-09
;  PRIOR APPLICATION NUMBER: PCT/US94/06198
;  PRIOR FILING DATE: 1994-06-01
;  PRIOR APPLICATION NUMBER: 08/070,116
;  PRIOR FILING DATE: 1993-06-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-11-221-900-11

  Query Match             95.8%;  Score 160;  DB 7;  Length 126;
  Best Local Similarity   96.8%;  Pred. No. 1.4e-14;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||:||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 97


RESULT 3
US-11-080-587-6
; Sequence 6, Application US/11080587
; Publication No. US20060002942A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  TITLE OF INVENTION: Calicheamicin Conjugates
;  FILE REFERENCE: AM101462
;  CURRENT APPLICATION NUMBER: US/11/080,587
;  CURRENT FILING DATE:  2005-03-15
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Human/murine chimera
;   FEATURE:
;   OTHER INFORMATION: Human/Murine Chimera G193 Heavy Chain
US-11-080-587-6

  Query Match             95.8%;  Score 160;  DB 7;  Length 449;
  Best Local Similarity   96.8%;  Pred. No. 5.1e-14;
  Matches   30;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||:||||||||||||||||||||||
Db         67 RFTISRDNSKNTLFLQMDSLRPEDTGVYFCA 97


RESULT 4
US-11-221-900-2
; Sequence 2, Application US/11221900
; Publication No. US20060002933A1
; GENERAL INFORMATION:
;  APPLICANT: BLUESTONE, JEFFREY A.
;  APPLICANT:  ZIVIN, ROBERT A.
;  APPLICANT:  JOLLIFFE, LINDA K.
;  TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
;  TITLE OF INVENTION:  IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: TOLT:004USC1
;  CURRENT APPLICATION NUMBER: US/11/221,900
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: US/10/267,286
;  PRIOR FILING DATE: 2003-01-28
;  PRIOR APPLICATION NUMBER: 08/557,050
;  PRIOR FILING DATE: 1998-10-09
;  PRIOR APPLICATION NUMBER: PCT/US94/06198
;  PRIOR FILING DATE: 1994-06-01
;  PRIOR APPLICATION NUMBER: 08/070,116
;  PRIOR FILING DATE: 1993-06-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-11-221-900-2

  Query Match             92.8%;  Score 155;  DB 7;  Length 236;
  Best Local Similarity   93.5%;  Pred. No. 1.3e-13;
  Matches   29;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||||:||| ||||||||||||||||||
Db         86 RFTISRDNSKNTAFLQMDSLRPEDTGVYFCA 116


RESULT 5
US-10-496-845A-4
; Sequence 4, Application US/10496845A
; Publication No. US20060051292A1
; GENERAL INFORMATION:
;  APPLICANT: Mackenzie, Roger C
;  APPLICANT:  Zhang, Jianbing
;  TITLE OF INVENTION: Self-Assembly Molecules
;  FILE REFERENCE: 36361-0038
;  CURRENT APPLICATION NUMBER: US/10/496,845A
;  CURRENT FILING DATE:  2004-05-27
;  PRIOR APPLICATION NUMBER: US 60/334,098
;  PRIOR FILING DATE: 2001-11-30
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 116
;   TYPE: PRT
;   ORGANISM: llama
;   FEATURE:
;   OTHER INFORMATION: none
US-10-496-845A-4

  Query Match             91.0%;  Score 152;  DB 6;  Length 116;
  Best Local Similarity   84.4%;  Pred. No. 1.6e-13;
  Matches   27;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||::||||||:||||||||:||:
Db         67 RFTISRDNAKNTVYLQMDSLKPEDTGVYYCAA 98


RESULT 6
US-11-267-310-5
; Sequence 5, Application US/11267310
; Publication No. US20060037107A1
; GENERAL INFORMATION:
;  APPLICANT: Leo G.J. FRENKEN
;  APPLICANT:  Cornelis P.E. van der LOGT
```

```
;  APPLICANT:  Vin-Miin TEH
;  APPLICANT:  Martine E. VERHOEYEN
;  APPLICANT:  Joy E. WILKINSON
;  APPLICANT:  Stephen A. JOBLING
;  TITLE OF INVENTION: Production of Antibodies
;  FILE REFERENCE: PNK/060113/0275850 - T7060C
;  CURRENT APPLICATION NUMBER: US/11/267,310
;  CURRENT FILING DATE:  2005-11-07
;  PRIOR APPLICATION NUMBER: US/09/737,476
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: EP 99310188.0
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 67
;  SOFTWARE: MS Word
; SEQ ID NO 5
;   LENGTH: 153
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VHH with linker
US-11-267-310-5

  Query Match             87.4%;  Score 146;  DB 7;  Length 153;
  Best Local Similarity   81.2%;  Pred. No. 1.3e-12;
  Matches   26;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||::||||||:|||| ||:||:
Db         66 RFTISRDNAKNTVYLQMDSLKPEDTAVYYCAA 97


RESULT 7
US-11-054-515-977
; Sequence 977, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 977
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-977

  Query Match             86.2%;  Score 144;  DB 7;  Length 254;
  Best Local Similarity   81.2%;  Pred. No. 4e-12;
  Matches   26;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||:||||:|||:|||||| ||:||:
Db         67 RFTISRDNSKNTLYLQMNSLRPEDTAVYYCAT 98


RESULT 8
US-11-224-623-10
; Sequence 10, Application US/11224623
; Publication No. US20060039906A1
; GENERAL INFORMATION:
;  APPLICANT: ELI LILLY AND COMPANY and WASHINGTON UNIVERSITY
;  TITLE OF INVENTION: Humanized Antibodies that Sequester Amyloid Beta Peptide
;  FILE REFERENCE: 8792/293
;  CURRENT APPLICATION NUMBER: US/11/224,623
;  CURRENT FILING DATE:  2005-09-12
;  PRIOR APPLICATION NUMBER: US/10/226,435
;  PRIOR FILING DATE: 2002-11-13
;  PRIOR APPLICATION NUMBER: PCT/US01/06191
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: 60/184,601
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/254,465
;  PRIOR FILING DATE: 2000-12-08
;  PRIOR APPLICATION NUMBER: 60/254,498
;  PRIOR FILING DATE: 2000-12-08
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 112
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Humanized antibodies
US-11-224-623-10

  Query Match             85.0%;  Score 142;  DB 7;  Length 112;
  Best Local Similarity   84.4%;  Pred. No. 3.3e-12;
  Matches   27;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||:|||:||| ||| ||:|||
Db         67 RFTISRDNAKNTLYLQMNSLRAEDTAVYYCAS 98


RESULT 9
US-11-224-623-12
; Sequence 12, Application US/11224623
; Publication No. US20060039906A1
; GENERAL INFORMATION:
;  APPLICANT: ELI LILLY AND COMPANY and WASHINGTON UNIVERSITY
;  TITLE OF INVENTION: Humanized Antibodies that Sequester Amyloid Beta Peptide
;  FILE REFERENCE: 8792/293
;  CURRENT APPLICATION NUMBER: US/11/224,623
;  CURRENT FILING DATE:  2005-09-12
;  PRIOR APPLICATION NUMBER: US/10/226,435
;  PRIOR FILING DATE: 2002-11-13
;  PRIOR APPLICATION NUMBER: PCT/US01/06191
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: 60/184,601
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: 60/254,465
;  PRIOR FILING DATE: 2000-12-08
;  PRIOR APPLICATION NUMBER: 60/254,498
;  PRIOR FILING DATE: 2000-12-08
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
;   LENGTH: 442
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Humanized antibodies
US-11-224-623-12
```

```
  Query Match             85.0%;  Score 142;  DB 7;  Length 442;
  Best Local Similarity   84.4%;  Pred. No. 1.3e-11;
  Matches   27;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||||||||:|||:||| ||| ||:|||
Db         67 RFTISRDNAKNTLYLQMNSLRAEDTAVYYCAS 98


RESULT 10
US-10-993-543-132
; Sequence 132, Application US/10993543
; Publication No. US20060036076A1
; GENERAL INFORMATION:
;  APPLICANT: Dransfield, Daniel T.
;  APPLICANT:  Rookey, Kristin
;  APPLICANT:  Ladner, Robert C.
;  TITLE OF INVENTION: Metalloproteinase-Binding Proteins
;  FILE REFERENCE: 10280-088001
;  CURRENT APPLICATION NUMBER: US/10/993,543
;  CURRENT FILING DATE:  2004-11-19
;  PRIOR APPLICATION NUMBER: US 60/523,745
;  PRIOR FILING DATE: 2003-11-19
;  NUMBER OF SEQ ID NOS: 299
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 132
;   LENGTH: 142
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-993-543-132

  Query Match             84.4%;  Score 141;  DB 6;  Length 142;
  Best Local Similarity   83.9%;  Pred. No. 5.6e-12;
  Matches   26;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              ||||||||:||||:|||:||| |||||||:||
Db         67 RFTISRDNSKNTLYLQMNSLRAEDTGVYYCA 97


RESULT 11
US-11-054-515-1886
; Sequence 1886, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1886
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1886

  Query Match             84.4%;  Score 141;  DB 7;  Length 240;
  Best Local Similarity   78.1%;  Pred. No. 9.5e-12;
  Matches   25;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||::|||::|||||| ||:|||
Db         67 RFTISRDNSKNTVYLQMNNLRPEDTAVYYCAS 98


RESULT 12
US-11-054-515-2052
; Sequence 2052, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2052
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-2052

  Query Match             84.4%;  Score 141;  DB 7;  Length 240;
  Best Local Similarity   78.1%;  Pred. No. 9.5e-12;
  Matches   25;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              ||||||||:|||::|||::|||||| ||:|||
Db         67 RFTISRDNSKNTVYLQMNNLRPEDTAVYYCAS 98


RESULT 13
US-11-054-515-2059
; Sequence 2059, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
```

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;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2059
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-2059

  Query Match             84.4%;  Score 141;  DB 7;  Length 240;
  Best Local Similarity   78.1%;  Pred. No. 9.5e-12;
  Matches   25;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||:|||::|||::|||||| ||:|||
Db         67 RFTISRDNSKNTVYLQMNNLRPEDTAVYYCAS 98


RESULT 14
US-11-054-515-2061
; Sequence 2061, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2061
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-2061

  Query Match             84.4%;  Score 141;  DB 7;  Length 240;
  Best Local Similarity   78.1%;  Pred. No. 9.5e-12;
  Matches   25;  Conservative    6;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCAS 32
              |||||||:|||::|||::|||||| ||:|||
Db         67 RFTISRDNSKNTVYLQMNNLRPEDTAVYYCAS 98


RESULT 15
US-11-040-159-16
; Sequence 16, Application US/11040159
; Publication No. US20050255552A1
; GENERAL INFORMATION:
;  APPLICANT: Flynn, Peter
;  APPLICANT:  Luehrsen, Kenneth
;  APPLICANT:  Balint, Robert F.
;  APPLICANT:  Her, Jeng-Horng
;  APPLICANT:  Bebbington, Christopher R.
;  APPLICANT:  Yarranton, Geoffrey T.
;  APPLICANT:  KaloBios, Inc.
;  TITLE OF INVENTION: Antibody Specificity Transfer Using Minimal Essential
;  TITLE OF INVENTION:  Binding Determinants
;  FILE REFERENCE: 021167-001730US
;  CURRENT APPLICATION NUMBER: US/11/040,159
;  CURRENT FILING DATE:  2005-01-20
;  PRIOR APPLICATION NUMBER: US 60/537,364
;  PRIOR FILING DATE: 2004-01-20
;  PRIOR APPLICATION NUMBER: US 60/546,216
;  PRIOR FILING DATE: 2004-02-23
;  NUMBER OF SEQ ID NOS: 133
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 124
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:V-region of
;   OTHER INFORMATION: anti-PcrV antibody 1F1 VH
US-11-040-159-16

  Query Match             83.8%;  Score 140;  DB 7;  Length 124;
  Best Local Similarity   80.6%;  Pred. No. 6.7e-12;
  Matches   25;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 RFTISRDNAKNTLFLQMDSLRPEDTGVYFCA 31
              |||||||:||||:|:|:|||||| ||:||
Db         67 RFTISRDNSKNTLYLEMNSLRPEDTAVYYCA 97


Search completed: March 25, 2006, 10:09:20
Job time : 11.5602 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:10 ; Search time 40.5445 Seconds
(without alignments)
119.206 Million cell updates/sec

Title: US-10-755-382-39
Perfect score: 61
Sequence: 1 WGQGTPVTVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	61	100.0	11	2	AAR97332	Aar97332 Humanised
2	61	100.0	11	9	AEA45801	Aea45801 Apolipopr
3	61	100.0	117	2	AAR38612	Aar38612 KOL heavy
4	61	100.0	117	2	AAR77305	Aar77305 Variable
5	61	100.0	117	2	AAW13532	Aaw13532 Anti-mela
6	61	100.0	117	2	AAW10230	Aaw10230 CDR-graft
7	61	100.0	117	2	AAW10228	Aaw10228 CDR-graft
8	61	100.0	119	2	AAR67449	Aar67449 OKT3 huma
9	61	100.0	119	2	AAR75224	Aar75224 OKT3 huma
10	61	100.0	119	2	AAR67447	Aar67447 OKT3 huma
11	61	100.0	119	2	AAR82964	Aar82964 3S193HuVH
12	61	100.0	119	2	AAR82965	Aar82965 3S193HuVH
13	61	100.0	119	2	AAR82966	Aar82966 3S193HuVH
14	61	100.0	119	2	AAR82962	Aar82962 Humanised
15	61	100.0	119	2	AAW11919	Aaw11919 Humanised
16	61	100.0	119	2	AAR82982	Aar82982 LK26 huma
17	61	100.0	119	2	AAR97336	Aar97336 Humanised
18	61	100.0	119	2	AAW13514	Aaw13514 Anti-mela
19	61	100.0	119	2	AAW73531	Aaw73531 Humanised
20	61	100.0	119	2	AAW73529	Aaw73529 Humanised
21	61	100.0	119	8	ADM95101	Adm95101 Humanised
22	61	100.0	119	8	ADM98324	Adm98324 Humanised
23	61	100.0	119	8	ADR48645	Adr48645 Novel bis
24	61	100.0	119	8	ADW14396	Adw14396 Human Flt
25	61	100.0	119	8	ADW69664	Adw69664 Humanized
26	61	100.0	119	9	ADX37189	Adx37189 Human SM5
27	61	100.0	119	9	ADX37181	Adx37181 SM5-1 hum
28	61	100.0	119	9	AEA88706	Aea88706 Human ant
29	61	100.0	119	9	AEA88698	Aea88698 Humanized
30	61	100.0	120	2	AAR54930	Aar54930 Fc recept
31	61	100.0	122	2	AAR04135	Aar04135 Anti-Leu
32	61	100.0	122	2	AAW23437	Aaw23437 Modified
33	61	100.0	122	2	AAW23441	Aaw23441 hWI2 heav
34	61	100.0	122	2	AAW23438	Aaw23438 Modified
35	61	100.0	122	8	ADI22091	Adi22091 Anti-plat
36	61	100.0	124	4	AAB62750	Aab62750 Human HIV
37	61	100.0	124	8	ADP09946	Adp09946 Anti-mous
38	61	100.0	124	8	ADO25696	Ado25696 Anti-TNF-
39	61	100.0	125	4	AAU02614	Aau02614 Anti-adip
40	61	100.0	125	9	AEA24165	Aea24165 Anti-HAAH
41	61	100.0	126	2	AAR28746	Aar28746 Heavy cha
42	61	100.0	126	2	AAR38613	Aar38613 KOL heavy
43	61	100.0	126	2	AAW13534	Aaw13534 Anti-mela
44	61	100.0	126	2	AAW58489	Aaw58489 Human KOL
45	61	100.0	126	2	AAW73527	Aaw73527 Humanised

ALIGNMENTS

RESULT 1
AAR97332
ID AAR97332 standard; peptide; 11 AA.
XX
AC AAR97332;
XX
DT 15-OCT-1996 (first entry)
XX
DE Humanised monoclonal antibody heavy chain framework region.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Homo sapiens.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Claim 7; Page 40; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. This sequence corresponds to the fourth framework region of the
CC heavy chain of the humanised MAb. See AAR97313-97333

XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTPVTVSS 11
||||||||||||
Db 1 WGQGTPVTVSS 11

RESULT 2
AEA45801
ID AEA45801 standard; peptide; 11 AA.
XX
AC AEA45801;
XX
DT 11-AUG-2005 (first entry)
XX
DE Apolipoprotein E C-terminal domain antibody VH-FR4 peptide #3.
XX
KW Neuroprotective; Nootropic; Antidiabetic; Endocrine-Gen.; Nephrotropic;
KW Antiparkinsonian; Anticonvulsant; Respiratory-Gen; Apolipoprotein E;
KW Alzheimers disease; amyloidosis; Parkinsons disease; Huntingtons chorea;
KW Kuru; Dementia; non-insulin dependent diabetes; Down syndrome;
KW Spongiform encephalopathy; Creutzfeldt Jakob disease;
KW motor neurone disease; chronic obstructive pulmonary disease.
XX
OS Homo sapiens.
XX
PN GB2408508-A.
XX
PD 01-JUN-2005.
XX
PF 26-NOV-2004; 2004GB-00026043.
XX
PR 28-NOV-2003; 2003US-0525174P.
XX
PA (ASTR) ASTRAZENECA AB.
PA (DYAX-) DYAX CORP.
XX
PI Nordstedt C, Goldschmidt T, Henderikx M, Hoet R, Hoogenboom H;
PI Hufton S, Andersson CV, Lindquist J, Sunnemark D, Leonov S;
XX
DR WPI; 2005-408785/42.
XX
PT New human antibody or antibody fragment which binds to a sequence of the
PT C-terminal domain of Apolipoprotein E (ApoE-CTD), useful for
PT manufacturing a medicament for treating or preventing an amyloid disorder
PT e.g. Alzheimers disease.
XX
PS Example 8; Page 102; 392pp; English.
XX
CC The present invention relates to a human antibody or antibody fragment,
CC which binds to the C-terminal domain of Apolipoprotein E (ApoE-CTD;
CC AEA44803) and also to human plaques. The antibody or its fragment is
CC useful for manufacturing a medicament for treating or preventing an
CC amyloid disorder such as Alzheimers disease, primary systemic
CC amyloidosis, secondary systemic amyloidosis, senile systemic amyloidosis,
CC familial amyloid polyneuropathy I, familial amyloid polyneuropathy III,
CC familial non-neuropathic amyloidosis, hereditary cerebral amyloid
CC angiopathy, Familial British Dementia, Hemodialysis-related amyloidosis,
CC Familial amyloidosis (Finnish type), Familial subepithelial corneal
CC amyloid, type II diabetes, Hereditary renal amyloidosis, Pituitary-gland
CC amyloidosis, injection localized amyloidosis, Medullary carcinoma of the
CC thyroid, Atrial amyloidosis, Familial Danish dementia (FDD), Downs
CC syndrome, Spongiform encephalopathies, Sporadic Creutzfeldt-Jakob
CC disease, Gerstmann-Straussler-Scheinker Disease (GSS), Kuru, Parkinsons
CC disease, Huntingtons disease, Familial amyotrophic lateral sclerosis, and
CC chronic obstructive pulmonary disease. The present sequence was used to
CC illustrate the invention.
XX

SQ Sequence 11 AA;

Query Match 100.0%; Score 61; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTPVTVSS 11
||||||||||||
Db 1 WGQGTPVTVSS 11

RESULT 3
AAR38612
ID AAR38612 standard; peptide; 117 AA.
XX
AC AAR38612;
XX
DT 25-MAR-2003 (revised)
DT 28-OCT-1993 (first entry)
XX
DE KOL heavy chain.
XX
KW Antibody; variable domain; light; L; heavy; H; consensus; affinity;
KW antigen; immunogenicity; humanisation; framework.
XX
OS Homo sapiens.
XX
PN WO9311794-A1.
XX
PD 24-JUN-1993.
XX
PF 14-DEC-1992; 92WO-US010906.
XX
PR 13-DEC-1991; 91US-00808464.
XX
PA (XOMA) XOMA CORP.
XX
PI Studnicka GM, Little RG, Fishwild DM, Kohn FR;
XX
DR WPI; 1993-213827/26.
XX
PT Antibodies prepn. used for treatment of auto-immune diseases - by
PT replacement of critical residues to reduce immunogenicity but retain
PT binding affinity, etc.
XX
PS Disclosure; Fig 1B; 160pp; English.
XX
CC The amino acid sequences of the light and heavy chains of the variable
CC domains from antibodies HYH [HYHEL-10 Fab-lysosyme complex] (AAR38601 and
CC AAR38608, respectively), MCPC [IgA Fab MCPC603-phosphocholine complex]
CC (AAR38602-03 and AAR38609-10, respectively), NEWM [Ig Fab' NEW] (AAR38604
CC -05 and AAR38611, respectively) and KOL [IgG1 KOL] (AAR38606-07 and
CC AAR38612, respectively) may be used to determine an alignment from which
CC appropriate changes may be made. Unlike other methods of humanisation,
CC which advocate the replacement of entire antibody framework regions with
CC those of human antibodies, this method involves only the introduction of
CC human residues into those positions not critical for antigen binding.
CC This ensures that the binding properties of the modified antibody are not
CC diminished. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 117 AA;

Query Match 100.0%; Score 61; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTPVTVSS 11
||||||||||||
Db 107 WGQGTPVTVSS 117

RESULT 4
AAR77305

```
ID   AAR77305 standard; peptide; 117 AA.
XX
AC   AAR77305;
XX
DT   25-MAR-2003  (revised)
DT   23-NOV-1995  (first entry)
XX
DE   Variable heavy chain sequence of humanised antibody chain TM29 VH.
XX
KW   Humanised antibody; TM29; T cell; Crohn's disease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          31. .35
FT                   /label= CDR1
FT   Region          50. .66
FT                   /label= CDR2
FT   Region          99. .106
FT                   /label= CDR3
XX
PN   WO9516038-A2.
XX
PD   15-JUN-1995.
XX
PF   21-NOV-1994;   94WO-IB000387.
XX
PR   08-DEC-1993;   93GB-00025182.
XX
PA   (TCEL-) T CELL SCI INC.
PA   (MERC/) MERCER C P.
XX
PI   Lin A;
XX
DR   WPI; 1995-224322/29.
XX
PT   Humanised antibody specific for select sub-population of T cells - useful
PT   for treatment of Crohn's disease and Multiple Sclerosis.
XX
PS   Claim 5; Page 82; 92pp; English.
XX
CC   A mouse monoclonal antibody (mAb), 16G8, which recognises human V beta
CC   8.1, was humanised by CDR grafting certain CDR and select framework
CC   residues from the murine mAb into KOL heavy chain and REI light chain
CC   frameworks. The cDNAs encoding humanised heavy (IgG1) and light (k)
CC   chains in mammamlian cell expression vectors with Neo and DHFR selection
CC   markers, respectively, were transfected into a DHFR- Chinese hamster
CC   fibroblast (CHO) cell line followed by selection and amplification. The
CC   humanised MAb that was secreted, designated "TM29", maintains the
CC   specificity for human TCR V beta 8.1. It is used as a therapeutic agent
CC   for Crohn's disease. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 117 AA;

  Query Match             100.0%;  Score 61;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db        107 WGQGTPVTVSS 117


RESULT 5
AAW13532
ID   AAW13532 standard; protein; 117 AA.
XX
AC   AAW13532;
XX
DT   28-OCT-1997  (first entry)
XX
DE   Anti-melanoma antibody C55 from VH antibody fusion phage library.
XX
KW   Human; monoclonal antitumour antibody; peripheral blood lymphocyte;
KW   cancer; tumourigenesis; anticancer vaccine.
XX
OS   Homo sapiens.
XX
PN   WO9702479-A2.
XX
PD   23-JAN-1997.
XX
PF   28-JUN-1996;   96WO-IB001032.
XX
PR   30-JUN-1995;   95US-00497647.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Garen A,  Cai X;
XX
DR   WPI; 1997-109061/10.
XX
PT   Prodn. of human monoclonal anti-tumour antibodies - by screening a fusion
PT   phage library produced using peripheral blood lymphocytes from a cancer
PT   patient.
XX
PS   Claim 19; Page 71; 82pp; English.
XX
CC   A process for isolating and synthesising human monoclonal anti-tumour
CC   antibodies has been produced. The process involves: (a) constructing at
CC   least one fusion phage library from the peripheral blood lymphocytes
CC   (PBLs) of a cancer patient; (b) screening for anti-tumour antibodies in
CC   the phage library in a binding assay with cultured tumour cells of the
CC   same type as the patient's tumour; (c) removing extraneous antibodies by
CC   absorption against normal human cells; (d) cloning the phage selected in
CC   step (b) and (c); (e) assaying the specificity of the cloned phage by
CC   incubating the phage with at least two types of cultured normal cells;
CC   and (f) further testing the specificity of cloned phage that do not bind
CC   to either cell line of cultured normal cells in further binding assays to
CC   cultured tumour cells derived from more than one other tumour that is not
CC   the patient's tumour. The present sequence represents a human heavy chain
CC   antibody, from a VH antibody fusion phage library, produced by a method
CC   as described above. The antibodies produced can be used for diagnostic
CC   and therapeutic applications and for isolating tumour antigens for
CC   studying tumourigenesis or for use as anti-cancer vaccines. The human
CC   antibodies have low immunogenicity in humans compared to murine
CC   monoclonal antibodies (MAbs). Since the antibodies are isolated from
CC   fusion phage libraries, their affinity and specificity for a tumour cell
CC   line can be improved by genetic manipulations
XX
SQ   Sequence 117 AA;

  Query Match             100.0%;  Score 61;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db        107 WGQGTPVTVSS 117


RESULT 6
AAW10230
ID   AAW10230 standard; protein; 117 AA.
XX
AC   AAW10230;
XX
DT   17-OCT-2003  (revised)
DT   01-APR-1997  (first entry)
XX
DE   CDR-grafted heavy chain variable region TF8HCDR20.
XX
KW   Tissue factor; complementarity determining region; CDR;
KW   humanised antibody; monoclonal antibody; TF8-5G9; coagulation;
KW   thrombosis; restenosis; arteriosclerosis; therapy.
XX
```

```
OS   Mus; sp.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .30
FT                   /label= KOH_framework
FT                   /note= "human KOH framework"
FT   Misc-difference 23
FT                   /note= "murine residue is retained at position 23"
FT   Misc-difference 24
FT                   /note= "murine residue is retained at position 24"
FT   Misc-difference 28
FT                   /note= "murine residue is retained at position 28"
FT   Misc-difference 29
FT                   /note= "murine residue is retained at position 29"
FT   Misc-difference 30
FT                   /note= "murine residue is retained at position 30"
FT   Region          31. .35
FT                   /label= CDR1
FT                   /note= "murine TF8-5G9 CDR1"
FT   Region          36. .49
FT                   /label= KOH_framework
FT                   /note= "human KOH framework"
FT   Misc-difference 48
FT                   /note= "murine residue is retained at position 48"
FT   Misc-difference 49
FT                   /note= "murine residue is retained at position 49"
FT   Region          50. .67
FT                   /label= CDR2
FT                   /note= "mouse TF8-5G9 CDR2"
FT   Region          68. .98
FT                   /label= KOH_framework
FT                   /note= "human KOH framework"
FT   Misc-difference 71
FT                   /note= "murine residue is retained at position 71"
FT   Misc-difference 88
FT                   /note= "murine residue is retained at position 88"
FT   Misc-difference 91
FT                   /note= "murine residue is retained at position 91"
FT   Region          99. .106
FT                   /label= CDR3
FT                   /note= "murine TF8-5G9 CDR3"
FT   Region          107. .117
FT                   /label= KOH_framework
FT                   /note= "human KOH framework"
XX
PN   WO9640921-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US009287.
XX
PR   07-JUN-1995;   95US-00480120.
XX
PA   (JOHJ ) JOHNSON & JOHNSON.
XX
PI   Joliffe LK,  Zivin RA,  Pulito VL;
XX
DR   WPI; 1997-099935/09.
XX
PT   CDR-grafted antibody capable of inhibiting human tissue factor - used in
PT   the treatment of thrombotic disorders, e.g.intravascular coagulation,
PT   arterial restenosis etc.
XX
PS   Claim 9; Page 72; 142pp; English.
XX
CC   CDR-grafted heavy chain variable regions TF8HCDR20 (AAW10230) and
CC   TF8HCDR1 (AAW10228) each have heavy chain CDRs (see also AAW10222-24) of
CC   mouse anti-tissue factor monoclonal antibody TF8-5G9 grafted into a human
CC   KOL antibody framework. They can be used with CDR- grafted light chain
CC   variable regions (AAW10229, AAW10231") and human constant regions to
CC   prepare humanised antibodies that inhibit human tissue factor (see also
CC   AAW10232-33). Such antibodies can be used to treat e.g. intravascular
CC   coagulation, arterial restenosis and arteriosclerosis. (Updated on 17-OCT
CC   -2003 to standardise OS field)
XX
SQ   Sequence 117 AA;

  Query Match             100.0%;  Score 61;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||||
Db        107 WGQGTPVTVSS 117


RESULT 7
AAW10228
ID   AAW10228 standard; protein; 117 AA.
XX
AC   AAW10228;
XX
DT   17-OCT-2003  (revised)
DT   01-APR-1997  (first entry)
XX
DE   CDR-grafted heavy chain variable region TF8HCDR1.
XX
KW   Tissue factor; complementarity determining region; CDR;
KW   humanised antibody; monoclonal antibody; TF8-5G9; coagulation;
KW   thrombosis; restenosis; arteriosclerosis; therapy.
XX
OS   Mus; sp.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .30
FT                   /label= KOH_framework
FT                   /note= "human KOH framework"
FT   Misc-difference 6
FT                   /note= "murine residue is retained at position 7"
FT   Misc-difference 17
FT                   /note= "murine residue is retained at position 17"
FT   Misc-difference 23
FT                   /note= "murine residue is retained at position 23"
FT   Misc-difference 24
FT                   /note= "murine residue is retained at position 24"
FT   Misc-difference 28
FT                   /note= "murine residue is retained at position 28"
FT   Misc-difference 29
FT                   /note= "murine residue is retained at position 29"
FT   Misc-difference 30
FT                   /note= "murine residue is retained at position 30"
FT   Region          31. .35
FT                   /label= CDR1
FT                   /note= "murine TF8-5G9 CDR1"
FT   Region          36. .49
FT                   /label= KOH_framework
FT                   /note= "human KOH framework"
FT   Misc-difference 48
FT                   /note= "murine residue is retained at position 48"
FT   Misc-difference 49
FT                   /note= "murine residue is retained at position 49"
FT   Region          50. .67
FT                   /label= CDR2
FT                   /note= "mouse TF8-5G9 CDR2"
FT   Region          68. .98
FT                   /label= KOH_framework
FT                   /note= "human KOH framework"
FT   Misc-difference 68
FT                   /note= "murine residue is retained at position 68"
FT   Misc-difference 71
FT                   /note= "murine residue is retained at position 71"
FT   Misc-difference 73
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FT                   /note= "murine residue is retained at position 73"
FT   Misc-difference 78
FT                   /note= "murine residue is retained at position 78"
FT   Misc-difference 88
FT                   /note= "murine residue is retained at position 88"
FT   Misc-difference 91
FT                   /note= "murine residue is retained at position 91"
FT   Region          99. .106
FT                   /label= CDR3
FT                   /note= "murine TF8-5G9 CDR3"
FT   Region          107. .117
FT                   /label= KOH_framework
FT                   /note= "human KOH framework"
XX
PN   WO9640921-A1.
XX
PD   19-DEC-1996.
XX
PF   06-JUN-1996;   96WO-US009287.
XX
PR   07-JUN-1995;   95US-00480120.
XX
PA   (JOHJ ) JOHNSON & JOHNSON.
XX
PI   Joliffe LK,  Zivin RA,  Pulito VL;
XX
DR   WPI; 1997-099935/09.
XX
PT   CDR-grafted antibody capable of inhibiting human tissue factor - used in
PT   the treatment of thrombotic disorders, e.g.intravascular coagulation,
PT   arterial restenosis etc.
XX
PS   Claim 7; Page 70-71; 142pp; English.
XX
CC   CDR-grafted heavy chain variable regions TF8HCDR1 (AAW10228) and
CC   TF8HCDR20 (AAW10230) each have heavy chain CDRs (see also AAW10222-24) of
CC   mouse anti-tissue factor monoclonal antibody TF8-5G9 grafted into a human
CC   KOL antibody framework. They can be used with CDR- grafted light chain
CC   variable regions (AAW10229, ") and human constant regions to prepare
CC   humanised antibodies that inhibit human tissue factor (see also AAW10232-
CC   33). Such antibodies can be used to treat e.g. intravascular coagulation,
CC   arterial restenosis and arteriosclerosis. (Updated on 17-OCT-2003 to
CC   standardise OS field)
XX
SQ   Sequence 117 AA;

  Query Match             100.0%;  Score 61;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db        107 WGQGTPVTVSS 117


RESULT 8
AAR67449
ID   AAR67449 standard; protein; 119 AA.
XX
AC   AAR67449;
XX
DT   16-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   08-JUL-1995  (first entry)
XX
DE   OKT3 humanized antibody heavy chain variable region (gHA).
XX
KW   OKT3; humanized antibody; 3C10; antibody engineering; immunosuppressive;
KW   monoclonal antibody.
XX
OS   Mus musculus.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          6
FT                   /note= "mouse residue"
FT   Region          23. .24
FT                   /note= "mouse residues"
FT   Region          27. .28
FT                   /note= "mouse residues"
FT   Region          29. .35
FT                   /note= "CDR region of 3C10 heavy chain"
FT   Region          30
FT                   /note= "mouse residue"
FT   Region          47. .48
FT                   /note= "mouse residues"
FT   Region          50. .66
FT                   /note= "CDR region of 3C10 heavy chain"
FT   Region          72
FT                   /note= "mouse residue"
FT   Region          74
FT                   /note= "mouse residue"
FT   Region          77
FT                   /note= "mouse residue"
FT   Region          79
FT                   /note= "mouse residue"
FT   Region          92
FT                   /note= "mouse residue"
FT   Region          95
FT                   /note= "mouse residue"
FT   Region          99. .108
FT                   /note= "CDR region of 3C10 heavy chain"
XX
PN   WO9428027-A1.
XX
PD   08-DEC-1994.
XX
PF   01-JUN-1994;   94WO-US006198.
XX
PR   01-JUN-1993;   93US-00070116.
XX
PA   (ARCH-) ARCH DEV CORP.
XX
PI   Bluestone JA,  Zivin RA,  Jolliffe L;
XX
DR   WPI; 1995-022721/03.
XX
PT   New humanised OKT3 antibody with mutated Fc receptor binding region -
PT   useful as immunosuppressant to reduce transplant rejection, lacks the T-
PT   cell activating side effects of wild type antibody.
XX
PS   Disclosure; Page 98-99; 135pp; English.
XX
CC   The anti-human CD3 mouse monoclonal antibody OKT3 (IgG2a) can be
CC   engineered to contain a human Fc region. By transferring the binding
CC   specificity into a human framework, the immunogenicity is reduced without
CC   affecting the immunosuppressive activity. (Updated on 25-MAR-2003 to
CC   correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 61;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db        109 WGQGTPVTVSS 119


RESULT 9
AAR75224
ID   AAR75224 standard; protein; 119 AA.
XX
AC   AAR75224;
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XX
DT   16-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   08-JUL-1995  (first entry)
XX
DE   OKT3 humanized antibody heavy chain variable region (gHG).
XX
KW   OKT3; humanized antibody; 3C10; antibody engineering; immunosuppressive;
KW   monoclonal antibody.
XX
OS   Mus musculus.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          6
FT                   /note= "mouse residue"
FT   Region          23. .24
FT                   /note= "mouse residues"
FT   Region          27. .28
FT                   /note= "mouse residues"
FT   Region          29. .35
FT                   /note= "CDR region of 3C10 heavy chain"
FT   Region          30
FT                   /note= "mouse residue"
FT   Region          47. .48
FT                   /note= "mouse residues"
FT   Region          50. .66
FT                   /note= "CDR region of 3C10 heavy chain"
FT   Region          79
FT                   /note= "mouse residue"
FT   Region          99. .108
FT                   /note= "CDR region of 3C10 heavy chain"
XX
PN   WO9428027-A1.
XX
PD   08-DEC-1994.
XX
PF   01-JUN-1994;   94WO-US006198.
XX
PR   01-JUN-1993;   93US-00070116.
XX
PA   (ARCH-) ARCH DEV CORP.
XX
PI   Bluestone JA,  Zivin RA,  Jolliffe L;
XX
DR   WPI; 1995-022721/03.
XX
PT   New humanised OKT3 antibody with mutated Fc receptor binding region -
PT   useful as immunosuppressant to reduce transplant rejection, lacks the T-
PT   cell activating side effects of wild type antibody.
XX
PS   Disclosure; Page 98-99; 135pp; English.
XX
CC   The anti-human CD3 mouse monoclonal antibody OKT3 (IgG2a) can be
CC   engineered to contain a human Fc region. By transferring the binding
CC   specificity into a human framework, the immunogenicity is reduced without
CC   affecting the immunosuppressive activity. (Updated on 25-MAR-2003 to
CC   correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 61;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||
Db        109 WGQGTPVTVSS 119


RESULT 10
AAR67447
ID   AAR67447 standard; protein; 119 AA.
XX
AC   AAR67447;
XX
DT   16-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   08-JUL-1995  (first entry)
XX
DE   OKT3 humanized antibody heavy chain variable region (gH).
XX
KW   OKT3; humanized antibody; 3C10; antibody engineering; immunosuppressive;
KW   monoclonal antibody.
XX
OS   Mus musculus.
OS   Homo sapiens.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          29. .35
FT                   /note= "CDR region of 3C10 heavy chain"
FT   Region          50. .66
FT                   /note= "CDR region of 3C10 heavy chain"
FT   Region          99. .108
FT                   /note= "CDR region of 3C10 heavy chain"
XX
PN   WO9428027-A1.
XX
PD   08-DEC-1994.
XX
PF   01-JUN-1994;   94WO-US006198.
XX
PR   01-JUN-1993;   93US-00070116.
XX
PA   (ARCH-) ARCH DEV CORP.
XX
PI   Bluestone JA,  Zivin RA,  Jolliffe L;
XX
DR   WPI; 1995-022721/03.
XX
PT   New humanised OKT3 antibody with mutated Fc receptor binding region -
PT   useful as immunosuppressant to reduce transplant rejection, lacks the T-
PT   cell activating side effects of wild type antibody.
XX
PS   Disclosure; Page 98-99; 135pp; English.
XX
CC   The anti-human CD3 mouse monoclonal antibody OKT3 (IgG2a) can be
CC   engineered to contain a human Fc region. By transferring the binding
CC   specificity into a human framework, the immunogenicity is reduced without
CC   affecting the immunosuppressive activity. (Updated on 25-MAR-2003 to
CC   correct PN field.) (Updated on 16-OCT-2003 to standardise OS field)
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 61;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||
Db        109 WGQGTPVTVSS 119


RESULT 11
AAR82964
ID   AAR82964 standard; protein; 119 AA.
XX
AC   AAR82964;
XX
DT   21-MAR-1996  (first entry)
XX
DE   3S193HuVHA humanised 3S193 heavy chain variable region.
XX
KW   Humanised antibody; Lewis Y antigen; monoclonal antibody 3S193;
```

```
KW   recombinant antibody; antibody engineering; heavy chain; CDR;
KW   complementarity determining region; cancer; diagnosis; therapy.
XX
OS   Synthetic.
XX
PN   WO9524484-A1.
XX
PD   14-SEP-1995.
XX
PF   08-MAR-1995;   95WO-US003096.
XX
PR   08-MAR-1994;   94US-00207861.
XX
PA   (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Wallace TP,  Harris WJ,  Carr FJ,  Old LJ,  Stockert E,  Welt S;
PI   Kitamura K,  Garin-Chesa P;
XX
DR   WPI; 1995-328275/42.
XX
PT   Recombinant humanised anti-Lewis Y antibody - has increased binding
PT   affinity and is used in the detection of cancer cells expressing Lewis Y
PT   antigen.
XX
PS   Example 4; Page 33; 48pp; English.
XX
CC   Primers (AAT05001-02) based on the murine IgG3 and kappa constant region
CC   genes, respectively, were used to produce cDNA from cytoplasmic RNA
CC   isolated from anti-Lewis Y antibody 3S192-producing hybridomas. The cDNA
CC   was amplified by PCR using primers (AAT05003-05) based on murine VH, V-
CC   kappa and heavy chain signal sequences to obtain clones coding for the
CC   3S192 heavy and light chain variable regions (AAT04997-98). CK2FOR (see
CC   AAT05002) primed DNA was amplified by PCR using primers (AAT05006-7)
CC   based on the framework 4 region of the clone shown in AAT04997. The
CC   amplified DNA lead to the isolation of the 3S193 clone (AAT04998), which
CC   was subjected to site directed mutagenisis to produce the sequences shown
CC   in AAR82964-8
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 61;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| |
Db        109 WGQGTPVTVSS 119


RESULT 12
AAR82965
ID   AAR82965 standard; protein; 119 AA.
XX
AC   AAR82965;
XX
DT   21-MAR-1996  (first entry)
XX
DE   3S193HuVHAS humanised 3S193 heavy chain variable region.
XX
KW   Humanised antibody; Lewis Y antigen; monoclonal antibody 3S193;
KW   recombinant antibody; antibody engineering; heavy chain; CDR;
KW   complementarity determining region; cancer; diagnosis; therapy.
XX
OS   Synthetic.
XX
PN   WO9524484-A1.
XX
PD   14-SEP-1995.
XX
PF   08-MAR-1995;   95WO-US003096.
XX
PR   08-MAR-1994;   94US-00207861.
XX
PA   (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Wallace TP,  Harris WJ,  Carr FJ,  Old LJ,  Stockert E,  Welt S;
PI   Kitamura K,  Garin-Chesa P;
XX
DR   WPI; 1995-328275/42.
XX
PT   Recombinant humanised anti-Lewis Y antibody - has increased binding
PT   affinity and is used in the detection of cancer cells expressing Lewis Y
PT   antigen.
XX
PS   Example 4; Page 33; 48pp; English.
XX
CC   Primers (AAT05001-02) based on the murine IgG3 and kappa constant region
CC   genes, respectively, were used to produce cDNA from cytoplasmic RNA
CC   isolated from anti-Lewis Y antibody 3S192-producing hybridomas. The cDNA
CC   was amplified by PCR using primers (AAT05003-05) based on murine VH, V-
CC   kappa and heavy chain signal sequences to obtain clones coding for the
CC   3S192 heavy and light chain variable regions (AAT04997-98). CK2FOR (see
CC   AAT05002) primed DNA was amplified by PCR using primers (AAT05006-7)
CC   based on the framework 4 region of the clone shown in AAT04997. The
CC   amplified DNA lead to the isolation of the 3S193 clone (AAT04998), which
CC   was subjected to site directed mutagenisis to produce the sequences shown
CC   in AAR82964-8
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 61;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| |
Db        109 WGQGTPVTVSS 119


RESULT 13
AAR82966
ID   AAR82966 standard; protein; 119 AA.
XX
AC   AAR82966;
XX
DT   21-MAR-1996  (first entry)
XX
DE   3S193HuVHASY humanised 3S193 heavy chain variable region.
XX
KW   Humanised antibody; Lewis Y antigen; monoclonal antibody 3S193;
KW   recombinant antibody; antibody engineering; heavy chain; CDR;
KW   complementarity determining region; cancer; diagnosis; therapy.
XX
OS   Synthetic.
XX
PN   WO9524484-A1.
XX
PD   14-SEP-1995.
XX
PF   08-MAR-1995;   95WO-US003096.
XX
PR   08-MAR-1994;   94US-00207861.
XX
PA   (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Wallace TP,  Harris WJ,  Carr FJ,  Old LJ,  Stockert E,  Welt S;
PI   Kitamura K,  Garin-Chesa P;
XX
DR   WPI; 1995-328275/42.
XX
PT   Recombinant humanised anti-Lewis Y antibody - has increased binding
PT   affinity and is used in the detection of cancer cells expressing Lewis Y
PT   antigen.
```

```
XX
PS   Example 4; Page 33; 48pp; English.
XX
CC   Primers (AAT05001-02) based on the murine IgG3 and kappa constant region
CC   genes, respectively, were used to produce cDNA from cytoplasmic RNA
CC   isolated from anti-Lewis Y antibody 3S192-producing hybridomas. The cDNA
CC   was amplified by PCR using primers (AAT05003-05) based on murine VH, V-
CC   kappa and heavy chain signal sequences to obtain clones coding for the
CC   3S192 heavy and light chain variable regions (AAT04997-98). CK2FOR (see
CC   AAT05002) primed DNA was amplified by PCR using primers (AAT05006-7)
CC   based on the framework 4 region of the clone shown in AAT04997. The
CC   amplified DNA lead to the isolation of the 3S193 clone (AAT04998), which
CC   was subjected to site directed mutagenisis to produce the sequences shown
CC   in AAR82964-8
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 61;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db        109 WGQGTPVTVSS 119


RESULT 14
AAR82962
ID   AAR82962 standard; protein; 119 AA.
XX
AC   AAR82962;
XX
DT   27-FEB-1996  (first entry)
XX
DE   Humanised antibody 3S193 heavy chain variable region.
XX
KW   Humanised antibody; Lewis Y antigen; monoclonal antibody 3S193;
KW   recombinant antibody; antibody engineering; heavy chain; CDR;
KW   complementary determining region; cancer; diagnosis; therapy.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          31. .35
FT                   /label= CDR
FT   Region          50. .66
FT                   /label= CDR
FT   Region          99. .108
FT                   /label= CDR
XX
PN   WO9524484-A1.
XX
PD   14-SEP-1995.
XX
PF   08-MAR-1995;   95WO-US003096.
XX
PR   08-MAR-1994;   94US-00207861.
XX
PA   (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Wallace TP,  Harris WJ,  Carr FJ,  Old LJ,  Stockert E,  Welt S;
PI   Kitamura K,  Garin-Chesa P;
XX
DR   WPI; 1995-328275/42.
DR   N-PSDB; AAT04999.
XX
PT   Recombinant humanised anti-Lewis Y antibody - has increased binding
PT   affinity and is used in the detection of cancer cells expressing Lewis Y
PT   antigen.
XX
PS   Example 3; Fig 3; 48pp; English.
XX
CC   A humanised antibody 3S193 heavy chain variable region (VH) (AAR82962) is
CC   composed of the human KOL framework (with Thr-28 from murine H-1 loop)
CC   with complementarity determining regions (CDRs) based on the CDRs of the
CC   murine 3S193 VH (AAR82960). Co-transfection of rat myeloma YB2/0 cells by
CC   DNA sequences (AAT04999, AAT05000) coding for the humanised VH and
CC   humanised V-kappa (AAR82963) allowed prodn. of anti-Lewis Y antigen 3S193
CC   humanised antibody
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 61;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.16;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db        109 WGQGTPVTVSS 119


RESULT 15
AAW11919
ID   AAW11919 standard; protein; 119 AA.
XX
AC   AAW11919;
XX
DT   16-OCT-2003  (revised)
DT   24-JUN-1997  (first entry)
XX
DE   Humanised MAb SK48-E26 heavy chain.
XX
KW   Interleukin-1 beta; IL-1 beta; recombinant antibody; humanised antibody;
KW   chimeric antibody; antibody engineering; monoclonal antibody; MAb;
KW   SK48-E26; inflammation; therapy.
XX
OS   Homo; sapiens.
OS   Mus sp.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .30
FT                   /label= FR1
FT                   /note= "framework region 1"
FT   Region          31. .35
FT                   /label= CDR1
FT                   /note= "complementarity determining region 1 (Claim 10,
FT                   page 48)"
FT   Region          36. .49
FT                   /label= FR2
FT                   /note= "framework region 2"
FT   Region          50. .66
FT                   /label= CDR2
FT                   /note= "complementarity determining region 2 (Claim 10,
FT                   page 48)"
FT   Region          67. .98
FT                   /label= FR3
FT                   /note= "framework region 3"
FT   Region          99. .108
FT                   /label= CDR3
FT                   /note= "complementarity determining region 3 (Claim 10,
FT                   page 48)"
FT   Region          109. .119
FT                   /label= FR4
FT                   /note= "framework region 4"
XX
PN   WO9501997-A1.
XX
PD   19-JAN-1995.
XX
PF   07-JUL-1994;   94WO-US007659.
XX
PR   09-JUL-1993;   93US-00090534.
PR   04-MAR-1994;   94US-00206190.
XX
```

PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Young PR, Gross MS, Jonak ZL, Theisen TW, Hurle MR, Jackson JR;
XX
DR WPI; 1995-066868/09.
DR N-PSDB; AAT51438.
XX
PT Recombinant and humanised chimeric antibodies against human interleukin-1
PT -beta - for preventing and treating interleukin-mediated inflammatory
PT disorders.
XX
PS Claim 39; Page 40-41; 62pp; English.
XX
CC The heavy chain variable region (AAW11919) and light chain variable
CC region (AAW11920) of humanised anti-human interleukin-1 beta (IL-1 beta)
CC murine monoclonal antibody (MAb) SK48-E26 comprise the complementarity
CC determining regions from MAb SK48-E26 (see also AAW11917-18) grafted into
CC human frameworks. The humanised antibody can be produced in e.g. COS
CC cells transfected with vectors carrying humanised heavy and light chain
CC nucleic acids (AAT51437-39) for use in the treatment and prevention of IL
CC -1 mediated inflammatory disorders. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 119 AA;

Query Match 100.0%; Score 61; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db        109 WGQGTPVTVSS 119
```

Search completed: March 25, 2006, 09:02:24
Job time : 41.6695 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:02:50 ; Search time 6.33508 Seconds
(without alignments)
167.067 Million cell updates/sec

Title: US-10-755-382-39
Perfect score: 61
Sequence: 1 WGQGTPVTVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	61	100.0	113	2	S57410	Ig heavy chain V-J
2	61	100.0	126	1	G1HUKL	Ig heavy chain V-I
3	58	95.1	140	1	HVMSG7	Ig heavy chain pre
4	57	93.4	120	1	G1HUCO	Ig heavy chain V-I
5	55	90.2	121	2	S09959	Ig heavy chain V r
6	53	86.9	17	2	S26747	Ig heavy chain J r
7	53	86.9	45	2	PL0093	Ig heavy chain V r
8	53	86.9	74	2	S26793	Ig heavy chain V r
9	53	86.9	99	2	S26326	Ig heavy chain V r
10	53	86.9	101	2	D24672	Ig heavy chain V r
11	53	86.9	106	2	S26315	Ig heavy chain V r
12	53	86.9	107	2	A49442	Ig heavy chain V r
13	53	86.9	108	2	S26316	Ig heavy chain V r
14	53	86.9	109	2	S26318	Ig heavy chain V r
15	53	86.9	110	2	PH1655	Ig heavy chain V r
16	53	86.9	110	2	S26323	Ig heavy chain V r
17	53	86.9	110	2	S26317	Ig heavy chain V r
18	53	86.9	111	2	S26324	Ig heavy chain V r
19	53	86.9	112	2	S33599	Ig gamma chain - A
20	53	86.9	113	2	S55533	Ig heavy chain V r
21	53	86.9	113	2	S55535	Ig heavy chain V r
22	53	86.9	113	2	S55530	Ig heavy chain V r
23	53	86.9	113	2	S55534	Ig heavy chain V r
24	53	86.9	113	2	S55528	Ig heavy chain V r
25	53	86.9	113	2	S55532	Ig heavy chain V r
26	53	86.9	113	2	S55531	Ig heavy chain V r
27	53	86.9	114	2	S46392	Ig heavy chain V r
28	53	86.9	114	2	S20707	Ig heavy chain V r
29	53	86.9	114	2	S11106	Ig heavy chain V r
30	53	86.9	114	2	S26319	Ig heavy chain V r
31	53	86.9	115	2	S11107	Ig heavy chain V r
32	53	86.9	115	2	PC6026	acetylcoline recep
33	53	86.9	115	2	S20706	Ig heavy chain V r
34	53	86.9	116	2	S15672	Ig heavy chain V r
35	53	86.9	116	2	S26309	Ig heavy chain V r
36	53	86.9	116	2	S55542	Ig heavy chain V r
37	53	86.9	117	1	G2MS73	Ig heavy chain V r
38	53	86.9	117	2	I57810	gene C72-3A1 prote
39	53	86.9	117	2	I28195	Ig heavy chain V r
40	53	86.9	117	2	B27563	Ig heavy chain V r
41	53	86.9	117	2	S55541	Ig heavy chain V r
42	53	86.9	118	2	S24702	Ig heavy chain V6
43	53	86.9	118	2	PH1666	Ig heavy chain V r
44	53	86.9	118	2	PH1660	Ig heavy chain V r
45	53	86.9	118	2	A47329	Ig heavy chain V r

ALIGNMENTS

RESULT 1
S57410
Ig heavy chain V-J region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S57410
R;Paterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.
submitted to the EMBL Data Library, June 1995
A;Description: Analysis of anti-GM1 ganglioside IgM antibodies cloned from motor neuropa
A;Reference number: S57408
A;Accession: S57410
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-113 <PAT>
A;Cross-references: UNIPARC:UPI00001137A9; EMBL:X87893; NID:g871363; PIDN:CAA61144.1; PI
C;Genetics:
A;Introns: 99/2
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 61; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db        103 WGQGTPVTVSS 113
```

RESULT 2
G1HUKL
Ig heavy chain V-III region (Kol) - human
C;Species: Homo sapiens (man)
C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jul-2004
C;Accession: A02055
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Accession: A02055
A;Molecule type: protein
A;Residues: 1-126 <SCH>
A;Cross-references: UNIPROT:P01772; UNIPARC:UPI000002D0C3
C;Genetics:
A;Gene: GDB:IGHV@
A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
F;15-98/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96,105-110/Disulfide bonds: #status experimental

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  Query Match             100.0%;  Score 61;  DB 1;  Length 126;
  Best Local Similarity   100.0%;  Pred. No. 0.0036;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db        116 WGQGTPVTVSS 126


RESULT 3
HVMSG7
Ig heavy chain precursor V region (93G7, 36-65) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A94264; A91261; A02028
R;Sims, J.; Rabbitts, T.H.; Estess, P.; Slaughter, C.; Tucker, P.W.; Capra, J.D.
Science 216, 309-311, 1982
A;Title: Somatic mutation in genes for the variable portion of the immunoglobulin heavy
A;Reference number: A94264; MUID:82152818; PMID:6801765
A;Accession: A94264
A;Molecule type: mRNA
A;Residues: 1-140 <SIM>
A;Cross-references: UNIPROT:P01746; UNIPARC:UPI00000270DA; GB:J00493; NID:g195006; PIDN:
A;Experimental source: strain A/J, hybridoma 93G7
R;Siekevitz, M.; Gefter, M.L.; Brodeur, P.; Riblet, R.; Marshak-Rothstein, A.
Eur. J. Immunol. 12, 1023-1032, 1982
A;Title: The genetic basis of antibody production: the dominant anti-arsonate idiotype r
A;Reference number: A91261; MUID:83131846; PMID:6186498
A;Accession: A91261
A;Molecule type: DNA
A;Residues: 20-76,'TK',79-118,'V',120-125,'Y',127-134,'T',136-140 <SIE>
A;Cross-references: UNIPARC:UPI0000114D5B; GB:M19292; NID:g196201; PIDN:AAA38625.1; PID:
A;Experimental source: strain A/J, hybridoma 36-65
A;Note: the sequence was determined from the differentiated gene
A;Note: from analysis of the sizes of several other differentiated genes that hybridize
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-140/Product: Ig heavy chain V region (93G7) #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;41-115/Disulfide bonds: #status predicted

  Query Match             95.1%;  Score 58;  DB 1;  Length 140;
  Best Local Similarity   90.9%;  Pred. No. 0.013;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||:|||| 
Db        130 WGQGTPLTVSS 140


RESULT 4
G1HUCO
Ig heavy chain V-II region (Cor) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
C;Accession: A02089
R;Press, E.M.; Hogg, N.M.
Biochem. J. 117, 641-660, 1970
A;Title: The amino acid sequences of the Fd fragments of two human gamma1 heavy chains.
A;Reference number: A90250; MUID:70258837; PMID:5449120
A;Accession: A02089
A;Molecule type: protein
A;Residues: 1-120 <PRE>
A;Cross-references: UNIPROT:P01815; UNIPARC:UPI000012CEE9
C;Comment: This chain was isolated from an IgG1 myeloma protein.
C;Genetics:
A;Gene: GDB:IGHV@
A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; pyroglutamic acid
F;15-96/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-94/Disulfide bonds: #status experimental
F;62/Binding site: carbohydrate (Asn) (covalent) #status experimental

  Query Match             93.4%;  Score 57;  DB 1;  Length 120;
  Best Local Similarity   90.9%;  Pred. No. 0.016;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||:||||||||| 
Db        110 WGRGTPVTVSS 120


RESULT 5
S09959
Ig heavy chain V region (31-9D) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
C;Accession: S09959
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies
A;Reference number: S09955; MUID:90269328; PMID:2347362
A;Accession: S09959
A;Molecule type: mRNA
A;Residues: 1-121 <REI>
A;Cross-references: UNIPARC:UPI0000115E5E; EMBL:X51847; NID:g55247; PIDN:CAA36140.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

  Query Match             90.2%;  Score 55;  DB 2;  Length 121;
  Best Local Similarity   90.9%;  Pred. No. 0.036;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              || ||||||||| 
Db        111 WGAGTPVTVSS 121


RESULT 6
S26747
Ig heavy chain J region JH4 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 17-Mar-1999
C;Accession: S26747
R;Solin, M.L.; Kaartinen, M.
Immunogenetics 36, 306-313, 1992
A;Title: Allelic polymorphism of mouse Igh-J locus, which encodes immunoglobulin heavy ch
A;Reference number: S26744; MUID:92355114; PMID:1644448
A;Accession: S26747
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-17 <SOL>
A;Cross-references: UNIPARC:UPI0000117CB8; EMBL:X63164
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             86.9%;  Score 53;  DB 2;  Length 17;
  Best Local Similarity   90.9%;  Pred. No. 0.011;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||| ||||| 
Db          7 WGQGTSVTVSS 17


RESULT 7
PL0093
Ig heavy chain V region (6B1) - mouse (fragment)
```

C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PL0093
R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
J. Exp. Med. 169, 519-533, 1989
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are
A;Reference number: PL0080; MUID:89094248; PMID:2492056
A;Accession: PL0093
A;Molecule type: mRNA
A;Residues: 1-45 <MEE>
A;Cross-references: UNIPARC:UPI0000115F21; GB:X58587; GB:Y00794; NID:g51563; PIDN:CAA414
A;Note: the authors translated the codon AGU for residues 6 and 7 as Asp
A;Note: the sequence shown here is from the VH region of a syngeneic antibody to anti-3-
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

 Query Match 86.9%; Score 53; DB 2; Length 45;
 Best Local Similarity 90.9%; Pred. No. 0.029;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WGQGTPVTVSS 11
 ||||| |||||
Db 35 WGQGTSVTVSS 45

RESULT 8
S26793
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26793
R;Mortari, F.; Newton, J.A.; Wang, J.Y.; Schroeder Jr., H.W.
Eur. J. Immunol. 22, 241-245, 1992
A;Title: The human cord blood antibody repertoire. Frequent usage of the V(H)7 gene fami
A;Reference number: S26786; MUID:92111632; PMID:1730251
A;Accession: S26793
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-74 <MOR>
A;Cross-references: UNIPARC:UPI0000115FCA; EMBL:X61019; NID:g32787; PIDN:CAA43353.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

 Query Match 86.9%; Score 53; DB 2; Length 74;
 Best Local Similarity 90.9%; Pred. No. 0.048;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WGQGTPVTVSS 11
 ||||| |||||
Db 64 WGQGTTVTVSS 74

RESULT 9
S26326
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
C;Accession: S26326
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26326
A;Molecule type: mRNA
A;Residues: 1-99 <STA>
A;Cross-references: UNIPARC:UPI00001769AC; EMBL:X59174
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

 Query Match 86.9%; Score 53; DB 2; Length 99;
 Best Local Similarity 90.9%; Pred. No. 0.064;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WGQGTPVTVSS 11
 ||||| |||||
Db 89 WGQGTSVTVSS 99

RESULT 10
D24672
Ig heavy chain V region (VGAM3-8) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-Jul-1999
C;Accession: D24672
R;Winter, E.; Radbruch, A.; Krawinkel, U.
EMBO J. 4, 2861-2867, 1985
A;Reference number: A91022; MUID:86055722; PMID:2998759
A;Accession: D24672
A;Molecule type: DNA
A;Residues: 1-101 <WIN>
A;Cross-references: UNIPARC:UPI0000113758; GB:X03301; NID:g51757; PIDN:CAA27040.1; PID:g
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

 Query Match 86.9%; Score 53; DB 2; Length 101;
 Best Local Similarity 90.9%; Pred. No. 0.065;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WGQGTPVTVSS 11
 ||||| |||||
Db 91 WGQGTSVTVSS 101

RESULT 11
S26315
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26315
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26315
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-106 <STA>
A;Cross-references: UNIPARC:UPI0000115F8B; EMBL:X59208; NID:g52079; PIDN:CAA41918.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;2-85/Domain: immunoglobulin homology <IMM>

 Query Match 86.9%; Score 53; DB 2; Length 106;
 Best Local Similarity 90.9%; Pred. No. 0.068;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WGQGTPVTVSS 11
 ||||| |||||
Db 96 WGQGTSVTVSS 106

RESULT 12
A49442
Ig heavy chain V region (50.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: A49442
R;Stura, E.A.; Stanfield, R.L.; Fieser, G.G.; Silver, S.; Roguska, M.; Hincapie, L.M.; S
Proteins 14, 499-508, 1992
A;Title: Crystallization, sequence, and preliminary crystallographic data for an antipep
A;Reference number: A49442; MUID:93066166; PMID:1438187
A;Accession: A49442
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-107 <STU>

A;Cross-references: UNIPARC:UPI00001768FD
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-91/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 53; DB 2; Length 107;
Best Local Similarity 90.9%; Pred. No. 0.069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WGQGTPVTVSS 11
||||| |||||
Db 97 WGQGTSVTVSS 107

RESULT 13
S26316
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26316
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26316
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <STA>
A;Cross-references: UNIPARC:UPI0000115F7E; EMBL:X59190; NID:g52066; PIDN:CAA41900.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;2-85/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 53; DB 2; Length 108;
Best Local Similarity 90.9%; Pred. No. 0.069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WGQGTPVTVSS 11
||||| |||||
Db 98 WGQGTSVTVSS 108

RESULT 14
S26318
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C;Accession: S26318
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26318
A;Molecule type: mRNA
A;Residues: 1-109 <STA>
A;Cross-references: UNIPARC:UPI00001769A7; EMBL:X59200
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;3-86/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 53; DB 2; Length 109;
Best Local Similarity 90.9%; Pred. No. 0.07;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WGQGTPVTVSS 11
||||| |||||
Db 99 WGQGTSVTVSS 109

RESULT 15
PH1655
Ig heavy chain V region (clone 2E8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1655
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1655
A;Molecule type: mRNA
A;Residues: 1-110 <HIL>
A;Cross-references: UNIPARC:UPI0000176BDC
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 86.9%; Score 53; DB 2; Length 110;
Best Local Similarity 90.9%; Pred. No. 0.071;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WGQGTPVTVSS 11
||||| |||||
Db 100 WGQGTTVTVSS 110

Search completed: March 25, 2006, 09:15:46
Job time : 6.33508 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 08:50:40 ; Search time 39.623 Seconds
(without alignments)
195.866 Million cell updates/sec

Title: US-10-755-382-39
Perfect score: 61
Sequence: 1 WGQGTPVTVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	61	100.0	126	1	HV3K_HUMAN	P01772 homo sapien
2	61	100.0	157	2	O95978_HUMAN	O95978 homo sapien
3	61	100.0	480	2	Q6PJF1_HUMAN	Q6pjf1 homo sapien
4	60	98.4	464	2	Q6PF95_MOUSE	Q6pf95 mus musculu
5	58	95.1	140	1	HV02_MOUSE	P01746 mus musculu
6	57	93.4	120	1	HV2B_HUMAN	P01815 homo sapien
7	56	91.8	476	2	Q6MZX7_HUMAN	Q6mzx7 homo sapien
8	53	86.9	110	2	Q9JL77_MOUSE	Q9jl77 mus musculu
9	53	86.9	111	2	Q5R3U9_MOUSE	Q5r3u9 mus musculu
10	53	86.9	114	2	Q5R3X1_MOUSE	Q5r3x1 mus musculu
11	53	86.9	117	1	HV42_MOUSE	P01812 mus musculu
12	53	86.9	117	2	Q9QXE9_MOUSE	Q9qxe9 mus musculu
13	53	86.9	119	2	Q9GYZ2_MOUSE	Q9gyz2 mus musculu
14	53	86.9	121	2	Q8CGS2_MOUSE	Q8cgs2 mus musculu
15	53	86.9	121	2	Q99NG4_MOUSE	Q99ng4 mus musculu
16	53	86.9	136	1	HV16_MOUSE	P01783 mus musculu
17	53	86.9	140	2	Q924R2_MOUSE	Q924r2 mus musculu
18	53	86.9	142	2	Q924Q2_MOUSE	Q924q2 mus musculu
19	53	86.9	142	2	Q924Q1_MOUSE	Q924q1 mus musculu
20	53	86.9	143	2	Q924P6_MOUSE	Q924p6 mus musculu
21	53	86.9	143	2	Q924R0_MOUSE	Q924r0 mus musculu
22	53	86.9	144	1	HV43_MOUSE	P01819 mus musculu
23	53	86.9	145	2	Q924P7_MOUSE	Q924p7 mus musculu
24	53	86.9	145	2	Q924Q6_MOUSE	Q924q6 mus musculu
25	53	86.9	145	2	Q924Q9_MOUSE	Q924q9 mus musculu
26	53	86.9	145	2	Q924R1_MOUSE	Q924r1 mus musculu
27	53	86.9	145	2	Q924R4_MOUSE	Q924r4 mus musculu
28	53	86.9	146	1	HV2I_HUMAN	P06331 homo sapien
29	53	86.9	146	2	Q924Q3_MOUSE	Q924q3 mus musculu
30	53	86.9	147	1	HV1C_HUMAN	P01744 homo sapien
31	53	86.9	147	2	Q925S3_MOUSE	Q925s3 mus musculu
32	53	86.9	159	2	Q96QS0_HUMAN	Q96qs0 homo sapien
33	53	86.9	170	2	Q925S2_MOUSE	Q925s2 mus musculu
34	53	86.9	218	2	Q925S1_MOUSE	Q925s1 mus musculu
35	53	86.9	241	2	Q921A6_MOUSE	Q921a6 mus musculu
36	53	86.9	262	2	Q65ZI1_MOUSE	Q65zi1 mus musculu
37	53	86.9	348	2	Q6PYX1_HUMAN	Q6pyx1 homo sapien
38	53	86.9	416	2	Q9NPP6_HUMAN	Q9npp6 homo sapien
39	53	86.9	426	2	Q9DCD9_MOUSE	Q9dcd9 mus musculu
40	53	86.9	458	2	Q5BK05_RAT	Q5bk05 rattus norv
41	53	86.9	464	2	Q6PIP8_MOUSE	Q6pip8 mus musculu
42	53	86.9	472	2	Q6N089_HUMAN	Q6n089 homo sapien
43	53	86.9	475	2	Q6N095_HUMAN	Q6n095 homo sapien
44	53	86.9	476	2	Q4V9Z4_MOUSE	Q4v9z4 mus musculu
45	53	86.9	482	2	Q8K172_MOUSE	Q8k172 mus musculu

ALIGNMENTS

RESULT 1
HV3K_HUMAN
ID HV3K_HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig heavy chain V-III region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule Kol and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC ---
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ---
DR PIR; A02055; G1HUKL.
DR PDB; 2FB4; X-ray; H=2-126.
DR PDB; 2IG2; X-ray; H=2-126.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT DISULFID 22 96
FT DISULFID 105 110
FT NON_TER 126 126
FT STRAND 3 7

```
FT   STRAND       11     12
FT   TURN         14     15
FT   STRAND       18     25
FT   HELIX        29     31
FT   STRAND       34     39
FT   TURN         41     42
FT   STRAND       45     51
FT   TURN         53     54
FT   STRAND       58     60
FT   HELIX        62     64
FT   STRAND       65     65
FT   TURN         66     67
FT   STRAND       68     73
FT   TURN         74     77
FT   STRAND       78     83
FT   HELIX        88     90
FT   STRAND       92     99
FT   STRAND      106    106
FT   TURN        107    108
FT   STRAND      109    109
FT   STRAND      113    116
FT   STRAND      120    124
SQ   SEQUENCE   126 AA;  13718 MW;  E4D71B52B16F8776 CRC64;

  Query Match             100.0%;  Score 61;  DB 1;  Length 126;
  Best Local Similarity   100.0%;  Pred. No. 0.0063;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| |
Db        116 WGQGTPVTVSS 126


RESULT 2
O95978_HUMAN
ID   O95978_HUMAN PRELIMINARY;      PRT;   157 AA.
AC   O95978;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VH1 protein precursor (Fragment).
GN   Name=VH1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Peripheral blood;
RA   Jox A., Zander T., Kueppers R., Irsch J., Kanzler H., Kornacker M.,
RA   Bohlen H., Diehl V., Wolf J.;
RT   "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
RT   patient with mixed cellularity Hodgkin's disease is associated with
RT   somatic mutations within the untranslated regions of rearranged and
RT   class switch recombinated Ig genes.";
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ005570; CAA06599.1; -; Genomic_DNA.
DR   HSSP; P01857; 1HZH.
DR   Ensembl; ENSG00000130076; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Signal.
FT   SIGNAL       1     21       Potential.
FT   NON_TER    157    157
SQ   SEQUENCE   157 AA;  17304 MW;  86986EDDA84D88B5 CRC64;

  Query Match             100.0%;  Score 61;  DB 2;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 0.008;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| |
Db        130 WGQGTPVTVSS 140


RESULT 3
Q6PJF1_HUMAN
ID   Q6PJF1_HUMAN PRELIMINARY;      PRT;   480 AA.
AC   Q6PJF1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC016381; AAH16381.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   480 AA;  52586 MW;  64DC641AE47CD6C8 CRC64;

  Query Match             100.0%;  Score 61;  DB 2;  Length 480;
  Best Local Similarity   100.0%;  Pred. No. 0.026;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| |
Db        140 WGQGTPVTVSS 150


RESULT 4
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```
Q6PF95_MOUSE
ID   Q6PF95_MOUSE PRELIMINARY;      PRT;   464 AA.
AC   Q6PF95;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
GN   Name=Igh-1a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CZECH II;
RC   TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
RC   Expression driven by an MMTV-LTR enhancer.;
RA   Strausberg R.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC057672; AAH57672.1; -; mRNA.
DR   HSSP; P01865; 1KB5.
DR   MGI; MGI:96443; Igh-1a.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   464 AA;  51096 MW;  5B837464D85A1888 CRC64;

  Query Match             98.4%;  Score 60;  DB 2;  Length 464;
  Best Local Similarity   90.9%;  Pred. No. 0.039;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              |||||||:||||
Db        124 WGQGTPITVSS 134
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RESULT 5
HV02_MOUSE
ID   HV02_MOUSE     STANDARD;      PRT;   140 AA.
AC   P01746;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region 93G7 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=82152818; PubMed=6801765;
RA   Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA   Capra J.D.;
RT   "Somatic mutation in genes for the variable portion of the
RT   immunoglobulin heavy chain.";
RL   Science 216:309-311(1982).
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; J00493; AAA38128.1; -; mRNA.
DR   HSSP; P01747; 1JFQ.
DR   SMR; P01746; 20-140.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    140       Ig heavy chain V region 93G7.
FT   DOMAIN      20    139       Ig-like.
FT   NON_TER    140    140
SQ   SEQUENCE   140 AA;  15514 MW;  25A4CBBE31DA5CE8 CRC64;

  Query Match             95.1%;  Score 58;  DB 1;  Length 140;
  Best Local Similarity   90.9%;  Pred. No. 0.025;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              |||||||:||||
Db        130 WGQGTPLTVSS 140
```

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RESULT 6
HV2B_HUMAN
ID   HV2B_HUMAN     STANDARD;      PRT;   120 AA.
AC   P01815;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V-II region COR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=70258837; PubMed=5449120;
RA   Press E.M., Hogg N.M.;
RT   "The amino acid sequences of the Fd fragments of two human gamma-1
RT   heavy chains.";
RL   Biochem. J. 117:641-660(1970).
```

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CC   -!- MISCELLANEOUS: This chain was isolated from an IgG1 myeloma
CC       protein.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A02089; G1HUCO.
DR   HSSP; P01820; 1A7N.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW   Immunoglobulin V region; Pyrrolidone carboxylic acid.
FT   DOMAIN        1    110       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   CARBOHYD     62     62       N-linked (GlcNAc. . .).
FT   DISULFID     22     94
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13226 MW;  158A8B29AE7EEB98 CRC64;

  Query Match             93.4%;  Score 57;  DB 1;  Length 120;
  Best Local Similarity   90.9%;  Pred. No. 0.032;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||:||||||||
Db        110 WGRGTPVTVSS 120


RESULT 7
Q6MZX7_HUMAN
ID   Q6MZX7_HUMAN PRELIMINARY;      PRT;   476 AA.
AC   Q6MZX7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp686M24218.
GN   Name=DKFZp686M24218;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Human rectum tumor;
RG   The German Human cDNA Consortium;
RA   Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA   Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640824; CAE45900.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   SMR; Q6MZX7; 28-472.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW   Hypothetical protein.
SQ   SEQUENCE   476 AA;  52420 MW;  0D3D1FFE5853958F CRC64;

  Query Match             91.8%;  Score 56;  DB 2;  Length 476;
  Best Local Similarity   90.9%;  Pred. No. 0.21;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              |||| ||||||
Db        139 WGQGAPVTVSS 149


RESULT 8
Q9JL77_MOUSE
ID   Q9JL77_MOUSE PRELIMINARY;      PRT;   110 AA.
AC   Q9JL77;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-myosin immunoglobulin heavy chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=DBA/2;
RX   MEDLINE=20448942; PubMed=10992488;
RX   DOI=10.1128/IAI.68.10.5803-5808.2000;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "T-Cell-dependent antibody response to the dominant epitope of
RT   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT   with cardiac myosin.";
RL   Infect. Immun. 68:5803-5808(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2499887;
RA   Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT   "Two murine natural polyreactive autoantibodies are encoded by
RT   nonmutated germ-line genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
DR   EMBL; AF206029; AAF69327.1; -; mRNA.
DR   PIR; F33932; F33932.
DR   HSSP; P01751; 1NQB.
DR   SMR; Q9JL77; 1-110.
DR   Ensembl; ENSMUSG00000021155; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     110    110
SQ   SEQUENCE   110 AA;  12138 MW;  2EDE81FB5862C9AF CRC64;

  Query Match             86.9%;  Score 53;  DB 2;  Length 110;
  Best Local Similarity   90.9%;  Pred. No. 0.15;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||| |||||
Db        100 WGQGTSVTVSS 110


RESULT 9
Q5R3U9_MOUSE
ID   Q5R3U9_MOUSE PRELIMINARY;      PRT;   111 AA.
AC   Q5R3U9;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   VH region of G7 Ab 2.9 (Fragment).
OS   Mus musculus (Mouse).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84057768; PubMed=6416834;
RA   Rocca-Serra J., Matthes H.W., Kaartinen M., Milstein C., Theze J.,
RA   Fougereau M.;
RT   "Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of
RT   four anti-GAT monoclonal antibodies. A paucigene system using
RT   alternate D-J recombinations to generate functionally similar
RT   hypervariable regions.";
RL   EMBO J. 2:867-872(1983).
DR   EMBL; X07144; CAA30149.1; -; mRNA.
DR   SMR; Q5R3U9; 1-111.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  12200 MW;  0E7C863998DAFADB CRC64;

  Query Match             86.9%;  Score 53;  DB 2;  Length 111;
  Best Local Similarity   90.9%;  Pred. No. 0.16;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||| |||||
Db        100 WGQGTSVTVSS 110


RESULT 10
Q5R3X1_MOUSE
ID   Q5R3X1_MOUSE PRELIMINARY;      PRT;   114 AA.
AC   Q5R3X1;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   V(H) region of G5 Bb 2.2 (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Balb-c;
RX   MEDLINE=84057768; PubMed=6416834;
RA   Rocca-Serra J., Matthes H.W., Kaartinen M., Milstein C., Theze J.,
RA   Fougereau M.;
RT   "Analysis of antibody diversity: V-D-J mRNA nucleotide sequence of
RT   four anti-GAT monoclonal antibodies. A paucigene system using
RT   alternate D-J recombinations to generate functionally similar
RT   hypervariable regions.";
RL   EMBO J. 2:867-872(1983).
DR   EMBL; X01820; CAA25962.1; -; mRNA.
DR   SMR; Q5R3X1; 1-114.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     114    114
SQ   SEQUENCE   114 AA;  12477 MW;  BD72D1082510BEAB CRC64;

  Query Match             86.9%;  Score 53;  DB 2;  Length 114;
  Best Local Similarity   90.9%;  Pred. No. 0.16;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||| |||||
Db        103 WGQGTSVTVSS 113


RESULT 11
HV42_MOUSE
ID   HV42_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01812;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region MOPC 173.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE OF 1-104.
RX   MEDLINE=72105531; PubMed=5062012;
RA   Bourgois A., Fougereau M., de Preval C.;
RT   "Sequence of amino acids of the NH 2 -terminal region of a mouse-
RT   clonal immunoglobulin heavy chain.";
RL   Eur. J. Biochem. 24:446-455(1972).
RN   [2]
RP   PROTEIN SEQUENCE OF 105-117.
RX   MEDLINE=76091933; PubMed=812695;
RA   Rocca-Serra J., Milili M., Fougereau M.;
RT   "Determination of the primary structure of a mouse IgG2a
RT   immunoglobulin. Amino-acid sequence of the H4 cyanogen-bromide
RT   fragment.";
RL   Eur. J. Biochem. 59:511-523(1975).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 96-117.
RX   MEDLINE=81223769; PubMed=6787590;
RA   Gough N.M., Bernard O.;
RT   "Sequences of the joining region genes for immunoglobulin heavy chains
RT   and their role in generation of antibody diversity.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:509-513(1981).
RN   [4]
RP   DISULFIDE BOND.
RX   PubMed=11947590;
RA   Bourgois A., Fougereau M.;
RT   "Partial amino acid sequence of the variable region of a mouse
RT   gammaG2a immunoglobulin heavy chain. Evidence for the existence of a
RT   third sub-group of variability for the heavy chain pool.";
RL   FEBS Lett. 8:265-268(1970).
CC   -!- MISCELLANEOUS: This gamma-2a chain was isolated from a myeloma
CC       protein.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A91190; G2MS73.
DR   HSSP; P01810; 2FBJ.
DR   SMR; P01812; 1-117.
DR   Ensembl; ENSMUSG00000003483; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    116       Ig-like.
FT   DISULFID     22     96
FT   CONFLICT    105    105       N -> D (in Ref. 2).
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FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13051 MW;  156DCCC259380F19 CRC64;

  Query Match             86.9%;  Score 53;  DB 1;  Length 117;
  Best Local Similarity   90.9%;  Pred. No. 0.16;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||| |||||
Db        107 WGQGTSVTVSS 117


RESULT 12
Q9QXE9_MOUSE
ID   Q9QXE9_MOUSE PRELIMINARY;      PRT;   117 AA.
AC   Q9QXE9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Immunoglobulin heavy chain V-D-J region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL   Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2499887;
RA   Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT   "Two murine natural polyreactive autoantibodies are encoded by
RT   nonmutated germ-line genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
DR   EMBL; AJ225174; CAB65237.1; -; mRNA.
DR   PIR; F33932; F33932.
DR   HSSP; P01751; 1NQB.
DR   SMR; Q9QXE9; 1-117.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13000 MW;  CDDE2AF84D499734 CRC64;

  Query Match             86.9%;  Score 53;  DB 2;  Length 117;
  Best Local Similarity   90.9%;  Pred. No. 0.16;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||| |||||
Db        107 WGQGTSVTVSS 117


RESULT 13
Q9GYZ2_MOUSE
ID   Q9GYZ2_MOUSE PRELIMINARY;      PRT;   119 AA.
AC   Q9GYZ2;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Monoclonal anti-idiotypic Schistosoma japonicum antibody NP30 heavy
DE   chain variable region (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Song X.T., Feng Z.Q., Guan X.H.;
RT   "Amplification, cloning and sequence analysis of the heavy chain
RT   variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT   Schistosoma japonicum.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF282622; AAG01452.1; -; mRNA.
DR   HSSP; P01751; 1A6W.
DR   SMR; Q9GYZ2; 1-119.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13567 MW;  BA893873FD5FA6AB CRC64;

  Query Match             86.9%;  Score 53;  DB 2;  Length 119;
  Best Local Similarity   90.9%;  Pred. No. 0.17;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||| |||||
Db        109 WGQGTTVTVSS 119


RESULT 14
Q8CGS2_MOUSE
ID   Q8CGS2_MOUSE PRELIMINARY;      PRT;   121 AA.
AC   Q8CGS2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-deoxynivalenol scFv lambda heavy chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BALB/c;
RA   Wang Z., Munshi K., Osawa F., Pestka J.J., Hart L.P.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY151140; AAN75452.1; -; mRNA.
DR   HSSP; P01751; 1NQB.
DR   Ensembl; ENSMUSG00000021155; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13475 MW;  84FE6CFA8053F5D6 CRC64;

  Query Match             86.9%;  Score 53;  DB 2;  Length 121;
  Best Local Similarity   90.9%;  Pred. No. 0.17;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||| |||||
Db        111 WGQGTTVTVSS 121


RESULT 15
Q99NG4_MOUSE
ID   Q99NG4_MOUSE PRELIMINARY;      PRT;   121 AA.
AC   Q99NG4;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Single chain Fv (Fragment).
OS   Mus musculus (Mouse).
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OG   Plasmid pHEN1.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BALB/C;
RX   MEDLINE=98169018; PubMed=9510199;
RA   Hawlisch H., Frank R., Hennecke M., Baensch M., Sohns B., Arseniev L.,
RA   Bautsch W., Kola A., Klos A., Koehl J.;
RT   "Site-Directed C3a-Receptor Antibodies from Phage Display Libraries.";
RL   J. Immunol. 160:2947-2958(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2499887;
RA   Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT   "Two murine natural polyreactive autoantibodies are encoded by
RT   nonmutated germ-line genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
DR   EMBL; AJ222590; CAA10890.1; -; mRNA.
DR   PIR; F33932; F33932.
DR   HSSP; P01820; 1G7J.
DR   SMR; Q99NG4; 1-121.
DR   Ensembl; ENSMUSG00000062080; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Plasmid.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  13255 MW;  D293E4EBC8C59D5B CRC64;

  Query Match             86.9%;  Score 53;  DB 2;  Length 121;
  Best Local Similarity   90.9%;  Pred. No. 0.17;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||| |||||
Db        110 WGQGTSVTVSS 120


Search completed: March 25, 2006, 09:13:52
Job time : 39.623 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:14:16 ; Search time 10.0209 Seconds
(without alignments)
90.753 Million cell updates/sec

Title: US-10-755-382-39
Perfect score: 61
Sequence: 1 WGQGTPVTVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	61	100.0	11	1	US-08-318-157B-39	Sequence 39, Appl
2	61	100.0	11	2	US-09-253-794-39	Sequence 39, Appl
3	61	100.0	117	1	US-08-652-558-3	Sequence 3, Appli
4	61	100.0	117	1	US-08-652-558-44	Sequence 44, Appl
5	61	100.0	117	1	US-08-652-558-45	Sequence 45, Appl
6	61	100.0	117	1	US-08-652-558-46	Sequence 46, Appl
7	61	100.0	117	2	US-08-983-607-46	Sequence 46, Appl
8	61	100.0	119	1	US-08-207-996-22	Sequence 22, Appl
9	61	100.0	119	1	US-08-859-649-20	Sequence 20, Appl
10	61	100.0	119	1	US-08-859-649-21	Sequence 21, Appl
11	61	100.0	119	1	US-08-859-649-22	Sequence 22, Appl
12	61	100.0	119	1	US-08-859-649-23	Sequence 23, Appl
13	61	100.0	119	1	US-08-859-649-24	Sequence 24, Appl
14	61	100.0	119	1	US-08-859-649-31	Sequence 31, Appl
15	61	100.0	119	1	US-08-318-157B-12	Sequence 12, Appl
16	61	100.0	119	1	US-08-318-157B-13	Sequence 13, Appl
17	61	100.0	119	1	US-08-318-157B-14	Sequence 14, Appl
18	61	100.0	119	1	US-08-318-157B-15	Sequence 15, Appl
19	61	100.0	119	1	US-08-318-157B-17	Sequence 17, Appl
20	61	100.0	119	1	US-08-318-157B-58	Sequence 58, Appl
21	61	100.0	119	1	US-08-070-116A-12	Sequence 12, Appl
22	61	100.0	119	1	US-08-070-116A-13	Sequence 13, Appl
23	61	100.0	119	1	US-08-070-116A-14	Sequence 14, Appl
24	61	100.0	119	1	US-08-760-840A-22	Sequence 22, Appl
25	61	100.0	119	2	US-09-266-119-22	Sequence 22, Appl
26	61	100.0	119	2	US-08-983-607-22	Sequence 22, Appl
27	61	100.0	119	2	US-08-207-861-20	Sequence 20, Appl
28	61	100.0	119	2	US-08-207-861-21	Sequence 21, Appl
29	61	100.0	119	2	US-08-207-861-22	Sequence 22, Appl
30	61	100.0	119	2	US-08-207-861-23	Sequence 23, Appl
31	61	100.0	119	2	US-08-207-861-24	Sequence 24, Appl
32	61	100.0	119	2	US-08-207-861-31	Sequence 31, Appl
33	61	100.0	119	2	US-09-602-709-22	Sequence 22, Appl
34	61	100.0	119	2	US-08-557-050-12	Sequence 12, Appl
35	61	100.0	119	2	US-08-557-050-13	Sequence 13, Appl
36	61	100.0	119	2	US-08-557-050-14	Sequence 14, Appl
37	61	100.0	119	2	US-08-859-648-20	Sequence 20, Appl
38	61	100.0	119	2	US-08-859-648-21	Sequence 21, Appl
39	61	100.0	119	2	US-08-859-648-22	Sequence 22, Appl
40	61	100.0	119	2	US-08-859-648-23	Sequence 23, Appl
41	61	100.0	119	2	US-08-859-648-24	Sequence 24, Appl
42	61	100.0	119	2	US-08-859-648-31	Sequence 31, Appl
43	61	100.0	119	2	US-09-253-794-12	Sequence 12, Appl
44	61	100.0	119	2	US-09-253-794-13	Sequence 13, Appl
45	61	100.0	119	2	US-09-253-794-14	Sequence 14, Appl

ALIGNMENTS

```
RESULT 1
US-08-318-157B-39
; Sequence 39, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  39:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-39

  Query Match             100.0%;  Score 61;  DB 1;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.0055;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db          1 WGQGTPVTVSS 11
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```
RESULT 2
US-09-253-794-39
; Sequence 39, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 39:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 11 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-253-794-39

  Query Match             100.0%;  Score 61;  DB 2;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.0055;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| |
Db          1 WGQGTPVTVSS 11


RESULT 3
US-08-652-558-3
; Sequence 3, Application US/08652558
; Patent No. 5861155
;  GENERAL INFORMATION:
;    APPLICANT:  LIN, AUGUSTINE YEE-THARN
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER & WITCOFF
;      STREET:  75 STATE STREET, 23RD FLOOR
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette, 1.4 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,558
;      FILING DATE:  JUNE 6, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB94/00387
;      FILING DATE:  NOVEMBER 21, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YANKWICH, LEON R.
;      REGISTRATION NUMBER:  30,237
;      REFERENCE/DOCKET NUMBER:  95,497-L
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-345-9100
;      TELEFAX:  617-345-9111
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-558-3

  Query Match             100.0%;  Score 61;  DB 1;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 0.051;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| |
Db        107 WGQGTPVTVSS 117


RESULT 4
US-08-652-558-44
; Sequence 44, Application US/08652558
; Patent No. 5861155
;  GENERAL INFORMATION:
;    APPLICANT:  LIN, AUGUSTINE YEE-THARN
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER & WITCOFF
;      STREET:  75 STATE STREET, 23RD FLOOR
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette, 1.4 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,558
;      FILING DATE:  JUNE 6, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB94/00387
;      FILING DATE:  NOVEMBER 21, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YANKWICH, LEON R.
;      REGISTRATION NUMBER:  30,237
;      REFERENCE/DOCKET NUMBER:  95,497-L
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-345-9100
;      TELEFAX:  617-345-9111
;  INFORMATION FOR SEQ ID NO:  44:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-558-44

  Query Match             100.0%;  Score 61;  DB 1;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 0.051;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||||
Db        107 WGQGTPVTVSS 117


RESULT 5
US-08-652-558-45
; Sequence 45, Application US/08652558
; Patent No. 5861155
;  GENERAL INFORMATION:
;    APPLICANT:  LIN, AUGUSTINE YEE-THARN
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER & WITCOFF
;      STREET:  75 STATE STREET, 23RD FLOOR
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette, 1.4 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,558
;      FILING DATE:  JUNE 6, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB94/00387
;      FILING DATE:  NOVEMBER 21, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YANKWICH, LEON R.
;      REGISTRATION NUMBER:  30,237
;      REFERENCE/DOCKET NUMBER:  95,497-L
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-345-9100
;      TELEFAX:  617-345-9111
;  INFORMATION FOR SEQ ID NO:  45:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-558-45

  Query Match             100.0%;  Score 61;  DB 1;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 0.051;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||||
Db        107 WGQGTPVTVSS 117


RESULT 6
US-08-652-558-46
; Sequence 46, Application US/08652558
; Patent No. 5861155
;  GENERAL INFORMATION:
;    APPLICANT:  LIN, AUGUSTINE YEE-THARN
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES AND USES
;    TITLE OF INVENTION:  THEREOF
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER & WITCOFF
;      STREET:  75 STATE STREET, 23RD FLOOR
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette, 1.4 Mb storage
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/652,558
;      FILING DATE:  JUNE 6, 1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB94/00387
;      FILING DATE:  NOVEMBER 21, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YANKWICH, LEON R.
;      REGISTRATION NUMBER:  30,237
;      REFERENCE/DOCKET NUMBER:  95,497-L
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-345-9100
;      TELEFAX:  617-345-9111
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-652-558-46

  Query Match             100.0%;  Score 61;  DB 1;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 0.051;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||||
Db        107 WGQGTPVTVSS 117


RESULT 7
US-08-983-607-46
; Sequence 46, Application US/08983607
; Patent No. 6140470
;  GENERAL INFORMATION:
;    APPLICANT:  Alan Garen
;    APPLICANT:  Xiaohong Cai
;    TITLE OF INVENTION:  Human Anti-Tumor Monoclonal Anti-
;    TITLE OF INVENTION:  bodies
;    NUMBER OF SEQUENCES:  51
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Department of Molecular Biophysics
;      ADDRESSEE:  and Biochemistry, Yale University
;      STREET:  266 Whitney Avenue
;      CITY:  New Haven
;      STATE:  Connecticut
;      COUNTRY:  United States of America
;      ZIP:  06520-8114
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" 1.44 Mb diskette
;      COMPUTER:  IBM PC
;      OPERATING SYSTEM:  MS DOS
;      SOFTWARE:  Word Processing
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/983,607
;      FILING DATE:  April 27, 1998
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;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/IB96/01032
;      FILING DATE:  June 28, 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mary M. Krinsky
;      REGISTRATION NUMBER:  32423
;      REFERENCE/DOCKET NUMBER:  OCR-679
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  203-773-9544
;      TELEFAX:  203-773-1183
;  INFORMATION FOR SEQ ID NO:  46:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 residues
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:
;      DESCRIPTION:  polypeptide
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens (melanoma patient
;      ORGANISM:  immunized with autologous tumor cells)
;      INDIVIDUAL ISOLATE:  peripheral blood lympho-
;      INDIVIDUAL ISOLATE:  cytes
;    IMMEDIATE SOURCE:
;      LIBRARY:  VH antibodies obtained from fUSE5
;      LIBRARY:  fusion phage construct
;      CLONE:  C55
;    FEATURE:
;      NAME/KEY:  heavy chain
US-08-983-607-46

  Query Match             100.0%;  Score 61;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 0.051;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||||
Db        107 WGQGTPVTVSS 117


RESULT 8
US-08-207-996-22
; Sequence 22, Application US/08207996
; Patent No. 5646253
;  GENERAL INFORMATION:
;    APPLICANT:  Scotgen Biopharmaceuticals,  Inc.
;    APPLICANT:  1014 Hamilton Court
;    APPLICANT:  Menlo Park, California 94025
;    APPLICANT:  United States of America
;    APPLICANT:  1345 Avenue of the Americas
;    APPLICANT:  New York, New York 10105
;    APPLICANT:  United States of America
;    TITLE OF INVENTION:  RECOMBINANT HUMAN ANTI-LK26
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.0/ASCII standard
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/207,996
;      FILING DATE:  08-MAR-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pasqualini, Patricia A.
;      REGISTRATION NUMBER:  34,894
;      REFERENCE/DOCKET NUMBER:  LUD-5363
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-688-9200
;      TELEFAX:  212-838-3884
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-207-996-22

  Query Match             100.0%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.052;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||||
Db        109 WGQGTPVTVSS 119


RESULT 9
US-08-859-649-20
; Sequence 20, Application US/08859649
; Patent No. 5874060
;  GENERAL INFORMATION:
;    APPLICANT:  Armour, Kathryn L.
;    APPLICANT:  Carr, Francis J.
;    APPLICANT:  Old, Lloyd J.
;    APPLICANT:  Kitamura, Kunio
;    APPLICANT:  Garin-Chesa, Pilar
;    TITLE OF INVENTION:  Recombinant Human Anti-Lewis Y
;    TITLE OF INVENTION:  Antibodies
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  2730 Sand Hill Road
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,649
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/207,861
;      FILING DATE:  08-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-859-649-20
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  Query Match           100.0%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.052;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db        109 WGQGTPVTVSS 119


RESULT 10
US-08-859-649-21
; Sequence 21, Application US/08859649
; Patent No. 5874060
;  GENERAL INFORMATION:
;    APPLICANT:  Armour, Kathryn L.
;    APPLICANT:  Carr, Francis J.
;    APPLICANT:  Old, Lloyd J.
;    APPLICANT:  Kitamura, Kunio
;    APPLICANT:  Garin-Chesa, Pilar
;    TITLE OF INVENTION:  Recombinant Human Anti-Lewis Y
;    TITLE OF INVENTION:  Antibodies
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  2730 Sand Hill Road
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,649
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/207,861
;      FILING DATE:  08-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-859-649-21

  Query Match           100.0%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.052;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db        109 WGQGTPVTVSS 119


RESULT 11
US-08-859-649-22
; Sequence 22, Application US/08859649
; Patent No. 5874060
;  GENERAL INFORMATION:
;    APPLICANT:  Armour, Kathryn L.
;    APPLICANT:  Carr, Francis J.
;    APPLICANT:  Old, Lloyd J.
;    APPLICANT:  Kitamura, Kunio
;    APPLICANT:  Garin-Chesa, Pilar
;    TITLE OF INVENTION:  Recombinant Human Anti-Lewis Y
;    TITLE OF INVENTION:  Antibodies
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  2730 Sand Hill Road
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,649
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/207,861
;      FILING DATE:  08-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-859-649-22

  Query Match           100.0%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.052;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db        109 WGQGTPVTVSS 119


RESULT 12
US-08-859-649-23
; Sequence 23, Application US/08859649
; Patent No. 5874060
;  GENERAL INFORMATION:
;    APPLICANT:  Armour, Kathryn L.
;    APPLICANT:  Carr, Francis J.
;    APPLICANT:  Old, Lloyd J.
;    APPLICANT:  Kitamura, Kunio
;    APPLICANT:  Garin-Chesa, Pilar
;    TITLE OF INVENTION:  Recombinant Human Anti-Lewis Y
;    TITLE OF INVENTION:  Antibodies
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  2730 Sand Hill Road
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  94025
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,649
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/207,861
;      FILING DATE:  08-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-859-649-23

  Query Match             100.0%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.052;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||||
Db        109 WGQGTPVTVSS 119


RESULT 13
US-08-859-649-24
; Sequence 24, Application US/08859649
; Patent No. 5874060
;  GENERAL INFORMATION:
;    APPLICANT:  Armour, Kathryn L.
;    APPLICANT:  Carr, Francis J.
;    APPLICANT:  Old, Lloyd J.
;    APPLICANT:  Kitamura, Kunio
;    APPLICANT:  Garin-Chesa, Pilar
;    TITLE OF INVENTION:  Recombinant Human Anti-Lewis Y
;    TITLE OF INVENTION:  Antibodies
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  2730 Sand Hill Road
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,649
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/207,861
;      FILING DATE:  08-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-859-649-24

  Query Match             100.0%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.052;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||||
Db        109 WGQGTPVTVSS 119


RESULT 14
US-08-859-649-31
; Sequence 31, Application US/08859649
; Patent No. 5874060
;  GENERAL INFORMATION:
;    APPLICANT:  Armour, Kathryn L.
;    APPLICANT:  Carr, Francis J.
;    APPLICANT:  Old, Lloyd J.
;    APPLICANT:  Kitamura, Kunio
;    APPLICANT:  Garin-Chesa, Pilar
;    TITLE OF INVENTION:  Recombinant Human Anti-Lewis Y
;    TITLE OF INVENTION:  Antibodies
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  2730 Sand Hill Road
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,649
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/207,861
;      FILING DATE:  08-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-027
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  31:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-859-649-31

  Query Match             100.0%;  Score 61;  DB 1;  Length 119;
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  Best Local Similarity   100.0%;  Pred. No. 0.052;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db        109 WGQGTPVTVSS 119


RESULT 15
US-08-318-157B-12
; Sequence 12, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-12

  Query Match             100.0%;  Score 61;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.052;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db        109 WGQGTPVTVSS 119


Search completed: March 25, 2006, 09:18:47
Job time : 10.0209 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:55:36 ; Search time 32.8272 Seconds
(without alignments)
140.009 Million cell updates/sec

Title: US-10-755-382-39
Perfect score: 61
Sequence: 1 WGQGTPVTVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	61	100.0	11	3	US-09-253-794-39	Sequence 39, Appl
2	61	100.0	11	5	US-10-755-382-39	Sequence 39, Appl
3	61	100.0	117	6	US-11-010-797-5	Sequence 5, Appli
4	61	100.0	119	3	US-09-253-794-12	Sequence 12, Appl
5	61	100.0	119	3	US-09-253-794-13	Sequence 13, Appl
6	61	100.0	119	3	US-09-253-794-14	Sequence 14, Appl
7	61	100.0	119	3	US-09-253-794-15	Sequence 15, Appl
8	61	100.0	119	3	US-09-253-794-17	Sequence 17, Appl
9	61	100.0	119	3	US-09-253-794-58	Sequence 58, Appl
10	61	100.0	119	4	US-10-267-286A-12	Sequence 12, Appl
11	61	100.0	119	4	US-10-267-286A-13	Sequence 13, Appl
12	61	100.0	119	4	US-10-267-286A-14	Sequence 14, Appl
13	61	100.0	119	4	US-10-680-734-12	Sequence 12, Appl
14	61	100.0	119	4	US-10-680-734-13	Sequence 13, Appl
15	61	100.0	119	4	US-10-680-734-14	Sequence 14, Appl
16	61	100.0	119	4	US-10-680-734-15	Sequence 15, Appl
17	61	100.0	119	4	US-10-680-734-17	Sequence 17, Appl
18	61	100.0	119	4	US-10-680-734-27	Sequence 27, Appl
19	61	100.0	119	5	US-10-722-849-1	Sequence 1, Appli
20	61	100.0	119	5	US-10-722-849-9	Sequence 9, Appli
21	61	100.0	119	5	US-10-755-382-12	Sequence 12, Appl
22	61	100.0	119	5	US-10-755-382-13	Sequence 13, Appl
23	61	100.0	119	5	US-10-755-382-14	Sequence 14, Appl
24	61	100.0	119	5	US-10-755-382-15	Sequence 15, Appl
25	61	100.0	119	5	US-10-755-382-17	Sequence 17, Appl
26	61	100.0	119	5	US-10-755-382-58	Sequence 58, Appl
27	61	100.0	119	6	US-11-056-776-4	Sequence 4, Appli
28	61	100.0	119	6	US-11-004-659-1	Sequence 1, Appli
29	61	100.0	119	6	US-11-004-659-9	Sequence 9, Appli
30	61	100.0	120	3	US-09-229-200A-9	Sequence 9, Appli
31	61	100.0	120	4	US-10-229-335-2	Sequence 2, Appli
32	61	100.0	122	3	US-09-155-106-17	Sequence 17, Appl
33	61	100.0	122	3	US-09-155-106-19	Sequence 19, Appl
34	61	100.0	122	3	US-09-155-106-20	Sequence 20, Appl
35	61	100.0	122	3	US-09-155-106-26	Sequence 26, Appl
36	61	100.0	122	5	US-10-808-538-17	Sequence 17, Appl
37	61	100.0	122	5	US-10-808-538-19	Sequence 19, Appl
38	61	100.0	122	5	US-10-808-538-20	Sequence 20, Appl
39	61	100.0	122	5	US-10-808-538-26	Sequence 26, Appl
40	61	100.0	122	6	US-11-021-715-54	Sequence 54, Appl
41	61	100.0	125	5	US-10-989-462-25	Sequence 25, Appl
42	61	100.0	126	3	US-09-253-794-7	Sequence 7, Appli
43	61	100.0	126	3	US-09-229-200A-8	Sequence 8, Appli
44	61	100.0	126	3	US-09-795-515-10	Sequence 10, Appl
45	61	100.0	126	4	US-10-267-286A-11	Sequence 11, Appl

ALIGNMENTS

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RESULT 1
US-09-253-794-39
; Sequence 39, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 39:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 11 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-253-794-39

  Query Match           100.0%;  Score 61;  DB 3;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 0.0039;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 WGQGTPVTVSS 11
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Db          1 WGQGTPVTVSS 11


RESULT 2
US-10-755-382-39
; Sequence 39, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 39:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 11 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-755-382-39

  Query Match             100.0%;  Score 61;  DB 5;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.0039;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||
Db          1 WGQGTPVTVSS 11


RESULT 3
US-11-010-797-5
; Sequence 5, Application US/11010797
; Publication No. US20050220793A1
; GENERAL INFORMATION:
;  APPLICANT: Centocor, Inc.
;  APPLICANT:  Anderson, Glenn M
;  TITLE OF INVENTION: ANTI-TISSUE FACTOR ANTIBODIES AND COMPOSITIONS
;  FILE REFERENCE: CEN5026CIP
;  CURRENT APPLICATION NUMBER: US/11/010,797
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: 60/475174
;  PRIOR FILING DATE: 2003-05-30
;  PRIOR APPLICATION NUMBER: 10/855664
;  PRIOR FILING DATE: 2004-05-27
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: humanized
US-11-010-797-5

  Query Match             100.0%;  Score 61;  DB 6;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 0.041;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||
Db        107 WGQGTPVTVSS 117


RESULT 4
US-09-253-794-12
; Sequence 12, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-253-794-12

  Query Match             100.0%;  Score 61;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 WGQGTPVTVSS 11
              ||||||||||
Db        109 WGQGTPVTVSS 119


RESULT 5
US-09-253-794-13
; Sequence 13, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-253-794-13

  Query Match             100.0%;  Score 61;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||
Db        109 WGQGTPVTVSS 119


RESULT 6
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

  Query Match             100.0%;  Score 61;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||
Db        109 WGQGTPVTVSS 119


RESULT 7
US-09-253-794-15
; Sequence 15, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
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;           FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;           NAME: SAXE, Bernhard D.
;           REGISTRATION NUMBER: 28,665
;           REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 119 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-253-794-15

  Query Match             100.0%;  Score 61;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||||
Db        109 WGQGTPVTVSS 119


RESULT 8
US-09-253-794-17
; Sequence 17, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Foley & Lardner
;           STREET: 3000 K Street, N.W., Suite 500
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/253,794
;           FILING DATE: 22-Feb-1999
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US 08/318,157
;           FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;           NAME: SAXE, Bernhard D.
;           REGISTRATION NUMBER: 28,665
;           REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 119 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-253-794-17

  Query Match             100.0%;  Score 61;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||||
Db        109 WGQGTPVTVSS 119


RESULT 9
US-09-253-794-58
; Sequence 58, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Foley & Lardner
;           STREET: 3000 K Street, N.W., Suite 500
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/253,794
;           FILING DATE: 22-Feb-1999
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US 08/318,157
;           FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;           NAME: SAXE, Bernhard D.
;           REGISTRATION NUMBER: 28,665
;           REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 58:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 119 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-253-794-58

  Query Match             100.0%;  Score 61;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||||
Db        109 WGQGTPVTVSS 119


RESULT 10
US-10-267-286A-12
; Sequence 12, Application US/10267286A
; Publication No. US20030108548A1
; GENERAL INFORMATION:
;  APPLICANT: BLUESTONE, JEFFREY A.
;  APPLICANT:  ZIVIN, ROBERT A.
;  APPLICANT:  JOLLIFFE, LINDA K.
```

```
;  TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
;  TITLE OF INVENTION:  IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: TOLT:004USC1
;  CURRENT APPLICATION NUMBER: US/10/267,286A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 08/557,050
;  PRIOR FILING DATE: 1998-10-09
;  PRIOR APPLICATION NUMBER: PCT/US94/06198
;  PRIOR FILING DATE: 1994-06-01
;  PRIOR APPLICATION NUMBER: 08/070,116
;  PRIOR FILING DATE: 1993-06-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-10-267-286A-12

  Query Match             100.0%;  Score 61;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||||
Db        109 WGQGTPVTVSS 119


RESULT 11
US-10-267-286A-13
; Sequence 13, Application US/10267286A
; Publication No. US20030108548A1
; GENERAL INFORMATION:
;  APPLICANT: BLUESTONE, JEFFREY A.
;  APPLICANT:  ZIVIN, ROBERT A.
;  APPLICANT:  JOLLIFFE, LINDA K.
;  TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
;  TITLE OF INVENTION:  IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: TOLT:004USC1
;  CURRENT APPLICATION NUMBER: US/10/267,286A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 08/557,050
;  PRIOR FILING DATE: 1998-10-09
;  PRIOR APPLICATION NUMBER: PCT/US94/06198
;  PRIOR FILING DATE: 1994-06-01
;  PRIOR APPLICATION NUMBER: 08/070,116
;  PRIOR FILING DATE: 1993-06-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-10-267-286A-13

  Query Match             100.0%;  Score 61;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||||
Db        109 WGQGTPVTVSS 119


RESULT 12
US-10-267-286A-14
; Sequence 14, Application US/10267286A
; Publication No. US20030108548A1
; GENERAL INFORMATION:
;  APPLICANT: BLUESTONE, JEFFREY A.
;  APPLICANT:  ZIVIN, ROBERT A.
;  APPLICANT:  JOLLIFFE, LINDA K.
;  TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
;  TITLE OF INVENTION:  IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: TOLT:004USC1
;  CURRENT APPLICATION NUMBER: US/10/267,286A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 08/557,050
;  PRIOR FILING DATE: 1998-10-09
;  PRIOR APPLICATION NUMBER: PCT/US94/06198
;  PRIOR FILING DATE: 1994-06-01
;  PRIOR APPLICATION NUMBER: 08/070,116
;  PRIOR FILING DATE: 1993-06-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-10-267-286A-14

  Query Match             100.0%;  Score 61;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||||
Db        109 WGQGTPVTVSS 119


RESULT 13
US-10-680-734-12
; Sequence 12, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-12

  Query Match             100.0%;  Score 61;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||||
Db        109 WGQGTPVTVSS 119
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RESULT 14
US-10-680-734-13
; Sequence 13, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-13

  Query Match             100.0%;  Score 61;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| |
Db        109 WGQGTPVTVSS 119


RESULT 15
US-10-680-734-14
; Sequence 14, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-14

  Query Match             100.0%;  Score 61;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| |
Db        109 WGQGTPVTVSS 119


Search completed: March 25, 2006, 10:08:06
Job time : 32.8272 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 25, 2006, 09:58:56 ; Search time 3.97382 Seconds
(without alignments)
81.644 Million cell updates/sec

Title: US-10-755-382-39
Perfect score: 61
Sequence: 1 WGQGTPVTVSS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 174695 seqs, 29494374 residues

Total number of hits satisfying chosen parameters: 174695

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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6: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	61	100.0	119	7	US-11-221-900-12	Sequence 12, Appl
2	61	100.0	119	7	US-11-221-900-13	Sequence 13, Appl
3	61	100.0	119	7	US-11-221-900-14	Sequence 14, Appl
4	61	100.0	126	7	US-11-221-900-11	Sequence 11, Appl
5	61	100.0	236	7	US-11-221-900-2	Sequence 2, Appli
6	61	100.0	247	7	US-11-054-515-1685	Sequence 1685, Ap
7	61	100.0	449	7	US-11-080-587-6	Sequence 6, Appli
8	57	93.4	119	7	US-11-076-395-19	Sequence 19, Appl
9	57	93.4	247	7	US-11-054-515-1934	Sequence 1934, Ap
10	57	93.4	248	7	US-11-054-515-1306	Sequence 1306, Ap
11	57	93.4	255	7	US-11-054-515-1054	Sequence 1054, Ap
12	57	93.4	255	7	US-11-054-515-1608	Sequence 1608, Ap
13	57	93.4	256	7	US-11-054-515-1607	Sequence 1607, Ap
14	55	90.2	11	6	US-10-880-238-167	Sequence 167, App
15	53	86.9	11	6	US-10-839-799-114	Sequence 114, App
16	53	86.9	11	6	US-10-839-799-129	Sequence 129, App
17	53	86.9	11	7	US-11-108-135-7	Sequence 7, Appli
18	53	86.9	11	7	US-11-226-325-179	Sequence 179, App
19	53	86.9	11	7	US-11-126-978-7	Sequence 7, Appli
20	53	86.9	11	7	US-11-222-745-35	Sequence 35, Appl
21	53	86.9	11	7	US-11-226-886-50	Sequence 50, Appl
22	53	86.9	12	7	US-11-009-840A-166	Sequence 166, App
23	53	86.9	12	7	US-11-009-840A-168	Sequence 168, App
24	53	86.9	12	7	US-11-009-873A-166	Sequence 166, App
25	53	86.9	12	7	US-11-009-873A-168	Sequence 168, App
26	53	86.9	12	7	US-11-009-769A-166	Sequence 166, App
27	53	86.9	12	7	US-11-009-769A-168	Sequence 168, App
28	53	86.9	19	7	US-11-089-266-6	Sequence 6, Appli
29	53	86.9	20	6	US-10-993-543-293	Sequence 293, App
30	53	86.9	20	7	US-11-040-159-4	Sequence 4, Appli
31	53	86.9	20	7	US-11-054-669-107	Sequence 107, App
32	53	86.9	20	7	US-11-061-848-31	Sequence 31, Appl
33	53	86.9	20	7	US-11-004-590-109	Sequence 109, App
34	53	86.9	26	7	US-11-040-159-3	Sequence 3, Appli
35	53	86.9	29	7	US-11-009-840A-118	Sequence 118, App
36	53	86.9	29	7	US-11-009-873A-118	Sequence 118, App
37	53	86.9	29	7	US-11-009-769A-118	Sequence 118, App
38	53	86.9	31	7	US-11-009-840A-128	Sequence 128, App
39	53	86.9	31	7	US-11-009-873A-128	Sequence 128, App
40	53	86.9	31	7	US-11-009-769A-128	Sequence 128, App
41	53	86.9	32	7	US-11-009-840A-137	Sequence 137, App
42	53	86.9	32	7	US-11-009-873A-137	Sequence 137, App
43	53	86.9	32	7	US-11-009-769A-137	Sequence 137, App
44	53	86.9	33	7	US-11-009-840A-123	Sequence 123, App
45	53	86.9	33	7	US-11-009-840A-134	Sequence 134, App

ALIGNMENTS

RESULT 1
US-11-221-900-12
; Sequence 12, Application US/11221900
; Publication No. US20060002933A1
; GENERAL INFORMATION:
; APPLICANT: BLUESTONE, JEFFREY A.
; APPLICANT: ZIVIN, ROBERT A.
; APPLICANT: JOLLIFFE, LINDA K.
; TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
; TITLE OF INVENTION: IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES
; FILE REFERENCE: TOLT:004USC1
; CURRENT APPLICATION NUMBER: US/11/221,900
; CURRENT FILING DATE: 2005-09-09
; PRIOR APPLICATION NUMBER: US/10/267,286
; PRIOR FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 08/557,050
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: PCT/US94/06198
; PRIOR FILING DATE: 1994-06-01
; PRIOR APPLICATION NUMBER: 08/070,116
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-11-221-900-12

Query Match 100.0%; Score 61; DB 7; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WGQGTPVTVSS 11
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Db 109 WGQGTPVTVSS 119

RESULT 2
US-11-221-900-13
; Sequence 13, Application US/11221900
; Publication No. US20060002933A1
; GENERAL INFORMATION:
; APPLICANT: BLUESTONE, JEFFREY A.

```
;  APPLICANT:  ZIVIN, ROBERT A.
;  APPLICANT:  JOLLIFFE, LINDA K.
;  TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
;  TITLE OF INVENTION:  IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: TOLT:004USC1
;  CURRENT APPLICATION NUMBER: US/11/221,900
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: US/10/267,286
;  PRIOR FILING DATE: 2003-01-28
;  PRIOR APPLICATION NUMBER: 08/557,050
;  PRIOR FILING DATE: 1998-10-09
;  PRIOR APPLICATION NUMBER: PCT/US94/06198
;  PRIOR FILING DATE: 1994-06-01
;  PRIOR APPLICATION NUMBER: 08/070,116
;  PRIOR FILING DATE: 1993-06-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-11-221-900-13

  Query Match           100.0%;  Score 61;  DB 7;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.0013;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||
Db        109 WGQGTPVTVSS 119


RESULT 3
US-11-221-900-14
; Sequence 14, Application US/11221900
; Publication No. US20060002933A1
; GENERAL INFORMATION:
;  APPLICANT: BLUESTONE, JEFFREY A.
;  APPLICANT:  ZIVIN, ROBERT A.
;  APPLICANT:  JOLLIFFE, LINDA K.
;  TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
;  TITLE OF INVENTION:  IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: TOLT:004USC1
;  CURRENT APPLICATION NUMBER: US/11/221,900
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: US/10/267,286
;  PRIOR FILING DATE: 2003-01-28
;  PRIOR APPLICATION NUMBER: 08/557,050
;  PRIOR FILING DATE: 1998-10-09
;  PRIOR APPLICATION NUMBER: PCT/US94/06198
;  PRIOR FILING DATE: 1994-06-01
;  PRIOR APPLICATION NUMBER: 08/070,116
;  PRIOR FILING DATE: 1993-06-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-11-221-900-14

  Query Match           100.0%;  Score 61;  DB 7;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.0013;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
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Db        109 WGQGTPVTVSS 119


RESULT 4
US-11-221-900-11
; Sequence 11, Application US/11221900
; Publication No. US20060002933A1
; GENERAL INFORMATION:
;  APPLICANT: BLUESTONE, JEFFREY A.
;  APPLICANT:  ZIVIN, ROBERT A.
;  APPLICANT:  JOLLIFFE, LINDA K.
;  TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
;  TITLE OF INVENTION:  IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: TOLT:004USC1
;  CURRENT APPLICATION NUMBER: US/11/221,900
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: US/10/267,286
;  PRIOR FILING DATE: 2003-01-28
;  PRIOR APPLICATION NUMBER: 08/557,050
;  PRIOR FILING DATE: 1998-10-09
;  PRIOR APPLICATION NUMBER: PCT/US94/06198
;  PRIOR FILING DATE: 1994-06-01
;  PRIOR APPLICATION NUMBER: 08/070,116
;  PRIOR FILING DATE: 1993-06-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 126
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-11-221-900-11

  Query Match           100.0%;  Score 61;  DB 7;  Length 126;
  Best Local Similarity  100.0%;  Pred. No. 0.0014;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
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Db        116 WGQGTPVTVSS 126


RESULT 5
US-11-221-900-2
; Sequence 2, Application US/11221900
; Publication No. US20060002933A1
; GENERAL INFORMATION:
;  APPLICANT: BLUESTONE, JEFFREY A.
;  APPLICANT:  ZIVIN, ROBERT A.
;  APPLICANT:  JOLLIFFE, LINDA K.
;  TITLE OF INVENTION: METHODS AND MATERIALS FOR MODULATION OF THE
;  TITLE OF INVENTION:  IMMUNOSUPPRESSIVE ACTIVITY AND TOXICITY OF MONOCLONAL
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: TOLT:004USC1
;  CURRENT APPLICATION NUMBER: US/11/221,900
;  CURRENT FILING DATE:  2005-09-09
;  PRIOR APPLICATION NUMBER: US/10/267,286
;  PRIOR FILING DATE: 2003-01-28
;  PRIOR APPLICATION NUMBER: 08/557,050
;  PRIOR FILING DATE: 1998-10-09
;  PRIOR APPLICATION NUMBER: PCT/US94/06198
;  PRIOR FILING DATE: 1994-06-01
;  PRIOR APPLICATION NUMBER: 08/070,116
;  PRIOR FILING DATE: 1993-06-01
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 236
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;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptide
US-11-221-900-2

  Query Match             100.0%;  Score 61;  DB 7;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 0.0025;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
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Db        128 WGQGTPVTVSS 138


RESULT 6
US-11-054-515-1685
; Sequence 1685, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1685
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1685

  Query Match             100.0%;  Score 61;  DB 7;  Length 247;
  Best Local Similarity   100.0%;  Pred. No. 0.0026;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||||||| 
Db        111 WGQGTPVTVSS 121


RESULT 7
US-11-080-587-6
; Sequence 6, Application US/11080587
; Publication No. US20060002942A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  TITLE OF INVENTION: Calicheamicin Conjugates
;  FILE REFERENCE: AM101462
;  CURRENT APPLICATION NUMBER: US/11/080,587
;  CURRENT FILING DATE:  2005-03-15
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 449
;   TYPE: PRT
;   ORGANISM: Human/murine chimera
;   FEATURE:
;   OTHER INFORMATION: Human/Murine Chimera G193 Heavy Chain
US-11-080-587-6

  Query Match             100.0%;  Score 61;  DB 7;  Length 449;
  Best Local Similarity   100.0%;  Pred. No. 0.0046;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
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Db        109 WGQGTPVTVSS 119


RESULT 8
US-11-076-395-19
; Sequence 19, Application US/11076395
; Publication No. US20060029594A1
;   GENERAL INFORMATION:
;        APPLICANT: Ames, Robert S.
;                   Appelbaum, Edward R.
;                   Chaiken, Irwin M.
;                   Cook, Richard M.
;                   Gross, Mitchell S.
;                   Holmes, Stephen D.
;                   McMillan, Lynette J.
;                   Theisen, Timothy W.
;        TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
;                            Treatment of IL5 Mediated Disorders
;        NUMBER OF SEQUENCES: 76
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: SmithKline Beecham Corp
;             STREET: P.O. Box 1539-UW2220
;             CITY: King of Prussia
;             STATE: Pennsylvania
;             COUNTRY: USA
;             ZIP: 19406-0939
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/076,395
;             FILING DATE: 09-Mar-2005
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/10/700,740
;             FILING DATE: 04-Nov-2003
;             APPLICATION NUMBER: US/10/144,644
;             FILING DATE: 2002-08-08
;             APPLICATION NUMBER: US 08/470110
;             FILING DATE: 06-JUN-1995
;             APPLICATION NUMBER: US 08/467420
;             FILING DATE: 06-JUN-1995
;             APPLICATION NUMBER: US 08/363131
;             FILING DATE: 23-DEC-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Sutton, Jeffrey A.
;             REGISTRATION NUMBER: 34,028
;             REFERENCE/DOCKET NUMBER: P50282-2
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 610-270-5024
;             TELEFAX: 610-270-5090
;   INFORMATION FOR SEQ ID NO: 19:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
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;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-11-076-395-19

  Query Match             93.4%;  Score 57;  DB 7;  Length 119;
  Best Local Similarity   90.9%;  Pred. No. 0.0062;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||:||||||||
Db        109 WGRGTPVTVSS 119


RESULT 9
US-11-054-515-1934
; Sequence 1934, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1934
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1934

  Query Match             93.4%;  Score 57;  DB 7;  Length 247;
  Best Local Similarity   90.9%;  Pred. No. 0.012;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||:||||||||
Db        111 WGRGTPVTVSS 121


RESULT 10
US-11-054-515-1306
; Sequence 1306, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1306
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1306

  Query Match             93.4%;  Score 57;  DB 7;  Length 248;
  Best Local Similarity   90.9%;  Pred. No. 0.012;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
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Db        115 WGKGTPVTVSS 125


RESULT 11
US-11-054-515-1054
; Sequence 1054, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1054
;   LENGTH: 255
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1054
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  Query Match             93.4%;  Score 57;  DB 7;  Length 255;
  Best Local Similarity   90.9%;  Pred. No. 0.013;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||:||||||||
Db        122 WGKGTPVTVSS 132


RESULT 12
US-11-054-515-1608
; Sequence 1608, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1608
;   LENGTH: 255
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1608

  Query Match             93.4%;  Score 57;  DB 7;  Length 255;
  Best Local Similarity   90.9%;  Pred. No. 0.013;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||:||||||||
Db        119 WGRGTPVTVSS 129


RESULT 13
US-11-054-515-1607
; Sequence 1607, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1607
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1607

  Query Match             93.4%;  Score 57;  DB 7;  Length 256;
  Best Local Similarity   90.9%;  Pred. No. 0.013;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||:||||||||
Db        120 WGRGTPVTVSS 130


RESULT 14
US-10-880-238-167
; Sequence 167, Application US/10880238
; Publication No. US20050287538A1
; GENERAL INFORMATION:
;  APPLICANT: Cheung , Wing-Tai
;  APPLICANT:  Cheng, Man
;  TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERMLINE
;  TITLE OF INVENTION:  IMMUNOGLOBULIN GENES RETRIEVAL AND ANTIBODY ENGINEERING
;  FILE REFERENCE: 17329-003001
;  CURRENT APPLICATION NUMBER: US/10/880,238
;  CURRENT FILING DATE:  2004-06-29
;  NUMBER OF SEQ ID NOS: 214
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 167
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetically generated peptide
US-10-880-238-167

  Query Match             90.2%;  Score 55;  DB 6;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 0.0014;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WGQGTPVTVSS 11
              ||||||:|||:
Db          1 WGQGTPLTVSA 11


RESULT 15
US-10-839-799-114
; Sequence 114, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/839,799
; FILING DATE: 06-May-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,265
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: WO PCT/JP94/01763
; FILING DATE: 19-OCT-1994
; APPLICATION NUMBER: JP 5-291078
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/184
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 114:
US-10-839-799-114

Query Match 86.9%; Score 53; DB 6; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.003;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WGQGTPVTVSS 11
||||| |||||
Db 1 WGQGTTVTVSS 11

Search completed: March 25, 2006, 10:09:21
Job time : 4.97382 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:17:30 ; Search time 190 Seconds
(without alignments)
275.190 Million cell updates/sec

Title: US-10-755-382-2
Perfect score: 641
Sequence: 1 EVKLLESGGGLVQSGGSLKL.....YFGFPWFAYWGQGTPVTVSA 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	641	100.0	119	2	AAR97334	Aar97334 Murine NE
2	641	100.0	119	8	ADM95095	Adm95095 Murine MN
3	641	100.0	119	8	ADM98318	Adm98318 Murine MN
4	568	88.6	119	8	ADM95101	Adm95101 Humanised
5	568	88.6	119	8	ADM98324	Adm98324 Humanised
6	568	88.6	138	6	ABG76489	Abg76489 Heavy cha
7	568	88.6	443	6	ABG76488	Abg76488 Humanised
8	568	88.6	443	6	ABG74240	Abg74240 Chimaeric
9	568	88.6	468	7	ADE64201	Ade64201 MN14HCF p
10	568	88.6	468	7	ADF60815	Adf60815 hMN-14 he
11	568	88.6	669	9	ADY97271	Ady97271 Exemplary
12	567	88.5	118	6	ABR42755	Abr42755 Anti-CEA
13	567	88.5	256	6	ABR42757	Abr42757 Anti-CEA
14	567	88.5	257	6	ABR42758	Abr42758 Anti-CEA
15	567	88.5	261	6	ABR42289	Abr42289 Diabody 6
16	567	88.5	261	6	ABR42754	Abr42754 Anti-CEA
17	567	88.5	261	6	ABR83645	Abr83645 hMN14-scF
18	567	88.5	267	6	ABR42292	Abr42292 Bispecifi
19	567	88.5	267	6	ABR42299	Abr42299 Bispecifi
20	567	88.5	267	6	ABR42296	Abr42296 Bispecifi
21	567	88.5	267	6	ABR42294	Abr42294 Bispecifi
22	567	88.5	358	8	ADU26571	Adu26571 Chimeric
23	567	88.5	363	8	ADU26561	Adu26561 Chimeric
24	567	88.5	364	8	ADU26570	Adu26570 Chimeric
25	567	88.5	370	8	ADU26560	Adu26560 Chimeric
26	567	88.5	415	6	ABR83648	Abr83648 TS1 VH ch
27	544.5	84.9	220	8	ADU86552	Adu86552 Immunoglo
28	539	84.1	119	2	AAR97336	Aar97336 Humanised
29	529.5	82.6	256	5	AAU72864	Aau72864 P4-15 sin
30	529.5	82.6	258	5	AAU72871	Aau72871 3B10xP4-3
31	529.5	82.6	503	5	AAU72873	Aau72873 3B10xP5-2
32	529.5	82.6	505	5	AAU72875	Aau72875 Human NKG
33	529	82.5	121	8	ADU86551	Adu86551 Immunoglo
34	529	82.5	121	8	ADU86550	Adu86550 Immunoglo
35	526.5	82.1	119	8	ADR15131	Adr15131 Mouse ant
36	526.5	82.1	120	7	ADD94119	Add94119 Mouse HUI
37	525.5	82.0	252	5	AAU72863	Aau72863 P4-14 sin
38	525.5	82.0	499	5	AAU72872	Aau72872 3B10xP4-1
39	525	81.9	142	9	AEB08073	Aeb08073 HLA-DR sp
40	525	81.9	468	9	AEB08072	Aeb08072 Murine/hu
41	523.5	81.7	239	2	AAY17963	Aay17963 Mouse scF
42	523	81.6	119	8	ADU87692	Adu87692 Mouse Luc
43	523	81.6	119	8	ADU87724	Adu87724 Heavy cha
44	523	81.6	119	8	ADU87731	Adu87731 VH region
45	523	81.6	137	8	ADU87714	Adu87714 Anti-CS1

ALIGNMENTS

RESULT 1
AAR97334
ID AAR97334 standard; protein; 119 AA.
XX
AC AAR97334;
XX
DT 15-OCT-1996 (first entry)
XX
DE Murine NEWM MN-14 variable region heavy chain.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Binding-site 31. .35
FT /label= CDR 1.
FT Binding-site 50. .66
FT /label= CDR 2.
FT Binding-site 99. .108
FT /label= CDR 3.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
DR N-PSDB; AAT29010.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Example 5; Fig 1; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a

CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. See AAR97313-97333 for the CDR sequence and framework regions
CC of the humanised MAbs
XX
SQ Sequence 119 AA;

Query Match 100.0%; Score 641; DB 2; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.2e-56;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
Db 1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy 61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
Db 61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119

RESULT 2
ADM95095
ID ADM95095 standard; protein; 119 AA.
XX
AC ADM95095;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 MAb heavy chain variable region.
XX
KW non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW complementarity determining region; pancreatic cancer; breast cancer;
KW ovarian cancer.
XX
OS Mus sp.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-364813/34.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Disclosure; Fig 11A-B; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the murine MN-
CC 14 antibody heavy chain variable region.
XX

SQ Sequence 119 AA;

Query Match 100.0%; Score 641; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 2.2e-56;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
Db 1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy 61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
Db 61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119

RESULT 3
ADM98318
ID ADM98318 standard; protein; 119 AA.
XX
AC ADM98318;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 antibody heavy chain variable region protein.
XX
KW carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW antibody; MN-14; non-medullary thyroid carcinoma;
KW medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW hepatocellular carcinoma; breast cancer; lung cancer;
KW antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW apoptosis.
XX
OS Mus sp.
XX
PN WO2004032857-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031801.
XX
PR 08-OCT-2002; 2002US-0416531P.
PR 11-OCT-2002; 2002WO-US032307.
PR 02-MAY-2003; 2003US-0467161P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-340797/31.
DR N-PSDB; ADM98317.
XX
PT Treating non-medullary or medullary thyroid carcinoma, involves
PT administering to subject, either concurrently or sequentially, anti-
PT carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS Disclosure; Fig 11; 122pp; English.
XX
CC This invention relates to methods for treating cancers that express
CC carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC antibodies that can be used following administration of an agent that
CC will increase antibody effector functions or following administration of
CC an amount of interferon effective to upregulate CEA expression in tumour
CC cells. The present invention describes the anti-CEA antibody as a class
CC III humanised murine monoclonal antibody that retains specificity for CEA
CC binding and is preferably an MN-14 antibody or fragment thereof.
CC Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC composition useful for the treatment of non-medullary or medullary
CC thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC carcinoma, as well as breast or lung cancer. Furthermore, it can
CC stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC cell growth and angiogenesis. This polypeptide sequence is murine MN-14

```
CC   antibody heavy chain variable region protein of the invention.
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 641;  DB 8;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-56;
  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119


RESULT 4
ADM95101
ID   ADM95101 standard; protein; 119 AA.
XX
AC   ADM95101;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 MAb heavy chain variable region coding sequence.
XX
KW   non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW   complementarity determining region; pancreatic cancer; breast cancer;
KW   ovarian cancer.
XX
OS   Mus sp.
OS   Homo sapiens.
XX
PN   WO2004032962-A1.
XX
PD   22-APR-2004.
XX
PF   11-OCT-2002; 2002WO-US032307.
XX
PR   08-OCT-2002; 2002US-0416531P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-364813/34.
DR   N-PSDB; ADM95099.
XX
PT   Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT   comprises administering, either concurrently or sequentially, Class III
PT   anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT   therapeutic agent(s).
XX
PS   Claim 14; Fig 16B; 88pp; English.
XX
CC   The invention relates to a method of treating a non-medullary thyroid
CC   carcinoma or treating medullary thyroid carcinoma involves administering
CC   to a subject, either concurrently or sequentially, a Class III anti-CEA
CC   (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC   least one therapeutic agent. The antibody or its fragment comprises the
CC   complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC   antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC   medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC   ovarian cancer, in a subject. This sequence corresponds to the humanised
CC   murine MN-14 antibody heavy chain variable region.
XX
SQ   Sequence 119 AA;

  Query Match             88.6%;  Score 568;  DB 8;  Length 119;
  Best Local Similarity   84.0%;  Pred. No. 4.7e-49;
  Matches  100;  Conservative   12;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :|||||||||:|||  :| ||| :|:|||||||||||||||||||||:
Db         61 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 5
ADM98324
ID   ADM98324 standard; protein; 119 AA.
XX
AC   ADM98324;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 antibody heavy chain variable region protein.
XX
KW   carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW   antibody; MN-14; non-medullary thyroid carcinoma;
KW   medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW   hepatocellular carcinoma; breast cancer; lung cancer;
KW   antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW   apoptosis; humanised.
XX
OS   Mus sp.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 33. .34
FT                   /note= "Encoded by TGGGATAGCAGTACGATTAACTATGCGATG"
FT   Misc-difference 53. .62
FT                   /note= "Encoded by CCACCG"
XX
PN   WO2004032857-A2.
XX
PD   22-APR-2004.
XX
PF   08-OCT-2003; 2003WO-US031801.
XX
PR   08-OCT-2002; 2002US-0416531P.
PR   11-OCT-2002; 2002WO-US032307.
PR   02-MAY-2003; 2003US-0467161P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-340797/31.
DR   N-PSDB; ADM98323.
XX.
PT   Treating non-medullary or medullary thyroid carcinoma, involves
PT   administering to subject, either concurrently or sequentially, anti-
PT   carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS   Disclosure; Fig 23b; 122pp; English.
XX
CC   This invention relates to methods for treating cancers that express
CC   carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC   therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC   antibodies that can be used following administration of an agent that
CC   will increase antibody effector functions or following administration of
CC   an amount of interferon effective to upregulate CEA expression in tumour
CC   cells. The present invention describes the anti-CEA antibody as a class
CC   III humanised murine monoclonal antibody that retains specificity for CEA
CC   binding and is preferably an MN-14 antibody or fragment thereof.
CC   Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC   composition useful for the treatment of non-medullary or medullary
CC   thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC   carcinoma, as well as breast or lung cancer. Furthermore, it can
CC   stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC   mediated lysis and apoptosis as well as inhibit cell cycle progression,
```

CC cell growth and angiogenesis. This polypeptide sequence is the humanised
CC murine MN-14 antibody heavy chain variable region protein of the
CC invention.
XX
SQ Sequence 119 AA;

Query Match 88.6%; Score 568; DB 8; Length 119;
Best Local Similarity 84.0%; Pred. No. 4.7e-49;
Matches 100; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :|||||||||:|||  :| ||| :|:|||||||||||||||||||||||:
Db         61 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119
```

RESULT 6
ABG76489
ID ABG76489 standard; protein; 138 AA.
XX
AC ABG76489;
XX
DT 13-MAY-2003 (first entry)
XX
DE Heavy chain variable, VH, region of antibody hMN14.
XX
KW CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW human; zeta signalling chain; CD8alpha hinge; humanised antibody;
KW heavy chain variable region; VH.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1. .19
FT /label= Signal_peptide
FT Protein 20. .138
FT /label= Mature_VH_of_hMN14
XX
PN US2002165360-A1.
XX
PD 07-NOV-2002.
XX
PF 10-DEC-2001; 2001US-00006771.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250090P.
XX
PA (JUNG/) JUNGHANS R P.
XX
PI Junghans RP;
XX
DR WPI; 2003-298705/29.
DR N-PSDB; ABX13169.
XX
PT New chimeric molecule from humanized antibody against carcinoembryonic
PT antigen and having signaling molecules of T cells and other effector
PT cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS Disclosure; Page 9; 20pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the
CC carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC which the cysteine residues have been mutated, with the IgTCR molecule
CC occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC NK (not defined) or other effector cells are useful in treating patients
CC with cancers expressing the CEA antigen, together with other or with
CC heterologous constructs to engage additional stimulatory and functional
CC properties of the effector cells to enhance the anti-tumour therapeutic
CC efficacy. The cancer disorder includes colorectal, breast and lung
CC cancers. The present sequence represents the heavy chain variable, VH,
CC region of antibody hMN14. The VH protein is humanised (complementarity
CC determining region-grafted) and has a leader peptide
XX
SQ Sequence 138 AA;

Query Match 88.6%; Score 568; DB 6; Length 138;
Best Local Similarity 84.0%; Pred. No. 5.6e-49;
Matches 100; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db         20 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 79

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :|||||||||:|||  :| ||| :|:|||||||||||||||||||||||:
Db         80 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 138
```

RESULT 7
ABG76488
ID ABG76488 standard; protein; 443 AA.
XX
AC ABG76488;
XX
DT 13-MAY-2003 (first entry)
XX
DE Humanised anti-CEA antibody, hMN14.
XX
KW CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW human; zeta signalling chain; CD8alpha hinge; humanised antibody.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
PN US2002165360-A1.
XX
PD 07-NOV-2002.
XX
PF 10-DEC-2001; 2001US-00006771.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250090P.
XX
PA (JUNG/) JUNGHANS R P.
XX
PI Junghans RP;
XX
DR WPI; 2003-298705/29.
DR N-PSDB; ABX13168.
XX
PT New chimeric molecule from humanized antibody against carcinoembryonic
PT antigen and having signaling molecules of T cells and other effector
PT cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS Disclosure; Page 7-8; 20pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the
CC carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC which the cysteine residues have been mutated, with the IgTCR molecule
CC occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC appearing as ABX13168. The new chimaeric molecule expressed in T cells,

CC NK (not defined) or other effector cells are useful in treating patients
CC with cancers expressing the CEA antigen, together with other or with
CC heterologous constructs to engage additional stimulatory and functional
CC properties of the effector cells to enhance the anti-tumour therapeutic
CC efficacy. The cancer disorder includes colorectal, breast and lung
CC cancers. The present sequence represents the chimaeric molecule of the
CC invention
XX
SQ Sequence 443 AA;

Query Match 88.6%; Score 568; DB 6; Length 443;
Best Local Similarity 84.0%; Pred. No. 2.2e-48;
Matches 100; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Qy 1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
Db 142 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 201

Qy 61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
Db 202 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 260

RESULT 8
ABG74240
ID ABG74240 standard; protein; 443 AA.
XX
AC ABG74240;
XX
DT 23-OCT-2003 (revised)
DT 22-APR-2003 (first entry)
XX
DE Chimaeric hMN14/T-cell receptor.
XX
KW Retroviral vector; T-cell receptor; hMN14; antibody; IgTCR; receptor;
KW cytostatic; dermatological; neuroprotective; immunostimulant; GD3;
KW ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4; 3E11;
KW prostate-specific membrane antigen; zeta signalling chain; human; cancer;
KW melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer;
KW mouse; CD8alpha hinge.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
PN US2002132983-A1.
XX
PD 19-SEP-2002.
XX
PF 10-DEC-2001; 2001US-00006773.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250089P.
XX
PA (JUNG/) JUNGHANS R P.
XX
PI Junghans RP;
XX
DR WPI; 2003-208946/20.
DR N-PSDB; ABX16565.
XX
PT New chimeric molecule useful in treating patients with disorders, such as
PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer
PT comprises GD3 and/or PSMA binding domains of antibody.
XX
PS Disclosure; Page 7-8; 35pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the GD3
CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)
CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC sequences, the zeta signalling chain of the T cell receptor and an
CC intervening CD8alpha hinge in which cysteine residues have been mutated.
CC The chimaeric molecules expressed in T cells or NK cells or other
CC effector cells are useful in treating patients with cancers expressing
CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC and/or together with each other or with heterologous constructs to engage
CC additional stimulatory and functional properties of the effector cells to
CC enhance the antitumour therapeutic efficacy (claimed). They are
CC particularly useful in disorders including melanoma, neuroendocrine
CC tumours and prostate and small cell lung cancer. The present sequence is
CC a hMN14 antibody (specific to CEA antigen) in a fusion protein with the
CC modified CD8alpha hinge and the T-cell receptor zeta chain (IgTCR)
CC encoded by a retroviral vector. The hMN14 antibody coding region is
CC replaced with the MB3.6, 3D8, 4D4 or 3E11 genes of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 443 AA;

Query Match 88.6%; Score 568; DB 6; Length 443;
Best Local Similarity 84.0%; Pred. No. 2.2e-48;
Matches 100; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Qy 1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
Db 142 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 201

Qy 61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
Db 202 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 260

RESULT 9
ADE64201
ID ADE64201 standard; protein; 468 AA.
XX
AC ADE64201;
XX
DT 29-JAN-2004 (first entry)
XX
DE MN14HCF protein related to a novel antibody library.
XX
KW antibody library; retroviral vector; antibody light chain;
KW antibody heavy chain; human therapy; multiplicity of infection; MOI;
KW plasmid; GATEWAY vector; MN14HCF.
XX
OS Unidentified.
XX
PN WO2003083077-A2.
XX
PD 09-OCT-2003.
XX
PF 28-MAR-2003; 2003WO-US009662.
XX
PR 28-MAR-2002; 2002US-0368808P.
PR 10-APR-2002; 2002US-0371299P.
PR 28-MAR-2003; 2003US-00371299.
XX
PA (GALA-) GALA DESIGN INC.
XX
PI Bremel RD, Eakle K, Imboden M;
XX
DR WPI; 2003-804051/75.
DR N-PSDB; ADE64206.
XX
PT New antibody library comprising cells comprising at least one integrated
PT retroviral vector expressing an antibody light or heavy chain, useful in
PT preparing a composition for diagnosing or treating disorders.
XX
PS Disclosure; Fig 6; 57pp; English.
XX
CC This invention relates to a new antibody library which comprises at least
CC 100 cells, each of which comprises at least one integrated retroviral
CC vector expressing an antibody light or heavy chain. Antibodies are of
CC increasing importance in human therapy, assay procedures and diagnostic
CC methods and a need exists for efficient methods of generating and

CC screening antibody libraries containing large numbers of antibodies. The
CC antibody library of the invention addresses this need, with the
CC additional advantage of strict control over multiplicity of infection
CC (MOI), and is useful in preparing a composition for diagnosing or
CC treating a wide variety of disorders. The present sequence is the amino
CC acid sequence of the MN14HCF protein, which was encoded by the Gateway
CC retroviral vectors used in the exemplification of the invention.
XX
SQ Sequence 468 AA;

Query Match 88.6%; Score 568; DB 7; Length 468;
Best Local Similarity 84.0%; Pred. No. 2.3e-48;
Matches 100; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db         20 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 79

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :|||||||||:|||  :| ||| :|:|||||||||||||||||||||:
Db         80 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 138
```

RESULT 10
ADF60815
ID ADF60815 standard; protein; 468 AA.
XX
AC ADF60815;
XX
DT 12-FEB-2004 (first entry)
XX
DE hMN-14 heavy chain amino acid sequence.
XX
KW Immunomodulatory; antidiabetic; immunosuppressive; cardiovascular;
KW neuroprotective; nootropic; fungicide; virucide; antimalarial;
KW antihelmintic; antiparasitic; haemostatic; muscular; antiinflammatory;
KW dermatological; antipyretic; antirheumatic; cytostatic; mutant;
KW bispecific antibody; immunoglobulin G; IgG; scFvs; Fvs; CH2 domain;
KW immune; autoimmune; disease; organ graft rejection; cardiovascular;
KW neurological; Alzheimer's disease; graft vs host disease;
KW systemic lupus erythematosus; diabetes mellitus.
XX
OS Homo sapiens.
XX
PN WO2003074569-A2.
XX
PD 12-SEP-2003.
XX
PF 03-MAR-2003; 2003WO-GB000871.
XX
PR 01-MAR-2002; 2002US-0361037P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (MCCA/) MCCALL J D.
XX
PI Qu Z, Hansen H, Goldenberg DM;
XX
DR WPI; 2003-902725/82.
DR N-PSDB; ADF60814.
XX
PT Mutant bispecific antibody which is rapidly cleared from a patient's
PT body, useful as a pretargeting agent in methods for diagnosing or
PT treating diseases, such as autoimmune disease, and disease caused by
PT infectious agents.
XX
PS Example; Fig 1; 68pp; English.
XX
CC The invention relates to a mutant bispecific antibody (mbAb1) comprising
CC at least a human hinge constant region from immunoglobulin G (IgG), two
CC single chain variable fragments (scFvs), and two variable fragments
CC (Fvs), where the constant region contains one or more amino acid
CC mutations in the heavy chain 2 (CH2) domain. The methods and antibody of
CC the invention are used to diagnose or treat an immune dysregulation
CC disease, an autoimmune disease, organ graft rejection, cardiovascular
CC disease, neurological disease (Alzheimer's disease) or graft vs. host
CC disease. The methods are also useful for treating a disease caused by a
CC fungus, virus, parasite, or bacterium. The methods may also be used for
CC intraoperative or endoscopic diagnosis to identify diseased tissue. The
CC autoimmune diseases that may be diagnosed or treated include acute or
CC chronic idiopathic thrombocytopenic purpura, dermatomyositis, Sydenham's
CC chorea, myasthenia gravis, systemic lupus erythematosus, lupus nephritis,
CC rheumatic fever, polyglandular syndromes and diabetes mellitus. The
CC current sequence represents the hMN-14 heavy chain amino acid sequence.
XX
SQ Sequence 468 AA;

Query Match 88.6%; Score 568; DB 7; Length 468;
Best Local Similarity 84.0%; Pred. No. 2.3e-48;
Matches 100; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db         20 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 79

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :|||||||||:|||  :| ||| :|:|||||||||||||||||||||:
Db         80 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 138
```

RESULT 11
ADY97271
ID ADY97271 standard; protein; 669 AA.
XX
AC ADY97271;
XX
DT 16-JUN-2005 (first entry)
XX
DE Exemplary antibody fusion protein SEQ ID NO:3.
XX
KW antibody engineering; fusion protein; cytostatic; antimicrobial;
KW virucide; antibacterial; cancer; infection.
XX
OS Synthetic.
XX
PN US2005069552-A1.
XX
PD 31-MAR-2005.
XX
PF 28-JUL-2004; 2004US-00900928.
XX
PR 28-JUL-2003; 2003US-0490569P.
XX
PA (BLEC/) BLECK G T.
PA (YORK/) YORK D.
PA (COLL/) COLLINS I.
XX
PI Bleck GT, York D, Collins I;
XX
DR WPI; 2005-261600/27.
DR N-PSDB; ADY97269.
XX
PT Composition useful as cancer vaccine, comprises polypeptide having
PT antibody heavy chain fused to antibody light chain, or multivalent
PT antibody having two polypeptides with antibody heavy chain fused to
PT antibody light chain.
XX
PS Disclosure; SEQ ID NO 3; 101pp; English.
XX
CC The invention describes a composition (I) comprising: (a) a polypeptide
CC comprising at least one antibody heavy chain fused to at least one
CC antibody light chain; or (b) a multivalent antibody comprising at least
CC two polypeptides, where each of the polypeptides comprises at least one
CC antibody heavy chain fused to at least one antibody light chain. Also
CC described: (1) a composition (II) comprising a nucleic acid comprising at
CC least one antibody heavy chain gene and at least one antibody light chain
CC gene, where the nucleic acid encodes a polypeptide comprising at least

CC one antibody heavy chain fused to at least one antibody light chain; (2)
CC a method (M1) of binding an antigen, involves providing a polypeptide
CC comprising at least one antibody heavy chain fused to at least one
CC antibody light chain, and contacting the polypeptide with a sample having
CC an antigen under conditions such that the polypeptide binds to the
CC antigen; (3) a method (M2), which involves providing a vector comprising
CC a bicistronic expression construct comprising genes encoding an antibody
CC heavy chain gene and an antibody light chain gene, and altering the
CC nucleic acid sequence of a splice acceptor sequence or a splice donor
CC sequence in the antibody light chain gene or the antibody heavy chain
CC gene under conditions such that splicing is prevented at the splice
CC acceptor sequence or donor sequence; (4) a nucleic acid sequence produced
CC by (M2); (5) a vector (III) comprising a modified antibody heavy or light
CC gene, where modification eliminates a splice donor or acceptor sequence
CC in antibody heavy or light chain gene; and (6) a host cell comprising
CC (III). (I) is useful in in vitro binding assays for identifying antigens
CC in a mixture or determining the presence or absence of expression of a
CC particular protein. (I) is also useful as vaccine for treating cancer and
CC infections caused by pathogens e.g. virus or bacteria. The present
CC sequence represents an exemplary antibody fusion protein from the present
CC invention.
XX
SQ Sequence 669 AA;

Query Match 88.6%; Score 568; DB 9; Length 669;
Best Local Similarity 84.0%; Pred. No. 3.5e-48;
Matches 100; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :|||||||||:|||  :| ||| :|:||||||||||||||||||||||:
Db         61 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119
```

RESULT 12
ABR42755
ID ABR42755 standard; protein; 118 AA.
XX
AC ABR42755;
XX
DT 26-AUG-2003 (first entry)
XX
DE Anti-CEA humanized monoclonal antibody hMN-14 VH region.
XX
KW Humanized; monoclonal antibody; antibody; hMN-14;
KW carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003033654-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032718.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
PR 08-JAN-2002; 2002US-0345641P.
PR 22-AUG-2002; 2002US-0404919P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg DM;
XX
DR WPI; 2003-513460/48.
XX
PT New multivalent, monospecific binding protein comprising two or more
PT binding sites having affinity for the same single target antigen, where
PT each binding site is associated with scFv fragments, useful for
PT diagnosing or treating tumor.
XX
PS Disclosure; Fig 12; 62pp; English.
XX
CC The present sequence is the protein sequence of the heavy chain variable
CC region of anti-carcinoembryonic antigen (CEA) humanized monoclonal
CC antibody hMN-14. scFv constructs comprising the hMN-14 VH and Vkappa
CC regions are used in novel multivalent, monospecific binding proteins
CC (diabody, triabody and tetrabody) of the invention (see also ABR42754,
CC ABR42757 and ABR42758). Claimed binding proteins are specific for a
CC tumour-associated antigen, and are used in the diagnosis and treatment of
CC a tumour, carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma,
CC lymphoma or myeloma, or a cancer selected from acute lymphoblastic
CC leukaemia, acute myelogenous leukaemia, biliary, breast, cervical,
CC chronic lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC prostate and bladder
XX
SQ Sequence 118 AA;

Query Match 88.5%; Score 567; DB 6; Length 118;
Best Local Similarity 84.7%; Pred. No. 5.9e-49;
Matches 100; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVS 118
              ||||||:| :|||||||||:|||  :| ||| :|:||||||||||||||||||||||
Db         61 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVS 118
```

RESULT 13
ABR42757
ID ABR42757 standard; protein; 256 AA.
XX
AC ABR42757;
XX
DT 26-AUG-2003 (first entry)
XX
DE Anti-CEA humanized monoclonal antibody hMN-14-0.
XX
KW Humanized; monoclonal antibody; antibody; hMN-14-0;
KW carcinoembryonic antigen; CEA; tumour; cytostatic; triabody.
XX
OS Homo sapiens.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .23
FT		/label= Signal_peptide
FT		/note= "pelB"
FT	Region	23. .141
FT		/label= hMN-14VH
FT	Protein	24. .256
FT		/label= hMN-14-0
FT	Region	142. .250
FT		/label= hMN-14Vkappa
FT	Region	251. .256
FT		/label= 6xHis_tag

XX
PN WO2003033654-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032718.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.

PR 08-JAN-2002; 2002US-0345641P.
PR 22-AUG-2002; 2002US-0404919P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg DM;
XX
DR WPI; 2003-513460/48.
DR N-PSDB; ACC58722.
XX
PT New multivalent, monospecific binding protein comprising two or more
PT binding sites having affinity for the same single target antigen, where
PT each binding site is associated with scFv fragments, useful for
PT diagnosing or treating tumor.
XX
PS Claim 39; Fig 13; 62pp; English.
XX
CC The present sequence is the protein sequence of hMN-14-0, which is
CC designed to form an hMN-14 triabody. The hMN-14-0 polypeptide comprises
CC the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC Vkappa without a peptide linker. The use of the zero linker enables the
CC secreted polypeptide to form a triabody, forming 3 binding sites for CEA.
CC The polypeptide also includes a pelB signal peptide, which precedes the
CC VH moiety to facilitate synthesis of the polypeptide in the periplasmic
CC space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC purification. This monospecific triabody is an example of claimed
CC multivalent binding proteins specific for a tumour-associated antigen.
CC The binding proteins are used in the diagnosis and treatment of a tumour,
CC carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC prostate and bladder
XX
SQ Sequence 256 AA;

Query Match 88.5%; Score 567; DB 6; Length 256;
Best Local Similarity 84.7%; Pred. No. 1.4e-48;
Matches 100; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:||||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 83

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVS 118
              ||||||:| :|||||||||:|||  :| ||| :|:|||||||||||||||||||||||
Db         84 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVS 141
```

RESULT 14
ABR42758
ID ABR42758 standard; protein; 257 AA.
XX
AC ABR42758;
XX
DT 26-AUG-2003 (first entry)
XX
DE Anti-CEA humanized monoclonal antibody hMN-14-1G.
XX
KW Humanized; monoclonal antibody; antibody; hMN-14-1G;
KW carcinoembryonic antigen; CEA; tumour; cytostatic; tetrabody.
XX
OS Homo sapiens.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1. .23
FT /label= Signal_peptide
FT /note= "pelB"
FT Region 23. .141
FT /label= hMN-14VH
FT Protein 24. .257
FT /label= hMN-14-0
FT Region 142
FT /label= 1G_linker
FT Region 143. .251
FT /label= hMN-14Vkappa
FT Region 252. .257
FT /label= 6xHis_tag
XX
PN WO2003033654-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032718.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
PR 08-JAN-2002; 2002US-0345641P.
PR 22-AUG-2002; 2002US-0404919P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg DM;
XX
DR WPI; 2003-513460/48.
XX
PT New multivalent, monospecific binding protein comprising two or more
PT binding sites having affinity for the same single target antigen, where
PT each binding site is associated with scFv fragments, useful for
PT diagnosing or treating tumor.
XX
PS Claim 48; Fig 14; 62pp; English.
XX
CC The present sequence is the protein sequence of hMN-14-1G, which is
CC designed to form an hMN-14 tetrabody. The hMN-14-1G polypeptide comprises
CC the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC Vkappa via a single glycine residues. Use of the 1G linker enables some
CC of the the secreted polypeptide to form a tetrabody with 4 binding sites
CC for CEA. The polypeptide also includes a pelB signal peptide, which
CC precedes the VH moiety to facilitate synthesis of the polypeptide in the
CC periplasmic space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC purification. This monospecific tetrabody is an example of claimed
CC multivalent binding proteins specific for a tumour-associated antigen.
CC The binding proteins are used in the diagnosis and treatment of a tumour,
CC carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC prostate and bladder
XX
SQ Sequence 257 AA;

Query Match 88.5%; Score 567; DB 6; Length 257;
Best Local Similarity 84.7%; Pred. No. 1.5e-48;
Matches 100; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:||||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 83

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVS 118
              ||||||:| :|||||||||:|||  :| ||| :|:|||||||||||||||||||||||
Db         84 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVS 141
```

RESULT 15
ABR42289

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ID   ABR42289 standard; protein; 261 AA.
XX
AC   ABR42289;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Diabody 679-scFv-L5 polypeptide (VH-I3Q/C101S mutant).
XX
KW   Diabody; antibody; 679-scFv-L5; histamine-succinyl-glycyl; HSG;
KW   affinity enhancement system; tumour; targeting; mutant; mutein.
XX
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB signal peptide"
FT   Misc-difference 3
FT                   /note= "wild-type Ile substituted by Gln"
FT   Protein         23. .268
FT                   /label= 679-scFv-L5
FT   Region          23. .142
FT                   /label= 679VH(I3Q/C101S)
FT   Misc-difference 101
FT                   /note= "wild-type Cys substituted by Ser"
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .260
FT                   /label= 679Vk
FT   Region          261. .268
FT                   /label= 6His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57803.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Disclosure; Fig 28; 87pp; English.
XX
CC   The present sequence is the protein sequence of a 679 mutant diabody in
CC   which antibody 679 VH has a Gln for Ile amino acid substitution at
CC   position 3 and a Ser for Gln amino acid substitution at position 101.
CC   Murine monoclonal antibody 679 binds with high affinity to molecules
CC   containing the moiety histamine-succinyl-glycyl (HSG). The present
CC   polypeptide comprises: 679 VH(I3Q) linked to 679 Vk via a peptide linker
CC   (enables the secreted polypeptide to dimerise into a diabody, forming 2
CC   sites for HSG); a pelB leader signal peptide (facilitates transport of
CC   the polypeptide into the periplasmic space of Escherichia coli); and 6
CC   His residues (allows purification by IMAC). The 679 diabody was expressed
CC   in E. coli at a level of 10 ug/l of culture, compared with 1 ug/l for the
CC   non-mutant polypeptide. The invention provides a bispecific diabody
CC   comprising an HSG binding site and a carcinoembryonic antigen (CEA)
CC   binding site. The HSG antigen binding site may comprise the VH and Vk
CC   polypeptides of 679 MAb. These diabodies are produced via recombinant DNA
CC   technology and create a novel affinity enhancement system that shows
CC   specific affinity for HSG and CEA. They pre-target CEA positive tumours
CC   for subsequent specific delivery of therapeutic radioisotopes carried by
CC   HSG-carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 261 AA;

  Query Match             88.5%;  Score 567;  DB 6;  Length 261;
  Best Local Similarity   84.7%;  Pred. No. 1.5e-48;
  Matches  100;  Conservative   11;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db         24 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 83

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVS 118
              ||||||:| :|||||||||:|||  :| ||| :|:|||||||||||||||||||||||
Db         84 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVS 141


Search completed: March 23, 2006, 01:21:02
Job time : 192 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:21:20 ; Search time 39 Seconds
(without alignments)
293.584 Million cell updates/sec

Title: US-10-755-382-2
Perfect score: 641
Sequence: 1 EVKLLESGGGLVQSGGSLKL.....YFGFPWFAYWGQGTPVTVSA 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	546.5	85.3	119	1	AVMSX4	Ig heavy chain V r
2	544.5	84.9	119	1	AVMSJ5	Ig heavy chain V r
3	532.5	83.1	119	1	AVMST6	Ig heavy chain V r
4	529	82.5	139	2	A25912	Ig heavy chain pre
5	521.5	81.4	136	2	S13791	Ig heavy chain V r
6	513	80.0	118	2	A47329	Ig heavy chain V r
7	509	79.4	121	2	A30560	Ig heavy chain V r
8	506	78.9	117	1	G2MS73	Ig heavy chain V r
9	503	78.5	117	1	G2MSU1	Ig heavy chain V r
10	485	75.7	116	1	HVMS44	Ig heavy chain pre
11	485	75.7	130	2	S06817	Ig heavy chain V r
12	463	72.2	140	2	S06816	Ig heavy chain pre
13	457	71.3	94	2	I67528	CD33 antigen homol
14	449	70.0	95	2	I67527	CD33 antigen homol
15	419.5	65.4	147	2	I37780	Ig variable region
16	419	65.4	125	2	S30531	Ig heavy chain V r
17	418	65.2	123	2	S31114	Ig heavy chain - h
18	417	65.1	140	2	S31686	Ig heavy chain V r
19	415	64.7	121	2	I55673	Ig heavy chain - h
20	415	64.7	139	2	I37781	Ig variable region
21	413	64.4	119	2	D36005	Ig heavy chain V r
22	412	64.3	143	2	S23624	Ig heavy chain V r
23	411.5	64.2	114	2	S31120	Ig heavy chain - h
24	411	64.1	138	2	S31666	Ig heavy chain V r
25	410.5	64.0	122	2	S31675	Ig heavy chain V r
26	410.5	64.0	136	2	S31587	Ig heavy chain V r
27	410.5	64.0	137	2	S03326	Ig heavy chain pre
28	409	63.8	117	2	S31109	Ig heavy chain - h
29	408.5	63.7	128	2	S26786	Ig heavy chain V r
30	408	63.7	117	2	S78486	Ig heavy chain V r
31	408	63.7	140	2	S31588	Ig heavy chain V r
32	407	63.5	123	2	S26794	Ig heavy chain V r
33	407	63.5	135	2	S31598	Ig heavy chain V r
34	406.5	63.4	124	2	S20782	Ig heavy chain V r
35	405.5	63.3	118	2	S31105	Ig heavy chain (su
36	405	63.2	119	2	S31107	Ig heavy chain - h
37	404.5	63.1	122	2	S20772	Ig heavy chain V r
38	404	63.0	119	2	C36005	Ig heavy chain V r
39	404	63.0	142	2	C34903	Ig heavy chain pre
40	403.5	62.9	140	2	S70442	Ig heavy chain pre
41	403	62.9	160	2	S05271	Ig heavy chain pre
42	402	62.7	119	2	S31108	Ig heavy chain - h
43	401.5	62.6	136	1	G1MS21	Ig heavy chain pre
44	401	62.6	138	2	S09258	Ig heavy chain V r
45	400.5	62.5	120	2	S48798	Ig heavy chain V r

ALIGNMENTS

RESULT 1
AVMSX4
Ig heavy chain V region (X44) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Apr-1980 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A02077; S06815
R;Rao, D.N.; Rudikoff, S.; Krutzsch, H.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 76, 2890-2894, 1979
A;Title: Structural evidence for independent joining region gene in immunoglobulin heavy
etermining regions.
A;Reference number: A93832; MUID:79223895; PMID:111245
A;Accession: A02077
A;Molecule type: protein
A;Residues: 1-119 <RAO>
A;Cross-references: UNIPROT:P01807; UNIPARC:UPI0000027250
A;Note: this chain was isolated from an IgA myeloma protein that binds galactan
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06815
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-118 <MIL>
A;Cross-references: UNIPARC:UPI0000173738
A;Experimental source: clone IIIB
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted

Query Match 85.3%; Score 546.5; DB 1; Length 119;
Best Local Similarity 88.3%; Pred. No. 6.4e-44;
Matches 106; Conservative 5; Mismatches 6; Indels 3; Gaps 2;

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Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              |||||||||||| |||||||||||||: ||||||||||||||||||||:||||||||
Db          1 EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASL-YFGFPWFAYWGQGTPVTVSA 119
                |||||||:|||||||||||||||||||||||||| | |:|:   ||||||| |||||
Db         61 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARLHYYGYA--AYWGQGTLVTVSA 118
```

RESULT 2
AVMSJ5
Ig heavy chain V region (J539) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Apr-1980 #sequence_revision 30-Apr-1980 #text_change 09-Jul-2004
C;Accession: A02080
R;Rao, D.N.; Rudikoff, S.; Krutzsch, H.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 76, 2890-2894, 1979

A;Title: Structural evidence for independent joining region gene in immunoglobulin heavy
etermining regions.
A;Reference number: A93832; MUID:79223895; PMID:111245
A;Accession: A02080
A;Molecule type: protein
A;Residues: 1-119 <RAO>
A;Cross-references: UNIPROT:P01810; UNIPARC:UPI0000027262
C;Comment: This chain was isolated from a myeloma protein that binds galactan.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted

Query Match 84.9%; Score 544.5; DB 1; Length 119;
Best Local Similarity 87.5%; Pred. No. 9.8e-44;
Matches 105; Conservative 5; Mismatches 7; Indels 3; Gaps 2;

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Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              |||||||||||||| |||||||||||||||: |||||||||||||||||||||||| ||||
Db          1 EVKLLESGGGLVQPGGSLKLSCAASGFDFSKYWMSWVRQAPGKGLEWIGEIHPDSGTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASL-YFGFPWFAYWGQGTPVTVSA 119
              ||||||||:|||||||:||||||||||||||||| | |:|:   ||||||| |||||
Db         61 TPSLKDKFIISRDNAKNSLYLQMSKVRSEDTALYYCARLHYYGYN--AYWGQGTLVTVSA 118
```

RESULT 3
AVMST6
Ig heavy chain V region (T601) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Apr-1980 #sequence_revision 30-Apr-1980 #text_change 09-Jul-2004
C;Accession: A02078
R;Rao, D.N.; Rudikoff, S.; Krutzsch, H.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 76, 2890-2894, 1979
A;Title: Structural evidence for independent joining region gene in immunoglobulin heavy
etermining regions.
A;Reference number: A93832; MUID:79223895; PMID:111245
A;Accession: A02078
A;Molecule type: protein
A;Residues: 1-119 <RAO>
A;Cross-references: UNIPROT:P01808; UNIPARC:UPI0000027253
C;Comment: This chain was isolated from an IgA myeloma protein that binds galactan.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted

Query Match 83.1%; Score 532.5; DB 1; Length 119;
Best Local Similarity 85.8%; Pred. No. 1.3e-42;
Matches 103; Conservative 6; Mismatches 8; Indels 3; Gaps 2;

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              |||||||||||||| |||||||||||||||: |||||||||||||||||||||||:||||||||
Db          1 EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASL-YFGFPWFAYWGQGTPVTVSA 119
              ||||||||:|||||||||||||||||||||||| | |:|:   |  || || ||||:
Db         61 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARLGYYGY--FDVWGAGTTVTVSS 118
```

RESULT 4
A25912
Ig heavy chain precursor V region (W3129) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999
C;Accession: A25912
R;Borden, P.; Kabat, E.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 2440-2443, 1987
A;Title: Nucleotide sequence of the cDNAs encoding the variable region heavy and light c
A;Reference number: A94147; MUID:87175689; PMID:2436230
A;Accession: A25912
A;Molecule type: mRNA
A;Residues: 1-139 <BOR>
A;Cross-references: UNIPARC:UPI0000114C7B; GB:M15873; NID:g195268; PIDN:AAA38228.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-139/Product: Ig heavy chain V region W3129 #status predicted <VAR>
F;33-116/Domain: immunoglobulin homology <IMM>

Query Match 82.5%; Score 529; DB 2; Length 139;
Best Local Similarity 83.5%; Pred. No. 3.2e-42;
Matches 101; Conservative 8; Mismatches 10; Indels 2; Gaps 1;

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Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              |||::|||||||| |||||||||||||||: |||||||||||||||||||:||||||||
Db         19 EVKVIESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 78

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFA--YWGQGTPVTVS 118
              ||||||||:|||||||||||||||||||||||||||||| |     ::|  |||||| ||||
Db         79 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARLGGDLHYYAMDYWGQGTSVTVS 138

Qy        119 A 119
              :
Db        139 S 139
```

RESULT 5
S13791
Ig heavy chain V region (X-24) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S13791
R;Arepalli, S.R.; Heller, M.; Glaudemans, C.P.J.
Nucleic Acids Res. 18, 7152, 1990
A;Title: Sequence of the V(H) gene for murine IgA X-24.
A;Reference number: S13791; MUID:91088313; PMID:2124679
A;Accession: S13791
A;Molecule type: DNA
A;Residues: 1-136 <ARE>
A;Cross-references: UNIPARC:UPI0000176C85; EMBL:X55984
A;Note: the authors translated the codon GGG for residue 15 as Lys
C;Genetics:
A;Introns: 15/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology <IMM>

Query Match 81.4%; Score 521.5; DB 2; Length 136;
Best Local Similarity 83.3%; Pred. No. 1.5e-41;
Matches 100; Conservative 7; Mismatches 10; Indels 3; Gaps 2;

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Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              |||||||||||| |||| |||||||||: ||||| ||||||| |||||||:| ||||||
Db         19 EVKLLESGGGLVQPGGSLNLSCAASGFDFSRYWMSWARQAPGKGQEWIGEINPGSSTINY 78

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASL-YFGFPWFAYWGQGTPVTVSA 119
              ||||||||:|||||||||||||||||||||||||||||| | |:|:  | |||||| :|||:
Db         79 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARLGYYGY--FDYWGQGTTLTVSS 136
```

RESULT 6
A47329
Ig heavy chain V region (PR1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 17-Jul-1994 #text_change 30-May-1997
C;Accession: A47329
R;Brinkmann, U.; Gallo, M.; Brinkmann, E.; Kunwar, S.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 90, 547-551, 1993
A;Title: A recombinant immunotoxin that is active on prostate cancer cells and that is c
A;Reference number: A47329; MUID:93133825; PMID:8421689
A;Accession: A47329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <BRI>
A;Cross-references: UNIPARC:UPI0000176E3C

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A;Experimental source: Balb/c
A;Note: sequence modified after extraction from NCBI backbone
A;Note: sequence extracted from NCBI backbone (NCBIN:122874)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-99/Domain: immunoglobulin homology <IMM>

  Query Match             80.0%;  Score 513;  DB 2;  Length 118;
  Best Local Similarity   82.4%;  Pred. No. 8.2e-41;
  Matches   98;  Conservative    8;  Mismatches   11;  Indels    2;  Gaps    1;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              :|:|:|||||||| ||||||||||||||: ||||||||||||||||||||:||||||||
Db          2 DVQLVESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 61

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
                ||||||||:| |||||||||||||||||||||||||    |:    |||||| ||||:
Db         62 TPSLKDKFIISSDNAKNTLYLQMSKVRSEDTALYYCARR--GYYAMDYWGQGTSVTVSS 118


RESULT 7
A30560
Ig heavy chain V region (16.4.12E) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 23-Jul-1999
C;Accession: A30560
R;Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclc
.
A;Reference number: A30560; MUID:89110062; PMID:2464028
A;Accession: A30560
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <MAT>
A;Cross-references: UNIPARC:UPI0000114E07; GB:M22955; NID:g195610; PIDN:AAA38368.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             79.4%;  Score 509;  DB 2;  Length 121;
  Best Local Similarity   81.0%;  Pred. No. 2e-40;
  Matches   98;  Conservative    7;  Mismatches   14;  Indels    2;  Gaps    1;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              |||||:||||||| |||||||||| ||: |||||||:||||||||||:|||| |||
Db          1 EVKLLQSGGGLVQPGGSLKLSCAASGIDFSRYWMSWVRRAPGKGLEWIGEINPDSSIINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPW--FAYWGQGTPVTVS 118
              || ||||||:|||||||||||||||||||||||||    |: |  |  || || ||||
Db         61 APFLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARPGNGYSWGYFDVWGTGTTVTVS 120

Qy        119 A 119
              :
Db        121 S 121


RESULT 8
G2MS73
Ig heavy chain V region (MOPC 173) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change 09-Jul-2004
C;Accession: A91190; A91235; A93886; A02082
R;Bourgois, A.; Fougereau, M.; de Preval, C.
Eur. J. Biochem. 24, 446-455, 1972
A;Title: Sequence of amino acids of the NH-2-terminal region of a mouse-clonal immunoglc
A;Reference number: A91190; MUID:72105531; PMID:5062012
A;Accession: A91190
A;Molecule type: protein
A;Residues: 1-104 <BOU>
A;Cross-references: UNIPROT:P01812; UNIPARC:UPI0000173739
R;Rocca-Serra, J.; Milili, M.; Fougereau, M.
Eur. J. Biochem. 59, 511-523, 1975
A;Title: Determination of the primary structure of a mouse IgG2a immunoglobulin. Amino-a
A;Reference number: A91235; MUID:76091933; PMID:812695
A;Accession: A91235
A;Molecule type: protein
A;Residues: 'D',106-117 <ROC>
A;Cross-references: UNIPARC:UPI000017373A
R;Gough, N.M.; Bernard, O.
Proc. Natl. Acad. Sci. U.S.A. 78, 509-513, 1981
A;Title: Sequences of the joining region genes for immunoglobulin heavy chains and their
A;Reference number: A93886; MUID:81223769; PMID:6787590
A;Accession: A93886
A;Molecule type: DNA
A;Residues: 96-117 <GOU>
A;Cross-references: UNIPARC:UPI000017373B
R;Bourgois, A.; Fougereau, M.
FEBS Lett. 8, 265-268, 1970
A;Title: Partial amino acid sequence of the variable region of a mouse gammaG2a immunogl
A;Reference number: A91439
A;Contents: annotation; disulfide bond
C;Comment: This gamma-2a chain was isolated from a myeloma protein.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status experimental

  Query Match             78.9%;  Score 506;  DB 1;  Length 117;
  Best Local Similarity   81.8%;  Pred. No. 3.6e-40;
  Matches   99;  Conservative    8;  Mismatches    8;  Indels    6;  Gaps    2;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||||||||| ||| |||||||||||||||: |||||||||||||||||||| |:||||||
Db          1 EVKLLESGGPLVQLGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEIDPNSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFA--YWGQGTPVTVS 118
                ||||||||:||::|||||||||||||||||||||||      |::|  |||||| ||||
Db         61 TPSLKDKFIISRNDAKNTLYLQMSKVRSEDTALYYCAR----SPYYAMNYWGQGTSVTVS 116

Qy        119 A 119
              :
Db        117 S 117


RESULT 9
G2MSU1
Ig heavy chain V region (UPC10) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C;Accession: A02081
R;Auffray, C.; Sikorav, J.L.; Ollo, R.; Rougeon, F.
Ann. Immunol. (Paris) 132D, 77-88, 1981
A;Title: Correlation between D region structure and antigen-binding specifity: evidences
A;Reference number: A02081; MUID:83021113; PMID:6181731
A;Accession: A02081
A;Molecule type: mRNA
A;Residues: 1-117 <AUF>
A;Cross-references: UNIPROT:P01811; UNIPARC:UPI0000027263
C;Comment: This chain was isolated from an Ig gamma-2a myeloma protein binding 2,6-levan
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted

  Query Match             78.5%;  Score 503;  DB 1;  Length 117;
  Best Local Similarity   80.3%;  Pred. No. 6.9e-40;
  Matches   98;  Conservative    7;  Mismatches    9;  Indels    8;  Gaps    2;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              |||||||||||| ||||||||||||||: |||||||||||||||||||:||||||||
Db          1 EVKLLESGGGLVQPGGSLKLSCAASGFDFSGYWMSWVRQAPGKGLEWIGEINPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPW---FAYWGQGTPVTV 117
              | |||||:|||||||||:|||||||||||||:||       |   | |||| | :||
Db         61 TPFLKDKFIISRDNAKNTLFLQMSKVRSEDTALYFCAR-----NWDVGFDYWGQVTTLTV 115
```

```
Qy        118 SA 119
              |:
Db        116 SS 117
```

RESULT 10
HVMS44
Ig heavy chain precursor V region (441) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A02076
R;Ollo, R.; Auffray, C.; Sikorav, J.L.; Rougeon, F.
Nucleic Acids Res. 9, 4099-4109, 1981
A;Title: Mouse heavy chain variable regions: nucleotide sequence of a germ-line V-H gene
A;Reference number: A02076; MUID:82059449; PMID:6795591
A;Accession: A02076
A;Molecule type: DNA
A;Residues: 1-116 <OLL>
A;Cross-references: UNIPROT:P01806; UNIPARC:UPI000002724C; GB:V00774; GB:J00541; NID:g51
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Introns: 15/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-116/Product: Ig heavy chain V region (441) #status predicted <MAT>
F;33-116/Domain: immunoglobulin homology <IMM>
F;40-114/Disulfide bonds: #status predicted

 Query Match 75.7%; Score 485; DB 1; Length 116;
 Best Local Similarity 93.8%; Pred. No. 3.2e-38;
 Matches 91; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              |||||||||||||| |||||||||||||||: |||||||||||||||||||:||||||||
Db         19 EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 78

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCA 97
              ||||||||:|||||||||||||||||||||||||||
Db         79 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCA 115
```

RESULT 11
S06817
Ig heavy chain V region (clone 11C7) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 11-Nov-1994 #text_change 23-Jul-1999
C;Accession: S06817
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06817
A;Molecule type: mRNA
A;Residues: 1-130 <MIL>
A;Cross-references: UNIPARC:UPI0000115E39; EMBL:X17165; NID:g51917; PIDN:CAA35043.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted

 Query Match 75.7%; Score 485; DB 2; Length 130;
 Best Local Similarity 75.2%; Pred. No. 3.7e-38;
 Matches 94; Conservative 13; Mismatches 12; Indels 6; Gaps 3;

```
Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              || |||||||||| |||||:|||||||||: :|||||||||||||||||:| |:|||||
Db          1 EVNLLESGGGLVQPGGSLKVSCAASGFDFSRFWMSWVRQAPGKGLEWIGEINPSSNTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCA---SLY-FG--FPWFAYWGQGTP 114
              ||||::||:|||||||||||||||||| ||| |||||   |:| :|  : :|  || ||
Db         61 TPSLKERFIISRDNAKNTLYLQMSKVRPEDTGLYYCAMTKSVYNYGSHYYYFDVWGAGTT 120
```

```
Qy        115 VTVSA 119
              ||||:
Db        121 VTVSS 125
```

RESULT 12
S06816
Ig heavy chain precursor V region (clone 10C3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 11-Nov-1994 #text_change 23-Jul-1999
C;Accession: S06816
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06816
A;Molecule type: mRNA
A;Residues: 1-140 <MIL>
A;Cross-references: UNIPARC:UPI0000115E38; EMBL:X17164; NID:g51916; PIDN:CAA35042.1; PID
A;Note: part of this sequence, including the amino end of the mature protein, was confir
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-140/Product: Ig heavy chain V region #status experimental <MAT>
F;33-115/Domain: immunoglobulin homology <IMM>
F;40-113/Disulfide bonds: #status predicted

 Query Match 72.2%; Score 463; DB 2; Length 140;
 Best Local Similarity 75.0%; Pred. No. 4.4e-36;
 Matches 93; Conservative 9; Mismatches 10; Indels 12; Gaps 3;

```
Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              |||||||||||||| |||||||||||||||: ||:  |||||||||||||||:| |:|| |
Db         19 EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWI-LVRQAPGKGLEWIGEINPHSTTIFY 77

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPW-----FAYWGQGTPV 115
              ||| ||||:|||||||||||:||||||||||||||       |     | :|||||| :
Db         78 TPSLMDKFIISRDNAKNTLYLQMTKVRSEDTALYYCAR------WGDKYLFDHWGQGTTL 131

Qy        116 TVSA 119
              |||:
Db        132 TVSS 135
```

RESULT 13
I67528
CD33 antigen homolog - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C;Accession: I67528
R;Chies, J.A.; Lembezat, M.P.; Freitas, A.A.
Eur. J. Immunol. 24, 1657-1664, 1994
A;Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is n
A;Reference number: I53392; MUID:94298870; PMID:8026526
A;Accession: I67528
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-94 <RES>
A;Cross-references: UNIPARC:UPI0000176EB4; GB:S71357; NID:g550040
C;Genetics:
A;Gene: Ig VHX24b
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;11-94/Domain: immunoglobulin homology <IMM>

 Query Match 71.3%; Score 457; DB 2; Length 94;
 Best Local Similarity 91.4%; Pred. No. 1e-35;
 Matches 85; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```
Qy          5 LESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINYAPSL 64
              ||||||||| |||||||||||||||: |||||||||||||||||||:|||||||| |||
Db          1 LESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINYTPSL 60
```

```
Qy          65 KDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCA 97
               ||||||:||||||||||||||||||: |||||||
Db          61 KDKFIISRDNAKNTLYLQMSKVRSDHTALYYCA 93


RESULT 14
I67527
CD33 antigen homolog - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C;Accession: I67527
R;Chies, J.A.; Lembezat, M.P.; Freitas, A.A.
Eur. J. Immunol. 24, 1657-1664, 1994
A;Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is r
A;Reference number: I53392; MUID:94298870; PMID:8026526
A;Accession: I67527
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-95 <RES>
A;Cross-references: UNIPARC:UPI0000176EB3; GB:S71351; NID:g550039
C;Genetics:
A;Gene: Ig VHX24a
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;12-95/Domain: immunoglobulin homology <IMM>

  Query Match             70.0%;  Score 449;  DB 2;  Length 95;
  Best Local Similarity   89.4%;  Pred. No. 5.9e-35;
  Matches   84;  Conservative    3;  Mismatches    7;  Indels    0;  Gaps    0;

Qy           4 LLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINYAPS 63
               |||||||||| |||| ||||||||||: ||||| ||||||| |||||||| |||||| ||
Db           1 LLESGGGLVQPGGSLNLSCAASGFDFSRYWMSWARQAPGKGQEWIGEINPGSSTINYTPS 60

Qy          64 LKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCA 97
               ||||||:||||||||||||||||||||||||||
Db          61 LKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCA 94


RESULT 15
I37780
Ig variable region (VDJ) (clone T20-11) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C;Accession: I37780; S25474
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by h
A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: I37780
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <RES>
A;Cross-references: UNIPARC:UPI00001160E7; EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;28-111/Domain: immunoglobulin homology <IMM>

  Query Match             65.4%;  Score 419.5;  DB 2;  Length 147;
  Best Local Similarity   64.5%;  Pred. No. 5.2e-32;
  Matches   80;  Conservative   17;  Mismatches   22;  Indels    5;  Gaps    1;

Qy           1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
               ||:|:|||||||| ||||:|||||||| |::|||||||||||||||:  |  | |  |
Db          14 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 73

Qy          61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAY-----WGQGTPV 115
               | |:| :| :||||:||||||||: :|:||||:||||    |:  : |     ||||| |
Db          74 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDGEGWGLYYYYGMDVWGQGTTV 133

Qy         116 TVSA 119
               ||||:
Db         134 TVSS 137
```

```
Search completed: March 23, 2006, 01:25:45
Job time : 40 secs
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:18:00 ; Search time 233 Seconds
(without alignments)
360.334 Million cell updates/sec

Title: US-10-755-382-2
Perfect score: 641
Sequence: 1 EVKLLESGGGLVQSGGSLKL.....YFGFPWFAYWGQGTPVTVSA 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	546.5	85.3	119	1	HV37_MOUSE	P01807 mus musculu
2	544.5	84.9	119	1	HV40_MOUSE	P01810 mus musculu
3	532.5	83.1	119	1	HV38_MOUSE	P01808 mus musculu
4	523	81.6	476	2	Q4V9Z4_MOUSE	Q4v9z4 mus musculu
5	511	79.7	118	1	HV39_MOUSE	P01809 mus musculu
6	506	78.9	117	1	HV42_MOUSE	P01812 mus musculu
7	503	78.5	117	1	HV41_MOUSE	P01811 mus musculu
8	485	75.7	116	1	HV36_MOUSE	P01806 mus musculu
9	410	64.0	470	2	Q6PJA4_HUMAN	Q6pja4 homo sapien
10	410	64.0	493	2	Q6GMX2_HUMAN	Q6gmx2 homo sapien
11	405.5	63.3	467	2	Q4VBH1_RAT	Q4vbh1 rattus norv
12	405	63.2	478	2	Q6PI81_HUMAN	Q6pi81 homo sapien
13	404.5	63.1	465	2	Q5I0J0_RAT	Q5i0j0 rattus norv
14	401.5	62.6	136	1	HV16_MOUSE	P01783 mus musculu
15	399	62.2	248	2	Q65ZQ7_9MURI	Q65zq7 mus sp. b3(
16	398	62.1	479	2	Q5PQK9_RAT	Q5pqk9 rattus norv
17	398	62.1	485	2	Q6PDB8_MOUSE	Q6pdb8 mus musculu
18	397.5	62.0	478	2	Q5FVQ3_RAT	Q5fvq3 rattus norv
19	397.5	62.0	606	2	Q6GMY2_HUMAN	Q6gmy2 homo sapien
20	395	61.6	142	1	HV01_RAT	P01805 rattus norv
21	393	61.3	113	2	Q9UL90_HUMAN	Q9ul90 homo sapien
22	392.5	61.2	465	2	Q6P6C4_HUMAN	Q6p6c4 homo sapien
23	390.5	60.9	119	2	Q5F2I8_MOUSE	Q5f2i8 mus musculu
24	390.5	60.9	473	2	Q6MZV7_HUMAN	Q6mzv7 homo sapien
25	390.5	60.9	473	2	Q91Z05_MOUSE	Q91z05 mus musculu
26	390.5	60.9	487	2	Q6ZVX0_HUMAN	Q6zvx0 homo sapien
27	390.5	60.9	573	2	Q8WU38_HUMAN	Q8wu38 homo sapien
28	390	60.8	479	2	Q5BK12_RAT	Q5bk12 rattus norv
29	389.5	60.8	487	2	Q99KA4_MOUSE	Q99ka4 mus musculu
30	387	60.4	597	2	Q96BB9_HUMAN	Q96bb9 homo sapien
31	386.5	60.3	118	2	Q9UL91_HUMAN	Q9ul91 homo sapien
32	386.5	60.3	147	2	Q9Y509_HUMAN	Q9y509 homo sapien
33	386	60.2	115	1	HV32_MOUSE	P01801 mus musculu
34	385.5	60.1	470	2	Q4G060_RAT	Q4g060 rattus norv
35	385.5	60.1	613	2	Q8WUK1_HUMAN	Q8wuk1 homo sapien
36	385	60.1	472	2	Q6N089_HUMAN	Q6n089 homo sapien
37	384	59.9	119	2	Q920E7_MOUSE	Q920e7 mus musculu
38	383	59.8	116	2	Q9UL93_HUMAN	Q9ul93 homo sapien
39	382.5	59.7	494	2	Q96K68_HUMAN	Q96k68 homo sapien
40	381.5	59.5	469	2	Q569F4_HUMAN	Q569f4 homo sapien
41	381.5	59.5	483	2	Q6MZX9_HUMAN	Q6mzx9 homo sapien
42	381	59.4	113	1	HV30_MOUSE	P01799 mus musculu
43	380.5	59.4	116	1	HV3T_HUMAN	P01781 homo sapien
44	380	59.3	115	1	HV3D_HUMAN	P01765 homo sapien
45	379.5	59.2	461	2	Q5M7V3_RAT	Q5m7v3 rattus norv

ALIGNMENTS

RESULT 1
HV37_MOUSE
ID HV37_MOUSE STANDARD; PRT; 119 AA.
AC P01807;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ig heavy chain V region X44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in complementarity-
RT determining regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 1-118.
RX MEDLINE=90064531; PubMed=2555519;
RA Miller A. III, Glasel J.A.;
RT "Comparative sequence and immunochemical analyses of murine monoclonal
RT anti-morphine antibodies.";
RL J. Mol. Biol. 209:763-778(1989).
CC -!- MISCELLANEOUS: This chain was isolated from an IgA myeloma protein
CC that binds galactan.
CC -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC ----------
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ----------
DR PIR; A02077; AVMSX4.
DR HSSP; P01810; 2FBJ.
DR SMR; P01807; 1-119.
DR Ensembl; ENSMUSG00000003483; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT DOMAIN 1 117 Ig-like.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13246 MW; BC34FC8F31CD41B3 CRC64;

Query Match 85.3%; Score 546.5; DB 1; Length 119;

```
  Best Local Similarity   88.3%;  Pred. No. 2.4e-50;
  Matches  106;  Conservative    5;  Mismatches    6;  Indels    3;  Gaps    2;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              |||||||||||| |||||||||||||: |||||||||||||||||||:||||||||
Db          1 EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASL-YFGFPWFAYWGQGTPVTVSA 119
              ||||||||:|||||||||||||||||||||| | |:|:   ||||||| |||||
Db         61 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARLHYYGYA--AYWGQGTLVTVSA 118


RESULT 2
HV40_MOUSE
ID   HV40_MOUSE     STANDARD;      PRT;   119 AA.
AC   P01810;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region J539.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PRELIMINARY PROTEIN SEQUENCE.
RX   MEDLINE=79223895; PubMed=111245;
RA   Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT   "Structural evidence for independent joining region gene in
RT   immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT   its potential role in generating diversity in complementarity-
RT   determining regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX   MEDLINE=88217852; PubMed=3449853; DOI=10.1002/prot.340010112;
RA   Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
RA   Davies D.R.;
RT   "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
RT   study at 2.6-A resolution.";
RL   Proteins 1:74-80(1986).
CC   -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC       binds galactan.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A02080; AVMSJ5.
DR   PDB; 2FBJ; X-ray; H=1-119.
DR   SMR; P01810; 1-119.
DR   Ensembl; ENSMUSG00000003483; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   NON_TER     119    119
FT   STRAND        3      7
FT   STRAND       10     12
FT   TURN         14     15
FT   STRAND       18     25
FT   HELIX        29     31
FT   STRAND       34     39
FT   TURN         41     42
FT   STRAND       45     51
FT   TURN         53     54
FT   STRAND       58     60
FT   TURN         62     67
FT   STRAND       68     72
FT   STRAND       78     83
FT   HELIX        88     90
FT   STRAND       92    100
FT   TURN        101    103
FT   STRAND      104    108
FT   STRAND      112    116
SQ   SEQUENCE   119 AA;  13240 MW;  577B4F1DB675C1F1 CRC64;

  Query Match             84.9%;  Score 544.5;  DB 1;  Length 119;
  Best Local Similarity   87.5%;  Pred. No. 4e-50;
  Matches  105;  Conservative    5;  Mismatches    7;  Indels    3;  Gaps    2;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              |||||||||||| |||||||||||||: |||||||||||||||||||||||| ||||
Db          1 EVKLLESGGGLVQPGGSLKLSCAASGFDFSKYWMSWVRQAPGKGLEWIGEIHPDSGTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASL-YFGFPWFAYWGQGTPVTVSA 119
              ||||||||:|||||||:|||||||||||||||||||| | |:|:   ||||||| |||||
Db         61 TPSLKDKFIISRDNAKNSLYLQMSKVRSEDTALYYCARLHYYGYN--AYWGQGTLVTVSA 118


RESULT 3
HV38_MOUSE
ID   HV38_MOUSE     STANDARD;      PRT;   119 AA.
AC   P01808;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region T601.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=79223895; PubMed=111245;
RA   Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT   "Structural evidence for independent joining region gene in
RT   immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT   its potential role in generating diversity in complementarity-
RT   determining regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgA myeloma protein
CC       that binds galactan.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   PIR; A02078; AVMST6.
DR   HSSP; P01810; 2FBJ.
DR   SMR; P01808; 1-119.
DR   Ensembl; ENSMUSG00000003483; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    112       Ig-like.
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13169 MW;  BC38CC84E6EA00E8 CRC64;

  Query Match             83.1%;  Score 532.5;  DB 1;  Length 119;
  Best Local Similarity   85.8%;  Pred. No. 7.7e-49;
  Matches  103;  Conservative    6;  Mismatches    8;  Indels    3;  Gaps    2;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
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                  ||||||||||||| ||||||||||||||||: ||||||||||||||||||||:||||||||
Db          1 EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASL-YFGFPWFAYWGQGTPVTVSA 119
              ||||||||:|||||||||||||||||||||||||| | |:|:  |  || || ||||:
Db         61 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARLGYYGY--FDVWGAGTTVTVSS 118


RESULT 4
Q4V9Z4_MOUSE
ID   Q4V9Z4_MOUSE PRELIMINARY;      PRT;   476 AA.
AC   Q4V9Z4;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   LOC544903 protein.
GN   Name=LOC544903;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC096617; AAH96617.1; -; mRNA.
SQ   SEQUENCE   476 AA;  51468 MW;  39E55334FAFCE5DA CRC64;

  Query Match             81.6%;  Score 523;  DB 2;  Length 476;
  Best Local Similarity   84.9%;  Pred. No. 4.1e-47;
  Matches  101;  Conservative    6;  Mismatches    6;  Indels    6;  Gaps    1;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||||||||||||| ||||||||||||||:  |||||||||||||||||||:||||||||
Db         19 EVKLLESGGGLVQPGGSLKLSCAASGFDFSKDWMSWVRQAPGKGLEWIGEINPDSSTINY 78

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              |||||||||:||:|||||||||||||||||||||||       : ||||||| ||||:
Db         79 APSLKDKFIISRENAKNTLYLQMSKVRSEDTALYYCAR------FLAYWGQGTSVTVSS 131


RESULT 5
HV39_MOUSE
ID   HV39_MOUSE     STANDARD;      PRT;   118 AA.
AC   P01809;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Ig heavy chain V region X24.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=79223895; PubMed=111245;
RA   Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT   "Structural evidence for independent joining region gene in
RT   immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT   its potential role in generating diversity in complementarity-
RT   determining regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 103-117.
RX   MEDLINE=92355114; PubMed=1644448; DOI=10.1007/BF00215659;
RA   Solin M.L., Kaartinen M.;
RT   "Allelic polymorphism of mouse Igh-J locus, which encodes
RT   immunoglobulin heavy chain joining (JH) segments.";
RL   Immunogenetics 36:306-313(1992).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgA myeloma protein
CC       that binds galactan.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   EMBL; X63164; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR   PIR; PT0394; AVMSX2.
DR   HSSP; P01810; 2FBJ.
DR   SMR; P01809; 1-118.
DR   Ensembl; ENSMUSG00000003483; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    111       Ig-like.
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13105 MW;  BB16A2DB677EF17F CRC64;

  Query Match             79.7%;  Score 511;  DB 1;  Length 118;
  Best Local Similarity   83.3%;  Pred. No. 1.5e-46;
  Matches  100;  Conservative    7;  Mismatches    9;  Indels    4;  Gaps    3;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||||||||||||| |||| |||||||||: ||||| ||||||| ||||||:| ||||||
Db          1 EVKLLESGGGLVQPGGSL-LSCAASGFDFSRYWMSWARQAPGKGQEWIGEINPGSSTINY 59

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASL-YFGFPWFAYWGQGTPVTVSA 119
              ||||||||:|||||||||||||||||||||||||| | |:|:  | ||||| :|||:
Db         60 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARLGYYGY--FDYWGQGTTLTVSS 117


RESULT 6
HV42_MOUSE
ID   HV42_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01812;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region MOPC 173.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
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OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE OF 1-104.
RX   MEDLINE=72105531; PubMed=5062012;
RA   Bourgois A., Fougereau M., de Preval C.;
RT   "Sequence of amino acids of the NH 2 -terminal region of a mouse-
RT   clonal immunoglobulin heavy chain.";
RL   Eur. J. Biochem. 24:446-455(1972).
RN   [2]
RP   PROTEIN SEQUENCE OF 105-117.
RX   MEDLINE=76091933; PubMed=812695;
RA   Rocca-Serra J., Milili M., Fougereau M.;
RT   "Determination of the primary structure of a mouse IgG2a
RT   immunoglobulin. Amino-acid sequence of the H4 cyanogen-bromide
RT   fragment.";
RL   Eur. J. Biochem. 59:511-523(1975).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 96-117.
RX   MEDLINE=81223769; PubMed=6787590;
RA   Gough N.M., Bernard O.;
RT   "Sequences of the joining region genes for immunoglobulin heavy chains
RT   and their role in generation of antibody diversity.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:509-513(1981).
RN   [4]
RP   DISULFIDE BOND.
RX   PubMed=11947590;
RA   Bourgois A., Fougereau M.;
RT   "Partial amino acid sequence of the variable region of a mouse
RT   gammaG2a immunoglobulin heavy chain. Evidence for the existence of a
RT   third sub-group of variability for the heavy chain pool.";
RL   FEBS Lett. 8:265-268(1970).
CC   -!- MISCELLANEOUS: This gamma-2a chain was isolated from a myeloma
CC       protein.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
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CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A91190; G2MS73.
DR   HSSP; P01810; 2FBJ.
DR   SMR; P01812; 1-117.
DR   Ensembl; ENSMUSG00000003483; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    116       Ig-like.
FT   DISULFID     22     96
FT   CONFLICT    105    105       N -> D (in Ref. 2).
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13051 MW;  156DCCC259380F19 CRC64;

  Query Match             78.9%;  Score 506;  DB 1;  Length 117;
  Best Local Similarity   81.8%;  Pred. No. 5.1e-46;
  Matches   99;  Conservative    8;  Mismatches    8;  Indels    6;  Gaps    2;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||||||||| ||| |||||||||||||||: |||||||||||||||||||| |:||||||
Db          1 EVKLLESGGPLVQLGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEIDPNSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFA--YWGQGTPVTVS 118
               ||||||||:||::||||||||||||||||||||      |::|  |||||| ||||
Db         61 TPSLKDKFIISRNDAKNTLYLQMSKVRSEDTALYYCAR----SPYYAMNYWGQGTSVTVS 116

Qy        119 A 119
               :
Db        117 S 117
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RESULT 7
HV41_MOUSE
ID   HV41_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01811;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region UPC10.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=83021113; PubMed=6181731;
RA   Auffray C., Sikorav J.L., Ollo R., Rougeon F.;
RT   "Correlation between D region structure and antigen-binding
RT   specificity: evidences from the comparison of closely related
RT   immunoglobulin VH sequences.";
RL   Ann. Immunol. (Paris) 132D:77-88(1981).
CC   -!- MISCELLANEOUS: This chain was isolated from an Ig gamma-2a myeloma
CC       protein binding 2,6-levan.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M36631; AAA38078.1; -; mRNA.
DR   PIR; A02081; G2MSU1.
DR   HSSP; P01810; 2FBJ.
DR   SMR; P01811; 1-117.
DR   Ensembl; ENSMUSG00000003483; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region.
FT   DOMAIN        1    116       Ig-like.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13001 MW;  B20A1074F8E99E7F CRC64;

  Query Match             78.5%;  Score 503;  DB 1;  Length 117;
  Best Local Similarity   80.3%;  Pred. No. 1.1e-45;
  Matches   98;  Conservative    7;  Mismatches    9;  Indels    8;  Gaps    2;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              |||||||||||| ||||||||||||||: |||||||||||||||||||:||||||||
Db          1 EVKLLESGGGLVQPGGSLKLSCAASGFDFSGYWMSWVRQAPGKGLEWIGEINPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPW---FAYWGQGTPVTV 117
               | ||||||:|||||||||:|||||||||||||||:||       |   | |||| | :||
Db         61 TPFLKDKFIISRDNAKNTLFLQMSKVRSEDTALYFCAR-----NWDVGFDYWGQVTTLTV 115

Qy        118 SA 119
               |:
Db        116 SS 117


RESULT 8
HV36_MOUSE
ID   HV36_MOUSE     STANDARD;      PRT;   116 AA.
AC   P01806;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region 441 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=82059449; PubMed=6795591;
RA   Ollo R., Auffray C., Sikorav J.-L., Rougeon F.;
RT   "Mouse heavy chain variable regions: nucleotide sequence of a germ-
RT   line VH gene segment.";
RL   Nucleic Acids Res. 9:4099-4109(1981).
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; V00774; CAA24152.1; -; Genomic_DNA.
DR   PIR; A02076; HVMS44.
DR   HSSP; P01810; 2FBJ.
DR   SMR; P01806; 19-116.
DR   Ensembl; ENSMUSG00000003483; Mus musculus.
DR   MGI; MGI:96492; Igh-VX24.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    116       Ig heavy chain V region 441.
FT   DOMAIN       19   >116       Ig-like.
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12911 MW;  6B4FF3EF9A95D9F3 CRC64;

  Query Match             75.7%;  Score 485;  DB 1;  Length 116;
  Best Local Similarity   93.8%;  Pred. No. 9e-44;
  Matches   91;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||||||||||||| |||||||||||||||: |||||||||||||||||||||:||||||||
Db         19 EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 78

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCA 97
              ||||||||:||||||||||||||||||||||||||||
Db         79 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCA 115


RESULT 9
Q6PJA4_HUMAN
ID   Q6PJA4_HUMAN PRELIMINARY;      PRT;   470 AA.
AC   Q6PJA4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGHG1 protein.
GN   Name=IGHG1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RG   NIH MGC Project;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018747; AAH18747.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   SMR; Q6PJA4; 20-470.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   470 AA;  51716 MW;  7B49556A11FD7D99 CRC64;

  Query Match             64.0%;  Score 410;  DB 2;  Length 470;
  Best Local Similarity   64.2%;  Pred. No. 5e-35;
  Matches   79;  Conservative   15;  Mismatches   23;  Indels    6;  Gaps    2;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||||| ||||:||| ||| |::|||||||||||||||:  |  | |   |
Db         20 EVQLVESGGGLVQPGGSLRLSCVVSGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCA----SLYFGFPWFAYWGQGTPVT 116
                |:| :| :|||||||:|||||: :|:||||:||||    | |    ||  ||||| ||
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDGSSWY--RDWFDPWGQGTLVT 137

Qy        117 VSA 119
              ||:
Db        138 VSS 140


RESULT 10
Q6GMX2_HUMAN
ID   Q6GMX2_HUMAN PRELIMINARY;      PRT;   493 AA.
AC   Q6GMX2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGHA1 protein.
GN   Name=IGHA1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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```
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RG   NIH MGC Project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073771; AAH73771.1; -; mRNA.
DR   SMR; Q6GMX2; 263-471.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 2.
DR   SMART; SM00409; IG; 4.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   493 AA;  52865 MW;  55B999305B286203 CRC64;

  Query Match             64.0%;  Score 410;  DB 2;  Length 493;
  Best Local Similarity   63.6%;  Pred. No. 5.2e-35;
  Matches   77;  Conservative   17;  Mismatches   25;  Indels    2;  Gaps    1;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||||| ||||:|||||||| |::||| |||||||||| |:  |: | |: :|
Db         20 EVQLVESGGGLVQPGGSLRLSCAASGFIFSSYWMHWVRQAPGKGLVWVSRINSDGSSTSY 79

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFP--WFAYWGQGTPVTVS 118
              | |:| :| :|||||||||||||: :| || |:|||| :  |     ||||| ||||
Db         80 ADSVKGRFTISRDNAKNTLYLQMNSLRGEDAAVYYCARGFVSLPRSTLDIWGQGTMVTVS 139

Qy        119 A 119
              :
Db        140 S 140


RESULT 11
Q4VBH1_RAT
ID   Q4VBH1_RAT  PRELIMINARY;      PRT;   467 AA.
AC   Q4VBH1;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   LOC299354 protein.
GN   Name=LOC299354;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC       histocompatibility complex class I molecules (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; BC095846; AAH95846.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
KW   Immunoglobulin domain; Repeat.
SQ   SEQUENCE   467 AA;  51651 MW;  1FF0328F50160ED3 CRC64;

  Query Match             63.3%;  Score 405.5;  DB 2;  Length 467;
  Best Local Similarity   61.5%;  Pred. No. 1.5e-34;
  Matches   75;  Conservative   20;  Mismatches   24;  Indels    3;  Gaps    2;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|:|||||| | |||||| |||| |::||| |:||||||||||:  |: |  :  |
Db         20 EVQLVETGGGLVQPGRSLKLSCVASGFTFSSYWMYWIRQAPGKGLEWVSSINTDGGSTYY 79

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCA--SLYFGFPW-FAYWGQGTPVTV 117
                |:| :| :|||||:||:||||: :|||||| ||||    |:|: : | |||||  |||
Db         80 PDSVKGRFTISRDNAENTVYLQMNSLRSEDTATYYCAKGGEYYGYNYPFDYWGQGVMVTV 139

Qy        118 SA 119
               |:
Db        140 SS 141


RESULT 12
Q6PI81_HUMAN
ID   Q6PI81_HUMAN PRELIMINARY;      PRT;   478 AA.
AC   Q6PI81;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGHM protein.
GN   Name=IGHM;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
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RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RG   NIH MGC Project;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC041037; AAH41037.1; -; mRNA.
DR   HSSP; P01861; 1ADQ.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 3.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ   SEQUENCE   478 AA;  52667 MW;  17BED38D917970D6 CRC64;

  Query Match             63.2%;  Score 405;  DB 2;  Length 478;
  Best Local Similarity   60.0%;  Pred. No. 1.7e-34;
  Matches   78;  Conservative   19;  Mismatches   21;  Indels   12;  Gaps    2;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||||| ||||:|||||||| |::|||||||||||||||:  |  | |   |
Db         20 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYY 79

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCA----------SLYFGFPWFAYW 109
                |:| :| :|||||||:|||||: :|:||||:||||          : |: | :   |
Db         80 VDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAREFESTMTTVNADYYYF-YMDVW 138

Qy        110 GQGTPVTVSA 119
                 |:|| ||||:
Db        139 GKGTTVTVSS 148


RESULT 13
Q5I0J0_RAT
ID   Q5I0J0_RAT  PRELIMINARY;      PRT;   465 AA.
AC   Q5I0J0;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical LOC299354.
GN   Name=LOC299354;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC       histocompatibility complex class I molecules (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; BC088271; AAH88271.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
KW   Hypothetical protein; Immunoglobulin domain; Repeat.
SQ   SEQUENCE   465 AA;  51699 MW;  97C4533A213A424F CRC64;

  Query Match             63.1%;  Score 404.5;  DB 2;  Length 465;
  Best Local Similarity   63.3%;  Pred. No. 1.9e-34;
  Matches   76;  Conservative   15;  Mismatches   28;  Indels    1;  Gaps    1;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||||| | |:|||||||| |: | |:|||||| |||||:  |  |     |
Db         20 EVQLVESGGGLVQPGRSMKLSCAASGFTFSNYGMAWVRQAPKKGLEWVAYISYDGGYTYY 79

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCAS-LYFGFPWFAYWGQGTPVTVSA 119
                :| :| :||||||||||||  :|||||| ||| :  |:|: || |||||| |:||:
Db         80 RDPVKGRFTISRDNAKNTLYLQMDSLRSEDTATYYCTTDRYYGYNWFTYWGQGTLVSVSS 139


RESULT 14
HV16_MOUSE
ID   HV16_MOUSE     STANDARD;      PRT;   136 AA.
AC   P01783;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region MOPC 21 precursor (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=81234548; PubMed=6788376; DOI=10.1016/0092-8674(81)90089-1;
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RA   Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA   Baltimore D.;
RT   "Heavy chain variable region contribution to the NPb family of
RT   antibodies: somatic mutation evident in a gamma 2a variable region.";
RL   Cell 24:625-637(1981).
RN   [2]
RP   PROTEIN SEQUENCE OF 17-136.
RX   MEDLINE=77100368; PubMed=401950;
RA   Adetugbo K., Milstein C., Secher D.S.;
RT   "Molecular analysis of spontaneous somatic mutants.";
RL   Nature 265:299-304(1977).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; J00522; AAD15290.1; -; mRNA.
DR   PIR; E90809; G1MS21.
DR   PDB; 1IGC; X-ray; H=17-136.
DR   Ensembl; ENSMUSG00000021155; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Signal.
FT   SIGNAL       <1     16
FT   CHAIN         17    136       Ig heavy chain V region MOPC 21.
FT   REGION       115    119       D segment.
FT   REGION       120    136       JH4 segment.
FT   DISULFID      38    112
FT   CONFLICT      75     78       HYAD -> DYAH (in Ref. 2).
FT   CONFLICT      89     90       DN -> ND (in Ref. 2).
FT   CONFLICT     115    115       W -> H (in Ref. 2).
FT   CONFLICT     120    120       Y -> W (in Ref. 2).
FT   NON_TER        1      1
FT   NON_TER      136    136
FT   STRAND        19     23
FT   STRAND        26     28
FT   TURN          30     31
FT   STRAND        34     41
FT   HELIX         45     47
FT   STRAND        50     55
FT   STRAND        61     67
FT   TURN          69     70
FT   STRAND        74     76
FT   HELIX         78     80
FT   STRAND        81     81
FT   TURN          82     83
FT   STRAND        84     89
FT   TURN          90     93
FT   STRAND        94     99
FT   HELIX        104    106
FT   STRAND       108    114
FT   TURN         118    119
FT   STRAND       125    126
FT   STRAND       130    134
SQ   SEQUENCE   136 AA;  15071 MW;  2276A98DBDBF7016 CRC64;

  Query Match             62.6%;  Score 401.5;  DB 1;  Length 136;
  Best Local Similarity   62.8%;  Pred. No. 9.4e-35;
  Matches   76;  Conservative   22;  Mismatches   20;  Indels    3;  Gaps    2;

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Qy        119 A 119
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Db        136 S 136


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ID   Q65ZQ7_9MURI PRELIMINARY;      PRT;   248 AA.
AC   Q65ZQ7;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   B3(Fv)-PE40 (Fragment).
GN   Name=B3(Fv)-PE40;
OS   Mus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10095;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=92020904; PubMed=1924323;
RA   Brinkmann U., Pai L.H., FitzGerald D.J., Willingham M., Pastan I.;
RT   "B3(Fv)-PE38KDEL, a single-chain immunotoxin that causes complete
RT   regression of a human carcinoma in mice.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
DR   EMBL; S57990; AAB19971.2; -; mRNA.
DR   SMR; Q65ZQ7; 4-247.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER      248    248
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  Best Local Similarity   64.2%;  Pred. No. 3.5e-34;
  Matches   77;  Conservative   18;  Mismatches   23;  Indels    2;  Gaps    2;

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Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCA-SLYFGFPWFAYWGQGTPVTVSA 119
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Search completed: March 23, 2006, 01:25:01
Job time : 235 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:25:15 ; Search time 47 Seconds
(without alignments)
209.328 Million cell updates/sec

Title: US-10-755-382-2
Perfect score: 641
Sequence: 1 EVKLLESGGGLVQSGGSLKL.....YFGFPWFAYWGQGTPVTVSA 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	641	100.0	119	1	US-08-318-157B-2	Sequence 2, Appli
2	641	100.0	119	2	US-09-253-794-2	Sequence 2, Appli
3	572	89.2	119	1	US-08-318-157B-15	Sequence 15, Appl
4	572	89.2	119	2	US-09-253-794-15	Sequence 15, Appl
5	568	88.6	119	1	US-08-318-157B-14	Sequence 14, Appl
6	568	88.6	119	2	US-09-253-794-14	Sequence 14, Appl
7	565	88.1	119	1	US-08-318-157B-13	Sequence 13, Appl
8	565	88.1	119	2	US-09-253-794-13	Sequence 13, Appl
9	555	86.6	119	1	US-08-318-157B-12	Sequence 12, Appl
10	555	86.6	119	1	US-08-318-157B-17	Sequence 17, Appl
11	555	86.6	119	2	US-09-253-794-12	Sequence 12, Appl
12	555	86.6	119	2	US-09-253-794-17	Sequence 17, Appl
13	548.5	85.6	118	2	US-09-232-290-53	Sequence 53, Appl
14	541.5	84.5	120	1	US-08-480-434-30	Sequence 30, Appl
15	541.5	84.5	120	1	US-08-053-451B-30	Sequence 30, Appl
16	541.5	84.5	120	1	US-08-053-451B-127	Sequence 127, App
17	533	83.2	119	1	US-08-318-157B-58	Sequence 58, Appl
18	533	83.2	119	2	US-09-253-794-58	Sequence 58, Appl
19	522.5	81.5	116	2	US-08-483-749A-18	Sequence 18, Appl
20	519	81.0	139	2	US-09-136-315-2	Sequence 2, Appli
21	519	81.0	139	2	US-09-767-888-2	Sequence 2, Appli
22	518.5	80.9	150	2	US-10-226-795-22	Sequence 22, Appl
23	513	80.0	117	1	US-07-958-140-3	Sequence 3, Appli
24	513	80.0	117	4	PCT-US93-09166-3	Sequence 3, Appli
25	513	80.0	243	1	US-07-958-140-2	Sequence 2, Appli
26	513	80.0	243	4	PCT-US93-09166-2	Sequence 2, Appli
27	510.5	79.6	109	1	US-07-942-245-17	Sequence 17, Appl
28	506	78.9	122	1	US-08-335-573-7	Sequence 7, Appli
29	505	78.8	119	1	US-08-318-157B-11	Sequence 11, Appl
30	505	78.8	119	2	US-09-253-794-11	Sequence 11, Appl
31	501	78.2	119	1	US-08-318-157B-10	Sequence 10, Appl
32	501	78.2	119	2	US-09-253-794-10	Sequence 10, Appl
33	500	78.0	119	1	US-08-318-157B-9	Sequence 9, Appli
34	500	78.0	119	2	US-09-253-794-9	Sequence 9, Appli
35	495	77.2	265	1	US-08-403-853-16	Sequence 16, Appl
36	494	77.1	139	2	US-09-136-315-6	Sequence 6, Appli
37	494	77.1	139	2	US-09-767-888-6	Sequence 6, Appli
38	491.5	76.7	124	1	US-07-958-140-4	Sequence 4, Appli
39	491.5	76.7	124	4	PCT-US93-09166-4	Sequence 4, Appli
40	485	75.7	98	2	US-09-840-459-47	Sequence 47, Appl
41	485	75.7	98	2	US-09-497-625A-47	Sequence 47, Appl
42	481	75.0	119	1	US-08-318-157B-8	Sequence 8, Appli
43	481	75.0	119	2	US-09-253-794-8	Sequence 8, Appli
44	463	72.2	98	2	US-09-840-459-52	Sequence 52, Appl
45	463	72.2	98	2	US-09-497-625A-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-08-318-157B-2
; Sequence 2, Application US/08318157B
; Patent No. 5874540
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; APPLICANT: ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; TITLE OF INVENTION: MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,157B
; FILING DATE: 05-OCT-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-157B-2

Query Match 100.0%; Score 641; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 3.1e-62;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-253-794-2
; Sequence 2, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
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US-09-253-794-2

  Query Match           100.0%;  Score 641;  DB 2;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-62;
  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 3
US-08-318-157B-15
; Sequence 15, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;     COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;     TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  15:
;     SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-318-157B-15

  Query Match           89.2%;  Score 572;  DB 1;  Length 119;
  Best Local Similarity  84.9%;  Pred. No. 1e-54;
  Matches  101;  Conservative   11;  Mismatches    7;  Indels    0;  Gaps    0;

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Db         61 APSLKDRFTISRDNAKNTLYLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 4
US-09-253-794-15
; Sequence 15, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;
```

```
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-253-794-15

  Query Match             89.2%;  Score 572;  DB 2;  Length 119;
  Best Local Similarity   84.9%;  Pred. No. 1e-54;
  Matches  101;  Conservative   11;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              |||||:| :||||||||||||  :| ||| :|:|||||||||||||||||||||:
Db         61 APSLKDRFTISRDNAKNTLYLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 5
US-08-318-157B-14
; Sequence 14, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-14

  Query Match             88.6%;  Score 568;  DB 1;  Length 119;
  Best Local Similarity   84.0%;  Pred. No. 2.8e-54;
  Matches  100;  Conservative   12;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :||||||||||:|||  :| ||| :|:|||||||||||||||||||||:
Db         61 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 6
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

  Query Match             88.6%;  Score 568;  DB 2;  Length 119;
  Best Local Similarity   84.0%;  Pred. No. 2.8e-54;
  Matches  100;  Conservative   12;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
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                ||||||:| :|||||||||:|||  :| ||| :|:|||||||||||||||||||||:
Db          61 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 7
US-08-318-157B-13
; Sequence 13, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-13

  Query Match             88.1%;  Score 565;  DB 1;  Length 119;
  Best Local Similarity   83.2%;  Pred. No. 5.9e-54;
  Matches   99;  Conservative   13;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :||||:||||:|||  :| ||| :|:|||||||||||||||||||||||:
Db         61 APSLKDRFTISRDNSKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 8
US-09-253-794-13
; Sequence 13, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-253-794-13

  Query Match             88.1%;  Score 565;  DB 2;  Length 119;
  Best Local Similarity   83.2%;  Pred. No. 5.9e-54;
  Matches   99;  Conservative   13;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :||||:||||:|||  :| ||| :|:|||||||||||||||||||||||:
Db         61 APSLKDRFTISRDNSKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 9
US-08-318-157B-12
; Sequence 12, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-12

  Query Match             86.6%;  Score 555;  DB 1;  Length 119;
  Best Local Similarity   80.7%;  Pred. No. 7.2e-53;
  Matches   96;  Conservative   15;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||::|||||||||||||||||||||: ||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFTTYWMSWVRQAPGKGLEWVAEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :||||:||||:|||  :| ||| :|:|||||||||||||||||||||:
Db         61 APSLKDRFTISRDNSKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 10
US-08-318-157B-17
; Sequence 17, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-17

  Query Match             86.6%;  Score 555;  DB 1;  Length 119;
  Best Local Similarity   80.7%;  Pred. No. 7.2e-53;
  Matches   96;  Conservative   15;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||::|||||||||||||||||||||: ||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFTTYWMSWVRQAPGKGLEWVAEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :||||:||||:|||  :| ||| :|:|||||||||||||||||||||:
Db         61 APSLKDRFTISRDNSKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 11
US-09-253-794-12
; Sequence 12, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-253-794-12

  Query Match             86.6%;  Score 555;  DB 2;  Length 119;
  Best Local Similarity   80.7%;  Pred. No. 7.2e-53;
  Matches   96;  Conservative   15;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||::|||||||||||||||||||||: ||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFTTYWMSWVRQAPGKGLEWVAEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :||||:||||:|||  :| ||| :|:|||||||||||||||||||||:
Db         61 APSLKDRFTISRDNSKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 12
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```
US-09-253-794-17
; Sequence 17, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-253-794-17

  Query Match             86.6%;  Score 555;  DB 2;  Length 119;
  Best Local Similarity   80.7%;  Pred. No. 7.2e-53;
  Matches   96;  Conservative   15;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||::|||||||||||||||||||||||: ||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSSSGFDFTTYWMSWVRQAPGKGLEWVAEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :||||:||||:|||  :| ||| :|:|||||||||||||||||||||:
Db         61 APSLKDRFTISRDNSKNTLFLQMDSLRPEDTGVYYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 13
US-09-232-290-53
; Sequence 53, Application US/09232290A
; Patent No. 6815540
; GENERAL INFORMATION:
;  APPLICANT: PLUCKTHUN, ANDREAS
;  APPLICANT: NIEBA, LARS
;  APPLICANT: HONEGGER, ANNEMARIE
;  TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
;  TITLE OF INVENTION: INCREASED SOLUBILITY
;  FILE REFERENCE: MORPHO/7
;  CURRENT APPLICATION NUMBER: US/09/232,290A
;  CURRENT FILING DATE: 1999-01-15
;  EARLIER APPLICATION NUMBER: PCT/EP96/02230
;  EARLIER FILING DATE: 1996-05-23
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Murine
US-09-232-290-53

  Query Match             85.6%;  Score 548.5;  DB 2;  Length 118;
  Best Local Similarity   88.3%;  Pred. No. 3.6e-52;
  Matches  106;  Conservative    4;  Mismatches    7;  Indels    3;  Gaps    2;

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RESULT 14
US-08-480-434-30
; Sequence 30, Application US/08480434
; Patent No. 5811248
; GENERAL INFORMATION:
;   APPLICANT:  Charles C. Ditlow, et al.
;   TITLE OF INVENTION:  ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
;   TITLE OF INVENTION:  ANTIBODIES THERETO, AND USES THEREOF
;   NUMBER OF SEQUENCES:  88
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Pennie & Edmonds
;     STREET:  1155 Avenue of the Americas
;     CITY:  New York
;     STATE:  New York
;     COUNTRY:  U.S.A.
;     ZIP:  10036
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.24
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/480,434
;     FILING DATE:  07-JUN-1995
;     CLASSIFICATION:  435
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Albert P. Halluin
;     REGISTRATION NUMBER:  25,227
;     REFERENCE/DOCKET NUMBER:  7606-053
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (415) 854-3660
;     TELEFAX:  (415) 854-3694
;     TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  30:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  120 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  unknown
;     TOPOLOGY:  unknown
;   MOLECULE TYPE:  DNA (genomic)
;   HYPOTHETICAL:  N
;   ANTI-SENSE:  N
US-08-480-434-30

  Query Match             84.5%;  Score 541.5;  DB 1;  Length 120;
  Best Local Similarity   86.9%;  Pred. No. 2.1e-51;
  Matches  106;  Conservative    6;  Mismatches    5;  Indels    5;  Gaps    3;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHP--DSSTI 58
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Db          1 EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPKADSSTI 60
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Qy          59 NYAPSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASL-YFGFPWFAYWGQGTPVTV 117
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Db          61 NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARLGYYGY--FAYWGQGTTVTV 118

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Db         119 SS 120


RESULT 15
US-08-053-451B-30
; Sequence 30, Application US/08053451B
; Patent No. 5955584
;  GENERAL INFORMATION:
;    APPLICANT:  Chen, Francis W.
;    APPLICANT:  Ditlow, Charles C.
;    APPLICANT:  Calenoff, Emanuel
;    TITLE OF INVENTION:  ATHEROSCLEROTIC PLAQUE SPECIFIC
;    TITLE OF INVENTION:  ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
;    NUMBER OF SEQUENCES:  176
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/053,451B
;      FILING DATE:  26-APR-1993
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-033-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
US-08-053-451B-30

  Query Match             84.5%;  Score 541.5;  DB 1;  Length 120;
  Best Local Similarity   86.9%;  Pred. No. 2.1e-51;
  Matches  106;  Conservative    6;  Mismatches    5;  Indels    5;  Gaps    3;

Qy           1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHP--DSSTI 58
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Qy          59 NYAPSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASL-YFGFPWFAYWGQGTPVTV 117
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Db          61 NYTPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARLGYYGY--FAYWGQGTTVTV 118

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Db         119 SS 120


Search completed: March 23, 2006, 01:26:38

Job time : 48 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:36:30 ; Search time 167 Seconds
(without alignments)
297.735 Million cell updates/sec

Title: US-10-755-382-2
Perfect score: 641
Sequence: 1 EVKLLESGGGLVQSGGSLKL.....YFGFPWFAYWGQGTPVTVSA 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	641	100.0	119	3	US-09-253-794-2	Sequence 2, Appli
2	641	100.0	119	4	US-10-680-734-2	Sequence 2, Appli
3	641	100.0	119	5	US-10-755-382-2	Sequence 2, Appli
4	572	89.2	119	3	US-09-253-794-15	Sequence 15, Appl
5	572	89.2	119	4	US-10-680-734-15	Sequence 15, Appl
6	572	89.2	119	5	US-10-755-382-15	Sequence 15, Appl
7	568	88.6	119	3	US-09-253-794-14	Sequence 14, Appl
8	568	88.6	119	4	US-10-680-734-14	Sequence 14, Appl
9	568	88.6	119	4	US-10-680-734-17	Sequence 17, Appl
10	568	88.6	119	5	US-10-755-382-14	Sequence 14, Appl
11	568	88.6	138	4	US-10-006-771A-4	Sequence 4, Appli
12	568	88.6	443	4	US-10-006-773-2	Sequence 2, Appli
13	568	88.6	443	4	US-10-006-771A-2	Sequence 2, Appli
14	568	88.6	468	4	US-10-377-109-2	Sequence 2, Appli
15	568	88.6	669	5	US-10-900-928-3	Sequence 3, Appli
16	567	88.5	118	4	US-10-270-073-3	Sequence 3, Appli
17	567	88.5	256	4	US-10-270-073-6	Sequence 6, Appli
18	567	88.5	257	4	US-10-270-073-8	Sequence 8, Appli
19	567	88.5	261	4	US-10-270-071-18	Sequence 18, Appl
20	567	88.5	261	4	US-10-270-073-2	Sequence 2, Appli
21	567	88.5	261	4	US-10-328-190-6	Sequence 6, Appli
22	567	88.5	267	4	US-10-270-071-22	Sequence 22, Appl
23	567	88.5	267	4	US-10-270-071-26	Sequence 26, Appl
24	567	88.5	267	4	US-10-270-071-30	Sequence 30, Appl
25	567	88.5	267	4	US-10-270-071-36	Sequence 36, Appl
26	567	88.5	358	5	US-10-829-388-12	Sequence 12, Appl
27	567	88.5	363	5	US-10-829-388-2	Sequence 2, Appli
28	567	88.5	364	5	US-10-829-388-11	Sequence 11, Appl
29	567	88.5	370	5	US-10-829-388-1	Sequence 1, Appli
30	567	88.5	415	4	US-10-328-190-12	Sequence 12, Appl
31	565	88.1	119	3	US-09-253-794-13	Sequence 13, Appl
32	565	88.1	119	4	US-10-680-734-13	Sequence 13, Appl
33	565	88.1	119	5	US-10-755-382-13	Sequence 13, Appl
34	555	86.6	119	3	US-09-253-794-12	Sequence 12, Appl
35	555	86.6	119	3	US-09-253-794-17	Sequence 17, Appl
36	555	86.6	119	4	US-10-680-734-12	Sequence 12, Appl
37	555	86.6	119	5	US-10-755-382-12	Sequence 12, Appl
38	555	86.6	119	5	US-10-755-382-17	Sequence 17, Appl
39	537	83.8	119	4	US-10-680-734-27	Sequence 27, Appl
40	533	83.2	119	3	US-09-253-794-58	Sequence 58, Appl
41	533	83.2	119	5	US-10-755-382-58	Sequence 58, Appl
42	529.5	82.6	256	4	US-10-239-656-57	Sequence 57, Appl
43	529.5	82.6	258	4	US-10-239-656-71	Sequence 71, Appl
44	529.5	82.6	503	4	US-10-239-656-75	Sequence 75, Appl
45	529.5	82.6	505	4	US-10-239-656-79	Sequence 79, Appl

ALIGNMENTS

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RESULT 1
US-09-253-794-2
; Sequence 2, Application US/09253794
; Patent No. US20020018750A1
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-253-794-2

  Query Match           100.0%;  Score 641;  DB 3;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-50;
  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
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Db         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119


RESULT 2
US-10-680-734-2
; Sequence 2, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-680-734-2

  Query Match             100.0%;  Score 641;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-50;
  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
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Db         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119


RESULT 3
US-10-755-382-2
; Sequence 2, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-755-382-2

  Query Match             100.0%;  Score 641;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-50;
  Matches  119;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
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Db         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119


RESULT 4
US-09-253-794-15
; Sequence 15, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
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;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-253-794-15

  Query Match             89.2%;  Score 572;  DB 3;  Length 119;
  Best Local Similarity   84.9%;  Pred. No. 2.1e-44;
  Matches  101;  Conservative   11;  Mismatches    7;  Indels    0;  Gaps    0;

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Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
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RESULT 5
US-10-680-734-15
; Sequence 15, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-15

  Query Match             89.2%;  Score 572;  DB 4;  Length 119;
  Best Local Similarity   84.9%;  Pred. No. 2.1e-44;
  Matches  101;  Conservative   11;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
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Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :|||||||||||||  :| ||| :|:|||||||||||||||||||||||:
Db         61 APSLKDRFTISRDNAKNTLYLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 6
US-10-755-382-15
; Sequence 15, Application US/10755382
; Publication No. US20050089538A1
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/755,382
;            FILING DATE: 13-Jan-2004
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 15:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-755-382-15

  Query Match             89.2%;  Score 572;  DB 5;  Length 119;
  Best Local Similarity   84.9%;  Pred. No. 2.1e-44;
  Matches  101;  Conservative   11;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :|||||||||||||  :| ||| :|:|||||||||||||||||||||||:
Db         61 APSLKDRFTISRDNAKNTLYLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 7
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. US20020018750A1
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
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;              FILING DATE: 22-Feb-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US 08/318,157
;              FILING DATE: 05-OCT-1994
;         ATTORNEY/AGENT INFORMATION:
;              NAME: SAXE, Bernhard D.
;              REGISTRATION NUMBER: 28,665
;              REFERENCE/DOCKET NUMBER: 18733/464
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (202)672-5300
;              TELEFAX: (202)672-5399
;              TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 14:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 119 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: <Unknown>
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

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  Best Local Similarity   84.0%;  Pred. No. 4.9e-44;
  Matches  100;  Conservative   12;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :|||||||||:|||  :| ||| :|:|||||||||||||||||||||||:
Db         61 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 8
US-10-680-734-14
; Sequence 14, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-14

  Query Match             88.6%;  Score 568;  DB 4;  Length 119;
  Best Local Similarity   84.0%;  Pred. No. 4.9e-44;
  Matches  100;  Conservative   12;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :|||||||||:|||  :| ||| :|:|||||||||||||||||||||||:
Db         61 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 9
US-10-680-734-17
; Sequence 17, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-17

  Query Match             88.6%;  Score 568;  DB 4;  Length 119;
  Best Local Similarity   84.0%;  Pred. No. 4.9e-44;
  Matches  100;  Conservative   12;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
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Db         61 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 10
US-10-755-382-14
; Sequence 14, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;         APPLICANT: HANSEN, Hans J.
;                    ARMOUR, Kathryn L.
;         TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                             MOUSE MONOCLONAL ANTIBODIES
;         NUMBER OF SEQUENCES: 58
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Foley & Lardner
;              STREET: 3000 K Street, N.W., Suite 500
;              CITY: Washington
;              STATE: D.C.
;              COUNTRY: USA
;              ZIP: 20007-5109
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/755,382
;              FILING DATE: 13-Jan-2004
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/09/253,794
;              FILING DATE: 22-Feb-1999
;              APPLICATION NUMBER: US 08/318,157
;              FILING DATE: 05-OCT-1994
;         ATTORNEY/AGENT INFORMATION:
;              NAME: SAXE, Bernhard D.
;              REGISTRATION NUMBER: 28,665
```

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;            REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-755-382-14

  Query Match             88.6%;  Score 568;  DB 5;  Length 119;
  Best Local Similarity   84.0%;  Pred. No. 4.9e-44;
  Matches  100;  Conservative   12;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db          1 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :|||||||||:|||  :| ||| :|:|||||||||||||||||||||||:
Db         61 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


RESULT 11
US-10-006-771A-4
; Sequence 4, Application US/10006771A
; Publication No. US20020165360A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen
;  FILE REFERENCE: 002
;  CURRENT APPLICATION NUMBER: US/10/006,771A
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: 60/250,090
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 138
;   TYPE: PRT
;   ORGANISM: Homo sapiens and Mus sp.
US-10-006-771A-4

  Query Match             88.6%;  Score 568;  DB 4;  Length 138;
  Best Local Similarity   84.0%;  Pred. No. 5.7e-44;
  Matches  100;  Conservative   12;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||:|| | ||:|||:||||||||||||||||||||||||||||||||||||
Db         20 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 79

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :|||||||||:|||  :| ||| :|:|||||||||||||||||||||||:
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RESULT 12
US-10-006-773-2
; Sequence 2, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
;  FILE REFERENCE: 003
;  CURRENT APPLICATION NUMBER: US/10/006,773
;  CURRENT FILING DATE:  2001-12-10
;  PRIOR APPLICATION NUMBER: 60/250,089
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 443
;   TYPE: PRT
;   ORGANISM: Homo sapiens and Mus sp.
US-10-006-773-2

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  Best Local Similarity   84.0%;  Pred. No. 1.9e-43;
  Matches  100;  Conservative   12;  Mismatches    7;  Indels    0;  Gaps    0;

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Db        142 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 201

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
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RESULT 13
US-10-006-771A-2
; Sequence 2, Application US/10006771A
; Publication No. US20020165360A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen
;  FILE REFERENCE: 002
;  CURRENT APPLICATION NUMBER: US/10/006,771A
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: 60/250,090
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 443
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-006-771A-2

  Query Match             88.6%;  Score 568;  DB 4;  Length 443;
  Best Local Similarity   84.0%;  Pred. No. 1.9e-43;
  Matches  100;  Conservative   12;  Mismatches    7;  Indels    0;  Gaps    0;

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Db        142 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 201

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
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RESULT 14
US-10-377-109-2
; Sequence 2, Application US/10377109
; Publication No. US20040018557A1
; GENERAL INFORMATION:
;  APPLICANT: QU, ZHENGXING
;  APPLICANT:  HANSEN, HANS
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: BISPECIFIC ANTIBODY POINT MUTATIONS FOR ENHANCING RATE
;  TITLE OF INVENTION:  OF CLEARANCE
;  FILE REFERENCE: 018733/1159
;  CURRENT APPLICATION NUMBER: US/10/377,109
;  CURRENT FILING DATE:  2003-03-03
;  PRIOR APPLICATION NUMBER: 60/361,037
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 468
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-377-109-2

  Query Match             88.6%;  Score 568;  DB 4;  Length 468;
  Best Local Similarity   84.0%;  Pred. No. 2e-43;
  Matches  100;  Conservative   12;  Mismatches    7;  Indels    0;  Gaps    0;

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Db         20 EVQLVESGGGVVQPGRSLRLSCSASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 79

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||:| :|||||||||:|||  :| ||| :|:|||||||||||||||||||||:
Db         80 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 138


RESULT 15
US-10-900-928-3
; Sequence 3, Application US/10900928
; Publication No. US20050069552A1
; GENERAL INFORMATION:
;  APPLICANT: Bleck, Gregory T.
;  APPLICANT:  York, Donna
;  APPLICANT:  Collins, Ian
;  TITLE OF INVENTION: Fusion Antibodies
;  FILE REFERENCE: GALA-09135
;  CURRENT APPLICATION NUMBER: US/10/900,928
;  CURRENT FILING DATE:  2004-07-28
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 669
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-900-928-3

  Query Match             88.6%;  Score 568;  DB 5;  Length 669;
  Best Local Similarity   84.0%;  Pred. No. 2.8e-43;
  Matches  100;  Conservative   12;  Mismatches    7;  Indels    0;  Gaps    0;

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Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
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Db         61 APSLKDRFTISRDNAKNTLFLQMDSLRPEDTGVYFCASLYFGFPWFAYWGQGTPVTVSS 119


Search completed: March 23, 2006, 01:39:56
Job time : 168 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:37:15 ; Search time 23 Seconds
(without alignments)
148.092 Million cell updates/sec

Title: US-10-755-382-2
Perfect score: 641
Sequence: 1 EVKLLESGGGLVQSGGSLKL.....YFGFPWFAYWGQGTPVTVSA 119

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	523	81.6	119	6	US-10-982-357-5	Sequence 5, Appli
2	523	81.6	119	6	US-10-982-357-38	Sequence 38, Appl
3	523	81.6	119	6	US-10-982-357-45	Sequence 45, Appl
4	523	81.6	137	6	US-10-982-357-27	Sequence 27, Appl
5	500	78.0	119	6	US-10-982-357-41	Sequence 41, Appl
6	500	78.0	119	6	US-10-982-357-47	Sequence 47, Appl
7	435	67.9	129	6	US-10-993-543-32	Sequence 32, Appl
8	431	67.2	121	6	US-10-665-658-5	Sequence 5, Appli
9	431	67.2	121	7	US-11-107-028-50	Sequence 50, Appl
10	431	67.2	121	7	US-11-149-031-2	Sequence 2, Appli
11	430.5	67.2	245	7	US-11-054-515-1826	Sequence 1826, Ap
12	428.5	66.8	122	7	US-11-049-536-186	Sequence 186, App
13	427.5	66.7	307	7	US-11-000-463-332	Sequence 332, App
14	427.5	66.7	363	7	US-11-000-463-335	Sequence 335, App
15	425	66.3	119	7	US-11-049-536-562	Sequence 562, App
16	425	66.3	121	6	US-10-665-658-24	Sequence 24, Appl
17	424.5	66.2	122	7	US-11-049-536-574	Sequence 574, App
18	423.5	66.1	124	7	US-11-049-536-210	Sequence 210, App
19	423	66.0	119	7	US-11-049-536-314	Sequence 314, App
20	422.5	65.9	119	6	US-10-925-366A-354	Sequence 354, App
21	422.5	65.9	119	6	US-10-925-366A-359	Sequence 359, App
22	421	65.7	147	7	US-11-049-536-52	Sequence 52, Appl
23	420.5	65.6	120	6	US-10-925-366A-286	Sequence 286, App
24	420	65.5	119	7	US-11-049-536-502	Sequence 502, App
25	419.5	65.4	116	6	US-10-925-366A-223	Sequence 223, App
26	419.5	65.4	126	7	US-11-049-536-430	Sequence 430, App
27	419	65.4	117	7	US-11-049-536-178	Sequence 178, App
28	419	65.4	117	7	US-11-049-536-222	Sequence 222, App
29	419	65.4	117	7	US-11-049-536-226	Sequence 226, App
30	418.5	65.3	124	7	US-11-049-536-310	Sequence 310, App
31	418	65.2	119	7	US-11-106-820-9	Sequence 9, Appli
32	418	65.2	119	7	US-11-154-337-6	Sequence 6, Appli
33	418	65.2	119	7	US-11-182-908-6	Sequence 6, Appli
34	418	65.2	119	7	US-11-049-536-542	Sequence 542, App
35	418	65.2	119	7	US-11-190-364-9	Sequence 9, Appli
36	418	65.2	119	7	US-11-102-120-6	Sequence 6, Appli
37	418	65.2	119	7	US-11-147-780-9	Sequence 9, Appli
38	418	65.2	119	7	US-11-223-361-6	Sequence 6, Appli
39	418	65.2	137	6	US-10-993-543-76	Sequence 76, Appl
40	417.5	65.1	116	7	US-11-125-837-38	Sequence 38, Appl
41	417.5	65.1	120	7	US-11-049-536-518	Sequence 518, App
42	417.5	65.1	133	6	US-10-993-543-4	Sequence 4, Appli
43	417	65.1	115	7	US-11-127-903-22	Sequence 22, Appl
44	417	65.1	123	7	US-11-127-903-48	Sequence 48, Appl
45	417	65.1	125	7	US-11-049-536-242	Sequence 242, App

ALIGNMENTS

RESULT 1
US-10-982-357-5
; Sequence 5, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/982,357
; CURRENT FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-982-357-5

Query Match 81.6%; Score 523; DB 6; Length 119;
Best Local Similarity 84.0%; Pred. No. 1.2e-39;
Matches 100; Conservative 6; Mismatches 13; Indels 0; Gaps 0;

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Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              |||||||||||||| ||||||||||||||: |||||||||||||||||||||:||||||||
Db          1 EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||||:|||||||||||||||||||||||||||     : :|  || || ||||:
Db         61 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARPDGNYWYFDVWGAGTTVTVSS 119
```

RESULT 2
US-10-982-357-38
; Sequence 38, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/982,357
; CURRENT FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-982-357-38

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  Query Match             81.6%;  Score 523;  DB 6;  Length 119;
  Best Local Similarity   84.0%;  Pred. No. 1.2e-39;
  Matches  100;  Conservative    6;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||||||||||||| |||||||||||||||: |||||||||||||||||||||:||||||||
Db          1 EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||||:||||||||||||||||||||||||     : :|  || || ||||:
Db         61 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARPDGNYWYFDVWGAGTTVTVSS 119


RESULT 3
US-10-982-357-45
; Sequence 45, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-45

  Query Match             81.6%;  Score 523;  DB 6;  Length 119;
  Best Local Similarity   84.0%;  Pred. No. 1.2e-39;
  Matches  100;  Conservative    6;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||||||||||||| |||||||||||||||: |||||||||||||||||||||:||||||||
Db          1 EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||||:||||||||||||||||||||||||     : :|  || || ||||:
Db         61 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARPDGNYWYFDVWGAGTTVTVSS 119


RESULT 4
US-10-982-357-27
; Sequence 27, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
;   LENGTH: 137
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-27

  Query Match             81.6%;  Score 523;  DB 6;  Length 137;
  Best Local Similarity   84.0%;  Pred. No. 1.4e-39;
  Matches  100;  Conservative    6;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||||||||||||| |||||||||||||||: |||||||||||||||||||||:||||||||
Db         19 EVKLLESGGGLVQPGGSLKLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 78

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              ||||||||:||||||||||||||||||||||||     : :|  || || ||||:
Db         79 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARPDGNYWYFDVWGAGTTVTVSS 137


RESULT 5
US-10-982-357-41
; Sequence 41, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-982-357-41

  Query Match             78.0%;  Score 500;  DB 6;  Length 119;
  Best Local Similarity   78.2%;  Pred. No. 1.3e-37;
  Matches   93;  Conservative   14;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:||||||| ||||:|||||||||: |||||||||||||||||||:||||||||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              |||||||||:|||||||:|||||: :|:||||:||||     : :|  ||||| ||||:
Db         61 APSLKDKFIISRDNAKNSLYLQMNSLRAEDTAVYYCARPDGNYWYFDVWGQGTLVTVSS 119


RESULT 6
US-10-982-357-47
; Sequence 47, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo saiens
US-10-982-357-47

  Query Match             78.0%;  Score 500;  DB 6;  Length 119;
  Best Local Similarity   78.2%;  Pred. No. 1.3e-37;
  Matches   93;  Conservative   14;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:||||||| ||||:|||||||||: |||||||||||||||||||:||||||||
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGFDFSRYWMSWVRQAPGKGLEWIGEINPDSSTINY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              |||||||||:|||||||:|||||: :|:||||:||||     : :|  ||||| ||||:
Db         61 APSLKDKFIISRDNAKNSLYLQMNSLRAEDTAVYYCARPDGNYWYFDVWGQGTLVTVSS 119


RESULT 7
US-10-993-543-32
; Sequence 32, Application US/10993543
; Publication No. US20060036076A1
; GENERAL INFORMATION:
;  APPLICANT: Dransfield, Daniel T.
;  APPLICANT:  Rookey, Kristin
;  APPLICANT:  Ladner, Robert C.
```

```
;  TITLE OF INVENTION: Metalloproteinase-Binding Proteins
;  FILE REFERENCE: 10280-088001
;  CURRENT APPLICATION NUMBER: US/10/993,543
;  CURRENT FILING DATE:  2004-11-19
;  PRIOR APPLICATION NUMBER: US 60/523,745
;  PRIOR FILING DATE: 2003-11-19
;  NUMBER OF SEQ ID NOS: 299
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-993-543-32

  Query Match             67.9%;  Score 435;  DB 6;  Length 129;
  Best Local Similarity   67.2%;  Pred. No. 7.5e-32;
  Matches   80;  Conservative   15;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|||||||||| ||||:|||||||| |: | | |||||||||||||:  |:|     ||
Db          1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSPYHMGWVRQAPGKGLEWVSGIYPSGGWTNY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              | |:| :| :||||:||||||||: :|:||||:||||   :   || |||||| ||||:
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDGYSSGWFRYWGQGTLVTVSS 119


RESULT 8
US-10-665-658-5
; Sequence 5, Application US/10665658
; Publication No. US20050276801A1
;   GENERAL INFORMATION:
;        APPLICANT: Jardieu, Paula M.
;                   Presta, Leonard G.
;        TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
;        NUMBER OF SEQUENCES: 71
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/665,658
;             FILING DATE: 19-Sep-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/031971
;             FILING DATE: 27-NOV-1996
;             APPLICATION NUMBER: 08/974899
;             FILING DATE: 20-NOV-1997
;             APPLICATION NUMBER: 09/420745
;             FILING DATE: 20-OCT-1999
;             APPLICATION NUMBER: 09/975798
;             FILING DATE: 28-FEB-2001
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Tan, Lee K.
;             REGISTRATION NUMBER: 39,447
;             REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-4462
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 121 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-665-658-5

  Query Match             67.2%;  Score 431;  DB 6;  Length 121;
  Best Local Similarity   66.1%;  Pred. No. 1.6e-31;
  Matches   80;  Conservative   17;  Mismatches   22;  Indels    2;  Gaps    2;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||||| ||||:|||||||: || :||:|||||||||||:| |||   |   |
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCA-SLYF-GFPWFAYWGQGTPVTVS 118
                  ||:| :| | :|||||||: :|:||||:||||  :|| |  :| ||||||| ||||
Db         61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120

Qy        119 A 119
              :
Db        121 S 121


RESULT 9
US-11-107-028-50
; Sequence 50, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
;  APPLICANT: CHAN, ANDREW C.
;  APPLICANT:  GONG, QIAN
;  APPLICANT:  MARTIN, FLAVIUS
;  TITLE OF INVENTION: Method for Augmenting B Cell Depletion
;  FILE REFERENCE: P2112R1
;  CURRENT APPLICATION NUMBER: US/11/107,028
;  CURRENT FILING DATE:  2005-04-15
;  PRIOR APPLICATION NUMBER: US 60/563,263
;  PRIOR FILING DATE: 2004-04-16
;  NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 50
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: sequence is synthesized
US-11-107-028-50

  Query Match             67.2%;  Score 431;  DB 7;  Length 121;
  Best Local Similarity   66.1%;  Pred. No. 1.6e-31;
  Matches   80;  Conservative   17;  Mismatches   22;  Indels    2;  Gaps    2;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||||| ||||:|||||||: || :||:|||||||||||:| |||   |   |
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCA-SLYF-GFPWFAYWGQGTPVTVS 118
                  ||:| :| | :|||||||: :|:||||:||||  :|| |  :| ||||||| ||||
Db         61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120

Qy        119 A 119
              :
Db        121 S 121


RESULT 10
US-11-149-031-2
; Sequence 2, Application US/11149031
; Publication No. US20060013818A1
; GENERAL INFORMATION:
;  APPLICANT: GOFFE, BERNARD S.
;  TITLE OF INVENTION: Method of Treating Granuloma Annulare or Sarcoid
;  FILE REFERENCE: P2129R1
;  CURRENT APPLICATION NUMBER: US/11/149,031
;  CURRENT FILING DATE:  2005-06-08
;  PRIOR APPLICATION NUMBER: US 60/578,768
;  PRIOR FILING DATE: 2004-06-09
;  PRIOR APPLICATION NUMBER: US 60/579,096
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;  PRIOR FILING DATE: 2004-06-10
;  NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 2
;   LENGTH: 121
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: sequence is synthesized
US-11-149-031-2

  Query Match             67.2%;  Score 431;  DB 7;  Length 121;
  Best Local Similarity   66.1%;  Pred. No. 1.6e-31;
  Matches   80;  Conservative   17;  Mismatches   22;  Indels    2;  Gaps    2;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|:|||||||| ||||:|||||||: || :||:|||||||||||||:| |||  |   |
Db          1 EVQLVESGGGLVQPGGSLRLSCAASGYSFTGHWMNWVRQAPGKGLEWVGMIHPSDSETRY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCA-SLYF-GFPWFAYWGQGTPVTVS 118
                ||:| :| | :|||||||||: :|:||||:||||  :|| |  :| |||||| ||||
Db         61 NQKFKDRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARGIYFYGTTYFDYWGQGTLVTVS 120

Qy        119 A 119
              :
Db        121 S 121


RESULT 11
US-11-054-515-1826
; Sequence 1826, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1826
;   LENGTH: 245
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1826

  Query Match             67.2%;  Score 430.5;  DB 7;  Length 245;
  Best Local Similarity   65.9%;  Pred. No. 3.4e-31;
  Matches   81;  Conservative   23;  Mismatches   14;  Indels    5;  Gaps    2;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              :|:|::|||||||| ||||:|||||||| |::: |:|||||||||||:  |   ||||:|
Db          1 QVQLVQSGGGLVQPGGSLRLSCAASGFSFSSHSMNWVRQAPGKGLEWVSYIDSSSSTIHY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYF----GFPWFAYWGQGTPVT 116
                | |:| :||:|||||||:|||||: :|:||||:||||| |:    |: :| |||||| ||
Db         61 ADSVKGRFIISRDNAKNSLYLQMNSLRAEDTAVYYCASTYYDILTGY-YFDYWGQGTLVT 119

Qy        117 VSA 119
              ||:
Db        120 VSS 122


RESULT 12
US-11-049-536-186
; Sequence 186, Application US/11049536
; Publication No. US20060024297A1
; GENERAL INFORMATION:
;  APPLICANT: Wood, Clive R.
;  APPLICANT:  Dransfield,  Daniel T.
;  APPLICANT:  Pieters, Henk
;  APPLICANT:  Hoet, Rene
;  APPLICANT:  Hufton, Simon E.
;  TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
;  FILE REFERENCE: 10280-128001
;  CURRENT APPLICATION NUMBER: US/11/049,536
;  CURRENT FILING DATE:  2005-02-02
;  PRIOR APPLICATION NUMBER: US 10/916,840
;  PRIOR FILING DATE: 2004-08-12
;  PRIOR APPLICATION NUMBER: US 60/494,713
;  PRIOR FILING DATE: 2003-08-12
;  NUMBER OF SEQ ID NOS: 721
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 186
;   LENGTH: 122
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: Antibody
US-11-049-536-186

  Query Match             66.8%;  Score 428.5;  DB 7;  Length 122;
  Best Local Similarity   66.4%;  Pred. No. 2.7e-31;
  Matches   81;  Conservative   17;  Mismatches   21;  Indels    3;  Gaps    1;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|||||||||| ||||:|||||||| |: | |:|||||||||||||:  |:|      |
Db          1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYKMNWVRQAPGKGLEWVSVIYPSGGWTYY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYF---GFPWFAYWGQGTPVTV 117
                | |:| :| :||||:||||||||: :|:||||:||||| |:   |:  | |||||| |||
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCASGYYDSSGYSRFDYWGQGTLVTV 120

Qy        118 SA 119
              |:
Db        121 SS 122


RESULT 13
US-11-000-463-332
; Sequence 332, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Chen, Rui-hong
;  APPLICANT:  Qian, Xiaohong B.
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Cao, Yi-Cheng
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
;  FILE REFERENCE: 785CIP4CN
;  CURRENT APPLICATION NUMBER: US/11/000,463
```

```
;  CURRENT FILING DATE:  2004-11-29
;  PRIOR APPLICATION NUMBER: 10/291,265
;  PRIOR FILING DATE: 2002-11-08
;  PRIOR APPLICATION NUMBER: PCT/US01/02623
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: 09/922,279
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 09/617,746
;  PRIOR FILING DATE: 2000-07-17
;  PRIOR APPLICATION NUMBER: 09/631,451
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: 09/633,870
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 944
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 332
;   LENGTH: 307
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-000-463-332

  Query Match             66.7%;  Score 427.5;  DB 7;  Length 307;
  Best Local Similarity   68.1%;  Pred. No. 7.7e-31;
  Matches   81;  Conservative   16;  Mismatches   19;  Indels    3;  Gaps    1;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|||||||||| |||||:|||||||| |::: |||||||||||||:  |   | |  |
Db         20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY 79

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              | |:| :| :||||:||||||||: :|:||||:||||     ||:| |||||| ||||:
Db         80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK---PFPYFDYWGQGTLVTVSS 135


RESULT 14
US-11-000-463-335
; Sequence 335, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Chen, Rui-hong
;  APPLICANT:  Qian, Xiaohong B.
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Cao, Yi-Cheng
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
;  FILE REFERENCE: 785CIP4CN
;  CURRENT APPLICATION NUMBER: US/11/000,463
;  CURRENT FILING DATE:  2004-11-29
;  PRIOR APPLICATION NUMBER: 10/291,265
;  PRIOR FILING DATE: 2002-11-08
;  PRIOR APPLICATION NUMBER: PCT/US01/02623
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: 09/922,279
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 09/617,746
;  PRIOR FILING DATE: 2000-07-17
;  PRIOR APPLICATION NUMBER: 09/631,451
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: 09/633,870
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 944
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 335
;   LENGTH: 363
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-000-463-335

  Query Match             66.7%;  Score 427.5;  DB 7;  Length 363;
  Best Local Similarity   68.1%;  Pred. No. 9e-31;
  Matches   81;  Conservative   16;  Mismatches   19;  Indels    3;  Gaps    1;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|||||||||| |||||:|||||||| |::: |||||||||||||:  |   | |  |
Db         20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSSFSMSWVRQAPGKGLEWVSSISGSSGTTYY 79

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              | |:| :| :||||:||||||||: :|:||||:||||     ||:| |||||| ||||:
Db         80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAK---PFPYFDYWGQGTLVTVSS 135


RESULT 15
US-11-049-536-562
; Sequence 562, Application US/11049536
; Publication No. US20060024297A1
; GENERAL INFORMATION:
;  APPLICANT: Wood, Clive R.
;  APPLICANT:  Dransfield,  Daniel T.
;  APPLICANT:  Pieters, Henk
;  APPLICANT:  Hoet, Rene
;  APPLICANT:  Hufton, Simon E.
;  TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
;  FILE REFERENCE: 10280-128001
;  CURRENT APPLICATION NUMBER: US/11/049,536
;  CURRENT FILING DATE:  2005-02-02
;  PRIOR APPLICATION NUMBER: US 10/916,840
;  PRIOR FILING DATE: 2004-08-12
;  PRIOR APPLICATION NUMBER: US 60/494,713
;  PRIOR FILING DATE: 2003-08-12
;  NUMBER OF SEQ ID NOS: 721
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 562
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: Antibody
US-11-049-536-562

  Query Match             66.3%;  Score 425;  DB 7;  Length 119;
  Best Local Similarity   66.4%;  Pred. No. 5.3e-31;
  Matches   79;  Conservative   15;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 EVKLLESGGGLVQSGGSLKLSCAASGFDFTTYWMSWVRQAPGKGLEWIGEIHPDSSTINY 60
              ||:|||||||||| |||||:|||||||| |: | | |||||||||||||:  |:|      |
Db          1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSKYKMHWVRQAPGKGLEWVSVIYPSGGKTYY 60

Qy         61 APSLKDKFIVSRDNAKNTLYLQMSKVRSEDTALYYCASLYFGFPWFAYWGQGTPVTVSA 119
              | |:| :| :||||:||||||||: :|:||||:||||     |  |: |||||| ||||:
Db         61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREMGGSGWYDYWGQGTLVTVSS 119


Search completed: March 23, 2006, 01:40:25
Job time : 24 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 00:44:09 ; Search time 313.891 Seconds
(without alignments)
148.377 Million cell updates/sec

Title: US-10-755-382-4
Perfect score: 557
Sequence: 1 EIQLTQSHKMMSTSVGDRVS.....FCQQYSLYRSFGGGTKLEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	557	100.0	106	8	ADM95097	Adm95097 Murine MN
2	557	100.0	106	8	ADM98320	Adm98320 Murine MN
3	553	99.3	106	2	AAR97335	Aar97335 Murine NE
4	509	91.4	213	5	AAU72819	Aau72819 DNA encod
5	509	91.4	213	6	AAO29887	Aao29887 LM6 fusio
6	509	91.4	213	7	ADJ79840	Adj79840 LM6-type
7	509	91.4	234	5	AAU72802	Aau72802 TRA-8 lig
8	509	91.4	234	6	AAO29870	Aao29870 Mouse ant
9	509	91.4	234	7	ADJ79788	Adj79788 TRA-8 ant
10	486	87.3	107	9	ADZ45501	Adz45501 Murine fa
11	485.5	87.2	107	8	ADU87728	Adu87728 Light cha
12	485.5	87.2	107	8	ADU87734	Adu87734 VL region
13	485.5	87.2	107	8	ADU87693	Adu87693 Mouse Luc
14	485.5	87.2	127	8	ADU87781	Adu87781 Anti-CS1
15	483.5	86.8	115	5	ABB07359	Abb07359 22A5 IgM
16	482	86.5	106	4	AAB86108	Aab86108 H. pylori
17	482	86.5	106	4	AAB86070	Aab86070 H. pylori
18	479.5	86.1	238	5	AAE27930	Aae27930 Human C5E
19	479.5	86.1	238	6	ABB82839	Abb82839 Antibody
20	478.5	85.9	105	8	ADT75007	Adt75007 Light cha
21	472.5	84.8	108	2	AAY21817	Aay21817 Anti-STX1
22	472.5	84.8	223	1	AAP40031	Aap40031 Kappa ant
23	472.5	84.8	247	1	AAP80155	Aap80155 FRs and C
24	472.5	84.8	247	1	AAP80156	Aap80156 Biosynthe
25	468.5	84.1	107	3	AAY79425	Aay79425 Tie2 rece
26	467.5	83.9	108	8	ADT75004	Adt75004 Light cha
27	467.5	83.9	108	8	ADT74999	Adt74999 Light cha
28	466.5	83.8	214	9	AEC20772	Aec20772 M-CSF spe
29	463.5	83.2	107	2	AAW47087	Aaw47087 Mouse J59
30	463.5	83.2	107	2	AAY90375	Aay90375 J591 mono
31	463.5	83.2	107	2	AAB36226	Aab36226 Monoclona
32	463.5	83.2	107	4	AAB69665	Aab69665 Murine Fd
33	463.5	83.2	107	6	ABO10703	Abo10703 Variable
34	463.5	83.2	107	6	ABR44647	Abr44647 Murine J5
35	463.5	83.2	107	8	ADO47768	Ado47768 Mouse Fd1
36	463.5	83.2	107	8	ADO47712	Ado47712 Mouse Fd1
37	462	82.9	108	8	ADT75006	Adt75006 Light cha
38	462	82.9	115	8	ADT74992	Adt74992 Light cha
39	461.5	82.9	108	9	AEB21883	Aeb21883 Human DC-
40	458.5	82.3	107	8	ADU67899	Adu67899 Mouse ant
41	457.5	82.1	107	2	AAR55121	Aar55121 Mouse ant
42	457.5	82.1	107	2	AAR60300	Aar60300 Anti HIV
43	455	81.7	213	5	AAU72818	Aau72818 DNA encod
44	455	81.7	213	6	AAO29886	Aao29886 LM5 fusio
45	455	81.7	213	7	ADJ79839	Adj79839 LM5-type

ALIGNMENTS

RESULT 1
ADM95097
ID ADM95097 standard; protein; 106 AA.
XX
AC ADM95097;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 MAb light chain variable region.
XX
KW non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW complementarity determining region; pancreatic cancer; breast cancer;
KW ovarian cancer.
XX
OS Mus sp.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-364813/34.
DR N-PSDB; ADM95096.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Disclosure; Fig 12A-B; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the murine MN-

```
CC   14 antibody light chain variable region.
XX
SQ   Sequence 106 AA;

  Query Match             100.0%;  Score 557;  DB 8;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-40;
  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
              ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106


RESULT 2
ADM98320
ID   ADM98320 standard; protein; 106 AA.
XX
AC   ADM98320;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Murine MN-14 antibody light chain variable region protein.
XX
KW   carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW   antibody; MN-14; non-medullary thyroid carcinoma;
KW   medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW   hepatocellular carcinoma; breast cancer; lung cancer;
KW   antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW   apoptosis.
XX
OS   Mus sp.
XX
PN   WO2004032857-A2.
XX
PD   22-APR-2004.
XX
PF   08-OCT-2003; 2003WO-US031801.
XX
PR   08-OCT-2002; 2002US-0416531P.
PR   11-OCT-2002; 2002WO-US032307.
PR   02-MAY-2003; 2003US-0467161P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-340797/31.
DR   N-PSDB; ADM98319.
XX
PT   Treating non-medullary or medullary thyroid carcinoma, involves
PT   administering to subject, either concurrently or sequentially, anti-
PT   carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS   Disclosure; Fig 12; 122pp; English.
XX
CC   This invention relates to methods for treating cancers that express
CC   carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC   therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC   antibodies that can be used following administration of an agent that
CC   will increase antibody effector functions or following administration of
CC   an amount of interferon effective to upregulate CEA expression in tumour
CC   cells. The present invention describes the anti-CEA antibody as a class
CC   III humanised murine monoclonal antibody that retains specificity for CEA
CC   binding and is preferably an MN-14 antibody or fragment thereof.
CC   Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC   composition useful for the treatment of non-medullary or medullary
CC   thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC   carcinoma, as well as breast or lung cancer. Furthermore, it can
CC   stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC   mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC   cell growth and angiogenesis. This polypeptide sequence is murine MN-14
CC   antibody light chain variable region protein of the invention.
XX
SQ   Sequence 106 AA;

  Query Match             100.0%;  Score 557;  DB 8;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-40;
  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
              ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106


RESULT 3
AAR97335
ID   AAR97335 standard; protein; 106 AA.
XX
AC   AAR97335;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Murine NEWM MN-14 variable region light chain.
XX
KW   Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW   complementary determining region; anti-carcinoembryonic antigen; CEA;
KW   diagnosis; imaging; therapy; immune response.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    24. .34
FT                   /label= CDR 1.
FT   Binding-site    50. .56
FT                   /label= CDR 2.
FT   Binding-site    89. .96
FT                   /label= CDR 3.
XX
PN   WO9611013-A1.
XX
PD   18-APR-1996.
XX
PF   28-SEP-1995;   95WO-US011964.
XX
PR   05-OCT-1994;   94US-00318157.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Hansen HJ,  Armour KL;
XX
DR   WPI; 1996-209653/21.
DR   N-PSDB; AAT29011.
XX
PT   New humanised anti-CEA monoclonal antibody - having engrafted murine
PT   CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS   Example 7; Fig 2; 62pp; English.
XX
CC   New humanised monoclonal antibodies (MAbs) comprising the complementary
CC   determining regions (CDRs) of a parental murine class III anti-
CC   carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC   heterologous antibody which can be derived from any species including
CC   human, retain the anti-CEA binding specificity of the parental murine MAb
CC   but are less immunogenic in a human subject than the parental MAb. The
CC   humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC   -producing cancers and patients receiving the humanised antibodies and
CC   conjugates show improved therapeutic results, decreased immune responses
CC   and decreased immune-mediated adverse effects compared to the parent
```

```
CC   antibody. See AAR97313-97333 for the CDR sequence and framework regions
CC   of the humanised MAbs
XX
SQ   Sequence 106 AA;

  Query Match             99.3%;  Score 553;  DB 2;  Length 106;
  Best Local Similarity   99.1%;  Pred. No. 4.5e-40;
  Matches  105;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
              |||||||||||||||||||||||||||||||||||||:|||||
Db         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGSKLEIK 106


RESULT 4
AAU72819
ID   AAU72819 standard; protein; 213 AA.
XX
AC   AAU72819;
XX
DT   26-FEB-2002  (first entry)
XX
DE   DNA encoding TRA-8 light chain/human Ig light chain fusion (LM6).
XX
KW   Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;
KW   TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;
KW   autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
KW   rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;
KW   Addison disease; scleroderma; Goodpasture's syndrome; sterility;
KW   myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
KW   allergy; arteriosclerosis; myocarditis; cardiomyopathy;
KW   glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.
XX
OS   Mus musculus.
OS   Homo sapiens.
XX
PN   WO200183560-A1.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014151.
XX
PR   02-MAY-2000; 2000US-0201344P.
XX
PA   (UABR-) UAB RES FOUND.
XX
PI   Zhou T,  Ichikawa K,  Kimberly RP,  Koopman WJ;
XX
DR   WPI; 2002-049338/06.
XX
PT   Novel antibody specific for tumor necrosis factor-related apoptosis-
PT   inducing ligand, useful for inhibiting cell proliferation in cancer.
XX
PS   Example 26; Page 219-220; 229pp; English.
XX
CC   The invention describes a novel antibody which recognizes a tumour
CC   necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC   DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
CC   activity to a cell expressing DR5 in vivo. It is also useful for
CC   preparing a therapeutic for selective apoptosis of abnormal or
CC   dysregulated cells, and for inhibiting cell proliferation in a cell,
CC   preferably a human breast, ovary, colon, haematopoietic, prostate,
CC   lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
CC   also be administered e.g. paclitaxel, taxol or cycloheximide. The
CC   antibody is used to treat an autoimmune disease, systemic lupus
CC   erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-
CC   host disease, Sjogren's syndrome, Chron's disease, pernicious anaemia,
CC   Addison disease, scleroderma, Goodpasture's syndrome, autoimmune
CC   haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,
CC   Basedow's disease, insulin-dependent diabetes mellitus, allergy, atopic
CC   disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC   nephritis, hypoplastic anaemia, rejection after organ transplantation,
CC   and numerous malignancies of lung, prostate, liver, ovary, lymphatic or
CC   breast tissue. Fusions of the TRA-8 light chain variable region with the
CC   human Ig constant region are shown in AAU72815-AAU72819 and AAU72810
XX
SQ   Sequence 213 AA;

  Query Match             91.4%;  Score 509;  DB 5;  Length 213;
  Best Local Similarity   89.6%;  Pred. No. 5.4e-36;
  Matches   95;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||:||||||:|||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
              ||||| |||||||||:||||||||||||||| ||:||||||||||
Db         61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYRTFGGGTKLEIK 106


RESULT 5
AAO29887
ID   AAO29887 standard; protein; 213 AA.
XX
AC   AAO29887;
XX
DT   23-OCT-2003  (revised)
DT   27-AUG-2003  (first entry)
XX
DE   LM6 fusion protein.
XX
KW   Tumour necrosis factor; TNF-related apoptosis-inducing ligand; allergy;
KW   inflammatory disease; TRAIL receptor; systemic lupus erythematosus; DR4;
KW   Hashimoto's disease; rheumatoid arthritis; inflammatory disease; cancer;
KW   multiple sclerosis; graft-versus-host disease; arteriosclerosis; asthma;
KW   Goodpasture's syndrome; autoimmune disease; glomerular nephritis; DR5;
KW   Crohn's disease; diabetes mellitus; antibody; mouse; fusion protein;
KW   human; LM6.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Chimeric.
XX
PN   WO2003037913-A2.
XX
PD   08-MAY-2003.
XX
PF   01-NOV-2002; 2002WO-US035333.
XX
PR   01-NOV-2001; 2001US-0346402P.
XX
PA   (UABR-) UAB RES FOUND.
XX
PI   Zhou T,  Kimberly RP,  Koopman WJ,  Lobuglio AF,  Buchsbaum DJ;
XX
DR   WPI; 2003-441350/41.
XX
PT   New purified antibody that specifically binds a TNF-related apoptosis-
PT   inducing ligand receptor DR4 or DR5, useful for treating cancer,
PT   inflammatory disease or autoimmune disease in a subject, e.g. asthma or
PT   rheumatoid arthritis.
XX
PS   Example 26; Page 244-245; 251pp; English.
XX
CC   The invention relates to an antibody that specifically binds a tumour
CC   necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC   DR4 or DR5. Antibodies of the invention are useful for selectively
CC   inducing apoptosis in target cells expressing DR4, for inhibiting
CC   proliferation of target cells expressing DR4 or for treating cancer,
CC   inflammatory disease or autoimmune disease in a subject e.g. systemic
CC   lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-
```

CC versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple
CC sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or
CC glomerular nephritis. The present sequence is LM6 fusion protein which
CC comprises humanised mouse anti-human DR5 antibody (TRA-8) light chain
CC variable region and human Ig light (kappa) chain constant region.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 213 AA;

Query Match 91.4%; Score 509; DB 6; Length 213;
Best Local Similarity 89.6%; Pred. No. 5.4e-36;
Matches 95; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
:| :||||| |||||||||||||||||||:||||||:|||||||||||| |||||||||
Db 1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy 61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
||||| |||||||||:|||||||||||||||| ||:||||||||||
Db 61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYRTFGGGTKLEIK 106

RESULT 6
ADJ79840
ID ADJ79840 standard; protein; 213 AA.
XX
AC ADJ79840;
XX
DT 06-MAY-2004 (first entry)
XX
DE LM6-type humanized TRA-8 light chain.
XX
KW nephrotropic; antiarteriosclerotic; cardiant; antiasthmatic;
KW antiallergic; antiinflammatory; antidiabetic; haemostatic;
KW neuroprotective; antiinfertility; immunosuppressive; dermatological;
KW antianaemic; antirheumatic; antiarthritic; thyromimetic; apoptosis;
KW proliferation;
KW tumor necrosis factor-related apoptosis-inducing ligand receptor; TNF;
KW TRAIL; synovial cell; lymphocyte; neutrophil;
KW systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis;
KW graft-versus-host disease; Sjogren's syndrome; pernicious anemia;
KW Addison disease; scleroderma; Goodpasture's syndrome; Crohn's disease;
KW autoimmune hemolytic anemia; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombotic; thrombocytopenia;
KW thrombopenia purpura; insulin dependent diabetes mellitus; allergy;
KW asthma; atopic disease; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anemia.
XX
OS Homo sapiens.
XX
PN WO2003038043-A2.
XX
PD 08-MAY-2003.
XX
PF 25-OCT-2002; 2002WO-US034420.
XX
PR 01-NOV-2001; 2001US-0346402P.
PR 24-JUN-2002; 2002US-0391478P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ, Oshumi J;
PI Lobuglio AF, Buchsbaum DJ;
XX
DR WPI; 2003-421518/39.
XX
PT Inducing apoptosis and inhibiting proliferation of target cells
PT expressing DR5, by contacting the target cell with an antibody that binds
PT TNF-related apoptosis-inducing ligand receptor DR5 and with therapeutic
PT agents.
XX
PS Example 26; SEQ ID NO 76; 274pp; English.
XX
CC The invention relates to a method of selectively inducing apoptosis in
CC and inhibiting (M1) proliferation of target cells expressing DR5,
CC comprising contacting the cell with an antibody that specifically binds
CC tumor necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL)
CC receptor DR5, where the antibody, in its soluble form, has in vivo and in
CC vitro apoptosis-inducing activity in the cell expressing DR5, and
CC contacting the cell with one or more therapeutic agents. M1 is useful for
CC inducing apoptosis in target cell and inhibiting proliferation of target
CC cell expressing DR5, where the target cell is an abnormally proliferating
CC synovial cells (e.g. rheumatoid arthritis synovial cell), activated
CC immune cell (e.g. activated lymphocyte), neutrophil, or virally infected
CC cell. M2 is useful for treating a subject having inflammatory and
CC autoimmune diseases. The inflammatory or autoimmune disease are selected
CC from systemic lupus erythematosus, Hashimoto's disease, rheumatoid
CC arthritis, graft-versus-host disease, Sjogren's syndrome, pernicious
CC anemia, Addison disease, scleroderma, Goodpasture's syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombotic, thrombocytopenia,
CC thrombopenia purpura, insulin dependent diabetes mellitus, allergy,
CC asthma, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerular nephritis, and hypoplastic anemia. This sequence represents a
CC protein used in the method of the invention.
XX
SQ Sequence 213 AA;

Query Match 91.4%; Score 509; DB 7; Length 213;
Best Local Similarity 89.6%; Pred. No. 5.4e-36;
Matches 95; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
:| :||||| |||||||||||||||||||:||||||:|||||||||||| |||||||||
Db 1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy 61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
||||| |||||||||:|||||||||||||||| ||:||||||||||
Db 61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYRTFGGGTKLEIK 106

RESULT 7
AAU72802
ID AAU72802 standard; protein; 234 AA.
XX
AC AAU72802;
XX
DT 26-FEB-2002 (first entry)
XX
DE TRA-8 light chain.
XX
KW Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;
KW TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;
KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;
KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;
KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.
XX
OS Mus musculus.
XX
PN WO200183560-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014151.
XX
PR 02-MAY-2000; 2000US-0201344P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;
XX
DR WPI; 2002-049338/06.
DR N-PSDB; AAS97063.

XX
PT Novel antibody specific for tumor necrosis factor-related apoptosis-
PT inducing ligand, useful for inhibiting cell proliferation in cancer.
XX
PS Claim 30; Page 200; 229pp; English.
XX
CC The invention describes a novel antibody which recognizes a tumour
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
CC activity to a cell expressing DR5 in vivo. It is also useful for
CC preparing a therapeutic for selective apoptosis of abnormal or
CC dysregulated cells, and for inhibiting cell proliferation in a cell,
CC preferably a human breast, ovary, colon, haematopoietic, prostate,
CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
CC also be administered e.g. paclitaxel, taxol or cycloheximide. The
CC antibody is used to treat an autoimmune disease, systemic lupus
CC erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-
CC host disease, Sjogren's syndrome, Chron's disease, pernicious anaemia,
CC Addison disease, scleroderma, Goodpasture's syndrome, autoimmune
CC haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,
CC Basedow's disease, insulin-dependent diabetes mellitus, allergy, atopic
CC disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, rejection after organ transplantation,
CC and numerous malignancies of lung, prostate, liver, ovary, lymphatic or
CC breast tissue. Peptides used to design primers for isolating heavy and
CC light chain cDNA of the mouse TRAIL (AAU72801 and AAU72802), TRA-8 are
CC shown in AAU72799 and AAU72800
XX
SQ Sequence 234 AA;

Query Match 91.4%; Score 509; DB 5; Length 234;
Best Local Similarity 89.6%; Pred. No. 5.9e-36;
Matches 95; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| ||||||||||||||||||||:||||||:|||||||||| |||||||||
Db         22 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 81

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
              ||||| |||||||||:||||||||||||||| ||:||||||||||
Db         82 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYRTFGGGTKLEIK 127
```

RESULT 8
AAO29870
ID AAO29870 standard; protein; 234 AA.
XX
AC AAO29870;
XX
DT 27-AUG-2003 (first entry)
XX
DE Mouse anti-human DR5 antibody (TRA-8) light chain.
XX
KW Tumour necrosis factor; TNF-related apoptosis-inducing ligand; allergy;
KW inflammatory disease; TRAIL receptor; systemic lupus erythematosus; DR4;
KW Hashimoto's disease; rheumatoid arthritis; inflammatory disease; cancer;
KW multiple sclerosis; graft-versus-host disease; arteriosclerosis; asthma;
KW Goodpasture's syndrome; autoimmune disease; glomerular nephritis; DR5;
KW Crohn's disease; diabetes mellitus; antibody; mouse.
XX
OS Mus sp.
XX
PN WO2003037913-A2.
XX
PD 08-MAY-2003.
XX
PF 01-NOV-2002; 2002WO-US035333.
XX
PR 01-NOV-2001; 2001US-0346402P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Zhou T, Kimberly RP, Koopman WJ, Lobuglio AF, Buchsbaum DJ;
XX
DR WPI; 2003-441350/41.
DR N-PSDB; AAL60478.
XX
PT New purified antibody that specifically binds a TNF-related apoptosis-
PT inducing ligand receptor DR4 or DR5, useful for treating cancer,
PT inflammatory disease or autoimmune disease in a subject, e.g. asthma or
PT rheumatoid arthritis.
XX
PS Example 16; Page 225-226; 251pp; English.
XX
CC The invention relates to an antibody that specifically binds a tumour
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR4 or DR5. Antibodies of the invention are useful for selectively
CC inducing apoptosis in target cells expressing DR4, for inhibiting
CC proliferation of target cells expressing DR4 or for treating cancer,
CC inflammatory disease or autoimmune disease in a subject e.g. systemic
CC lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-
CC versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple
CC sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or
CC glomerular nephritis. The present sequence is mouse anti-human DR5
CC antibody (TRA-8) light chain
XX
SQ Sequence 234 AA;

Query Match 91.4%; Score 509; DB 6; Length 234;
Best Local Similarity 89.6%; Pred. No. 5.9e-36;
Matches 95; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| ||||||||||||||||||||:||||||:|||||||||| |||||||||
Db         22 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 81

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
              ||||| |||||||||:||||||||||||||| ||:||||||||||
Db         82 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYRTFGGGTKLEIK 127
```

RESULT 9
ADJ79788
ID ADJ79788 standard; protein; 234 AA.
XX
AC ADJ79788;
XX
DT 06-MAY-2004 (first entry)
XX
DE TRA-8 antibody light chain.
XX
KW nephrotropic; antiarteriosclerotic; cardiant; antiasthmatic;
KW antiallergic; antiinflammatory; antidiabetic; haemostatic;
KW neuroprotective; antiinfertility; immunosuppressive; dermatological;
KW antianaemic; antirheumatic; antiarthritic; thyromimetic; apoptosis;
KW proliferation;
KW tumor necrosis factor-related apoptosis-inducing ligand receptor; TNF;
KW TRAIL; synovial cell; lymphocyte; neutrophil;
KW systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis;
KW graft-versus-host disease; Sjogren's syndrome; pernicious anemia;
KW Addison disease; scleroderma; Goodpasture's syndrome; Crohn's disease;
KW autoimmune hemolytic anemia; sterility; myasthenia gravis;
KW multiple sclerosis; Basedow's disease; thrombotic; thrombocytopenia;
KW thrombopenia purpura; insulin dependent diabetes mellitus; allergy;
KW asthma; atopic disease; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; hypoplastic anemia.
XX
OS Homo sapiens.
XX
PN WO2003038043-A2.
XX
PD 08-MAY-2003.
XX
PF 25-OCT-2002; 2002WO-US034420.
XX
PR 01-NOV-2001; 2001US-0346402P.

PR 24-JUN-2002; 2002US-0391478P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ, Oshumi J;
PI Lobuglio AF, Buchsbaum DJ;
XX
DR WPI; 2003-421518/39.
XX
PT Inducing apoptosis and inhibiting proliferation of target cells
PT expressing DR5, by contacting the target cell with an antibody that binds
PT TNF-related apoptosis-inducing ligand receptor DR5 and with therapeutic
PT agents.
XX
PS Example 16; SEQ ID NO 24; 274pp; English.
XX
CC The invention relates to a method of selectively inducing apoptosis in
CC and inhibiting (M1) proliferation of target cells expressing DR5,
CC comprising contacting the cell with an antibody that specifically binds
CC tumor necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL)
CC receptor DR5, where the antibody, in its soluble form, has in vivo and in
CC vitro apoptosis-inducing activity in the cell expressing DR5, and
CC contacting the cell with one or more therapeutic agents. M1 is useful for
CC inducing apoptosis in target cell and inhibiting proliferation of target
CC cell expressing DR5, where the target cell is an abnormally proliferating
CC synovial cells (e.g. rheumatoid arthritis synovial cell), activated
CC immune cell (e.g. activated lymphocyte), neutrophil, or virally infected
CC cell. M2 is useful for treating a subject having inflammatory and
CC autoimmune diseases. The inflammatory or autoimmune disease are selected
CC from systemic lupus erythematosus, Hashimoto's disease, rheumatoid
CC arthritis, graft-versus-host disease, Sjogren's syndrome, pernicious
CC anemia, Addison disease, scleroderma, Goodpasture's syndrome, Crohn's
CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC multiple sclerosis, Basedow's disease, thrombotic, thrombocytopenia,
CC thrombopenia purpura, insulin dependent diabetes mellitus, allergy,
CC asthma, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,
CC glomerular nephritis, and hypoplastic anemia. This sequence represents a
CC protein used in the method of the invention.
XX
SQ Sequence 234 AA;

Query Match 91.4%; Score 509; DB 7; Length 234;
Best Local Similarity 89.6%; Pred. No. 5.9e-36;
Matches 95; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
:| :||||| |||||||||||||||||||:||||||:|||||||||| |||||||||
Db 22 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 81

Qy 61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
||||| ||||||||:|||||||||||||||| ||:||||||||||
Db 82 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYRTFGGGTKLEIK 127

RESULT 10
ADZ45501
ID ADZ45501 standard; protein; 107 AA.
XX
AC ADZ45501;
XX
DT 30-JUN-2005 (first entry)
XX
DE Murine factor IX directed antibody fragment SEQ ID NO 205.
XX
KW bispecific antibody; blood coagulation factor VIII; bleeding;
KW fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;
KW factor VIII deficiency; von Willebrands disease; hemostatic;
KW immunostimulator; antibody engineering.
XX
OS Mus musculus.
XX
PN WO2005035756-A1.
XX
PD 21-APR-2005.
XX
PF 08-OCT-2004; 2004WO-JP014911.
XX
PR 10-OCT-2003; 2003WO-JP013062.
PR 14-OCT-2003; 2003WO-JP013123.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Hattori K, Kojima T, Miyazaki T, Soeda T;
XX
DR WPI; 2005-315563/32.
XX
PT Novel bispecific antibody substituting for function of cofactor that
PT enhances enzyme reaction, and recognizing both enzyme and substrates of
PT enzyme, useful for treating hemophilia A.
XX
PS Disclosure; SEQ ID NO 205; 69pp; Japanese.
XX
CC This invention describes a novel bispecific antibody which can act as a
CC cofactor to enhance an enzyme reaction and can recognize the enzyme and
CC the enzyme substrate. The antibody specifically binds to blood
CC coagulation factor VIII. The invention also describes a composition
CC comprising the antibody and a carrier, a kit useful in preventing and/or
CC treating bleeding associated with a disorder or from a disease caused by
CC bleeding. The composition includes blood coagulation factor VIII. The
CC antibody of the invention can be a blood-coagulation fibrinolysis related
CC factor including blood-coagulation factor VIII, blood coagulation factor
CC X, or blood-coagulation factor IX. The antibody comprises a complementary
CC determining region (CDR) of anti-blood-coagulation factor IX/IXa factor
CC antibody. The novel antibody or composition is useful for preventing
CC and/or treating a disease accompanying bleeding, or the disease resulting
CC from bleeding, where the disease accompanying bleeding or the disease
CC resulting from bleeding develops and/or progresses by an active reduction
CC or deletion of the blood coagulation factor VIII. The disease the
CC develops and/or progresses by an active reduction or deletion of the
CC blood coagulation factor VIII and/or activation blood coagulation factor
CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is
CC an acquired hemophilia A. This sequence represents a fragment of the
CC antibody described in the method of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 107 AA;

Query Match 87.3%; Score 486; DB 9; Length 107;
Best Local Similarity 85.8%; Pred. No. 2.7e-34;
Matches 91; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
:| :||||| |||||||||||||||||||:||||||:|||||||||| |||||||||
Db 1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy 61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
||||| ||||||||:|||||||||| ||||| | :||||||||:|
Db 61 RFTGSRYGTDFTLTISNVQSEDLADYLCQQYSNYITFGGGTKLELK 106

RESULT 11
ADU87728
ID ADU87728 standard; protein; 107 AA.
XX
AC ADU87728;
XX
DT 10-FEB-2005 (first entry)
XX
DE Light chain variable region of mouse Luc63.
XX
KW Antibody; CS1; SLAM family member 7; SLAMF7; immunoglobulin;
KW pharmaceutical; antibody-dependent cellular cytotoxicity;
KW FcgammaR receptor; cell proliferation; leukocyte; cancer;
KW multiple myeloma; multiple myeloma-related bone disorder; plasmacytoma;

KW macroglobulinemia; amyloidosis; chronic lymphocytic leukemia;
KW autoimmune disease; inflammatory bowel disease;
KW systemic lupus erythematosus; cytostatic; immunosuppressive;
KW antiinflammatory; gastrointestinal-gen.; dermatological; luc63;
KW light chain variable region.
XX
OS Mus sp.
XX
PN WO2004100898-A2.
XX
PD 25-NOV-2004.
XX
PF 10-MAY-2004; 2004WO-US014866.
XX
PR 08-MAY-2003; 2003US-0469211P.
PR 29-MAR-2004; 2004US-0557620P.
PR 29-MAR-2004; 2004US-0557621P.
PR 29-MAR-2004; 2004US-0557622P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Williams M, Tso YJ, Landolfi NF;
XX
DR WPI; 2004-821790/81.
XX
PT New anti-CS1 antibodies, useful for diagnosing, preventing or treating
PT cancer, myeloma, autoimmune disorder, inflammatory bowel disease, or
PT systemic lupus erythematosus.
XX
PS Claim 19; SEQ ID NO 42; 151pp; English.
XX
CC The invention relates to an antibody or its antigen-binding fragment,
CC which binds to CS1 (also known as SLAM family member 7, SLAMF7) and
CC inhibits immunoglobulin secretion, where the antibody binds to
CC substantially the same epitope as an antibody comprising an amino acid
CC sequence of any one of SEQ ID NOS: 3-26, the antibody comprises an amino
CC acid sequence of SEQ ID NOS: 27-44, and where the heavy chain variable
CC region comprises a complementarity determining region (CDR) of SEQ ID NO:
CC 33. Also disclosed are (i) a heavy chain CDR of an antibody comprising an
CC amino acid sequence of SEQ ID NOS: 9-11, 15-17, 21-23, 29-33, (ii) a
CC light chain CDR of an antibody comprising an amino acid sequence of SEQ
CC ID NOS: 12-14, 18-20, 24-26, 34-370, (iii) a pharmaceutical composition
CC comprising a pharmaceutical carrier and the antibody described above,
CC (iv) a method of inhibiting proliferation of CS1 expressing cells, (v)
CC inhibiting immunoglobulin secretion, and (vi) increasing antibody-
CC dependent cellular cytotoxicity (ADCC) activity of the antibody described
CC above, where the antibody has decreased levels of fucose or is mutated to
CC increase antibody affinity for a FcgammaR receptor. The antibody of the
CC invention inhibits the proliferation of leukocytes or cancer cells. The
CC antibody triggers cytotoxic effects on cells expressing CS1 or enhances
CC cytotoxicity mediated by immune cells, or triggers ADCC-mediated
CC cytotoxicity of cells expressing CS1. The antibody binds to substantially
CC the same epitope as the antibody produced by a hybridoma cell line having
CC ATCC accession number PTA-5091 or a Luc63 antibody. The antibody is
CC produced by a hybridoma cell line having ATCC accession number PTA-5091
CC or by a hybridoma cell line expressing Luc63 antibody. The antibody is a
CC monoclonal antibody, e.g. a chimeric antibody, a humanized antibody, or a
CC fully human antibody. The antibody is conjugated with a cytotoxic agent.
CC The antibody comprises a heavy chain variable region comprising amino
CC acid sequences of SEQ ID NOS: 3, 5, 7, or 27, and a light chain variable
CC region comprising amino acid sequences of SEQ ID NOS: 4, 6, 8, or 28. The
CC antibody, compositions, and methods are useful for diagnosing, preventing
CC or treating plasma cell cancer, e.g. myeloma, multiple myeloma, myeloma
CC of bone, extramedullary plasmacytoma, macroglobulinemia (including
CC Waldenstrom's macroglobulinemia), heavy-chain disease, primary
CC amyloidosis or monoclonal gammopathy of unknown significance, non-plasma
CC cell cancer (chronic lymphocytic leukemia), autoimmune disorder,
CC inflammatory bowel disease (IBD), or systemic lupus erythematosus (SLE).
CC This sequence represents the light chain variable region of mouse Luc63
CC (MuLuc63 VL).
XX
SQ Sequence 107 AA;

Query Match 87.2%; Score 485.5; DB 8; Length 107;
Best Local Similarity 86.9%; Pred. No. 2.9e-34;
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

Qy 1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
:| :||||| |||||||||||||||||| :||||||:|||||||||| |||||||||
Db 1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGIAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy 61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
||||| |||||||||:||||||||||||||| | :||||||||||
Db 61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 107

RESULT 12
ADU87734
ID ADU87734 standard; protein; 107 AA.
XX
AC ADU87734;
XX
DT 10-FEB-2005 (first entry)
XX
DE VL region of mouse Luc63.
XX
KW Antibody; CS1; SLAM family member 7; SLAMF7; immunoglobulin;
KW pharmaceutical; antibody-dependent cellular cytotoxicity;
KW FcgammaR receptor; cell proliferation; leukocyte; cancer;
KW multiple myeloma; multiple myeloma-related bone disorder; plasmacytoma;
KW macroglobulinemia; amyloidosis; chronic lymphocytic leukemia;
KW autoimmune disease; inflammatory bowel disease;
KW systemic lupus erythematosus; cytostatic; immunosuppressive;
KW antiinflammatory; gastrointestinal-gen.; dermatological; luc63;
KW light chain variable region.
XX
OS Mus sp.
XX
PN WO2004100898-A2.
XX
PD 25-NOV-2004.
XX
PF 10-MAY-2004; 2004WO-US014866.
XX
PR 08-MAY-2003; 2003US-0469211P.
PR 29-MAR-2004; 2004US-0557620P.
PR 29-MAR-2004; 2004US-0557621P.
PR 29-MAR-2004; 2004US-0557622P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Williams M, Tso YJ, Landolfi NF;
XX
DR WPI; 2004-821790/81.
XX
PT New anti-CS1 antibodies, useful for diagnosing, preventing or treating
PT cancer, myeloma, autoimmune disorder, inflammatory bowel disease, or
PT systemic lupus erythematosus.
XX
PS Example 5; SEQ ID NO 48; 151pp; English.
XX
CC The invention relates to an antibody or its antigen-binding fragment,
CC which binds to CS1 (also known as SLAM family member 7, SLAMF7) and
CC inhibits immunoglobulin secretion, where the antibody binds to
CC substantially the same epitope as an antibody comprising an amino acid
CC sequence of any one of SEQ ID NOS: 3-26, the antibody comprises an amino
CC acid sequence of SEQ ID NOS: 27-44, and where the heavy chain variable
CC region comprises a complementarity determining region (CDR) of SEQ ID NO:
CC 33. Also disclosed are (i) a heavy chain CDR of an antibody comprising an
CC amino acid sequence of SEQ ID NOS: 9-11, 15-17, 21-23, 29-33, (ii) a
CC light chain CDR of an antibody comprising an amino acid sequence of SEQ
CC ID NOS: 12-14, 18-20, 24-26, 34-370, (iii) a pharmaceutical composition
CC comprising a pharmaceutical carrier and the antibody described above,
CC (iv) a method of inhibiting proliferation of CS1 expressing cells, (v)
CC inhibiting immunoglobulin secretion, and (vi) increasing antibody-
CC dependent cellular cytotoxicity (ADCC) activity of the antibody described

CC above, where the antibody has decreased levels of fucose or is mutated to
CC increase antibody affinity for a FcgammaR receptor. The antibody of the
CC invention inhibits the proliferation of leukocytes or cancer cells. The
CC antibody triggers cytotoxic effects on cells expressing CS1 or enhances
CC cytotoxicity mediated by immune cells, or triggers ADCC-mediated
CC cytotoxicity of cells expressing CS1. The antibody binds to substantially
CC the same epitope as the antibody produced by a hybridoma cell line having
CC ATCC accession number PTA-5091 or a Luc63 antibody. The antibody is
CC produced by a hybridoma cell line having ATCC accession number PTA-5091
CC or by a hybridoma cell line expressing Luc63 antibody. The antibody is a
CC monoclonal antibody, e.g. a chimeric antibody, a humanized antibody, or a
CC fully human antibody. The antibody is conjugated with a cytotoxic agent.
CC The antibody comprises a heavy chain variable region comprising amino
CC acid sequences of SEQ ID NOS: 3, 5, 7, or 27, and a light chain variable
CC region comprising amino acid sequences of SEQ ID NOS: 4, 6, 8, or 28. The
CC antibody, compositions, and methods are useful for diagnosing, preventing
CC or treating plasma cell cancer, e.g. myeloma, multiple myeloma, myeloma
CC of bone, extramedullary plasmacytoma, macroglobulinemia (including
CC Waldenstrom's macroglobulinemia), heavy-chain disease, primary
CC amyloidosis or monoclonal gammopathy of unknown significance, non-plasma
CC cell cancer (chronic lymphocytic leukemia), autoimmune disorder,
CC inflammatory bowel disease (IBD), or systemic lupus erythematosus (SLE).
CC This sequence represents the light chain variable region of mouse Luc63
CC (MuLuc63 VL).
XX
SQ Sequence 107 AA;

Query Match 87.2%; Score 485.5; DB 8; Length 107;
Best Local Similarity 86.9%; Pred. No. 2.9e-34;
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

```
Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||| :||||||:|||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGIAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||:|||||||||||||||||  |  :||||||||||
Db         61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 107
```

RESULT 13
ADU87693
ID ADU87693 standard; protein; 107 AA.
XX
AC ADU87693;
XX
DT 10-FEB-2005 (first entry)
XX
DE Mouse Luc63 light chain variable region.
XX
KW Antibody; CS1; SLAM family member 7; SLAMF7; immunoglobulin;
KW pharmaceutical; antibody-dependent cellular cytotoxicity;
KW FcgammaR receptor; cell proliferation; leukocyte; cancer;
KW multiple myeloma; multiple myeloma-related bone disorder; plasmacytoma;
KW macroglobulinemia; amyloidosis; chronic lymphocytic leukemia;
KW autoimmune disease; inflammatory bowel disease;
KW systemic lupus erythematosus; cytostatic; immunosuppressive;
KW antiinflammatory; gastrointestinal-gen.; dermatological; luc63;
KW light chain variable region.
XX
OS Mus sp.
XX
PN WO2004100898-A2.
XX
PD 25-NOV-2004.
XX
PF 10-MAY-2004; 2004WO-US014866.
XX
PR 08-MAY-2003; 2003US-0469211P.
PR 29-MAR-2004; 2004US-0557620P.
PR 29-MAR-2004; 2004US-0557621P.
PR 29-MAR-2004; 2004US-0557622P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Williams M, Tso YJ, Landolfi NF;
XX
DR WPI; 2004-821790/81.
XX
PT New anti-CS1 antibodies, useful for diagnosing, preventing or treating
PT cancer, myeloma, autoimmune disorder, inflammatory bowel disease, or
PT systemic lupus erythematosus.
XX
PS Claim 12; SEQ ID NO 6; 151pp; English.
XX
CC The invention relates to an antibody or its antigen-binding fragment,
CC which binds to CS1 (also known as SLAM family member 7, SLAMF7) and
CC inhibits immunoglobulin secretion, where the antibody binds to
CC substantially the same epitope as an antibody comprising an amino acid
CC sequence of any one of SEQ ID NOS: 3-26, the antibody comprises an amino
CC acid sequence of SEQ ID NOS: 27-44, and where the heavy chain variable
CC region comprises a complementarity determining region (CDR) of SEQ ID NO:
CC 33. Also disclosed are (i) a heavy chain CDR of an antibody comprising an
CC amino acid sequence of SEQ ID NOS: 9-11, 15-17, 21-23, 29-33, (ii) a
CC light chain CDR of an antibody comprising an amino acid sequence of SEQ
CC ID NOS: 12-14, 18-20, 24-26, 34-370, (iii) a pharmaceutical composition
CC comprising a pharmaceutical carrier and the antibody described above,
CC (iv) a method of inhibiting proliferation of CS1 expressing cells, (v)
CC inhibiting immunoglobulin secretion, and (vi) increasing antibody-
CC dependent cellular cytotoxicity (ADCC) activity of the antibody described
CC above, where the antibody has decreased levels of fucose or is mutated to
CC increase antibody affinity for a FcgammaR receptor. The antibody of the
CC invention inhibits the proliferation of leukocytes or cancer cells. The
CC antibody triggers cytotoxic effects on cells expressing CS1 or enhances
CC cytotoxicity mediated by immune cells, or triggers ADCC-mediated
CC cytotoxicity of cells expressing CS1. The antibody binds to substantially
CC the same epitope as the antibody produced by a hybridoma cell line having
CC ATCC accession number PTA-5091 or a Luc63 antibody. The antibody is
CC produced by a hybridoma cell line having ATCC accession number PTA-5091
CC or by a hybridoma cell line expressing Luc63 antibody. The antibody is a
CC monoclonal antibody, e.g. a chimeric antibody, a humanized antibody, or a
CC fully human antibody. The antibody is conjugated with a cytotoxic agent.
CC The antibody comprises a heavy chain variable region comprising amino
CC acid sequences of SEQ ID NOS: 3, 5, 7, or 27, and a light chain variable
CC region comprising amino acid sequences of SEQ ID NOS: 4, 6, 8, or 28. The
CC antibody, compositions, and methods are useful for diagnosing, preventing
CC or treating plasma cell cancer, e.g. myeloma, multiple myeloma, myeloma
CC of bone, extramedullary plasmacytoma, macroglobulinemia (including
CC Waldenstrom's macroglobulinemia), heavy-chain disease, primary
CC amyloidosis or monoclonal gammopathy of unknown significance, non-plasma
CC cell cancer (chronic lymphocytic leukemia), autoimmune disorder,
CC inflammatory bowel disease (IBD), or systemic lupus erythematosus (SLE).
CC This sequence represents a CS1 antibody.
XX
SQ Sequence 107 AA;

Query Match 87.2%; Score 485.5; DB 8; Length 107;
Best Local Similarity 86.9%; Pred. No. 2.9e-34;
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

```
Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||| :||||||:|||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGIAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||:|||||||||||||||||  |  :||||||||||
Db         61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 107
```

RESULT 14
ADU87781
ID ADU87781 standard; protein; 127 AA.
XX
AC ADU87781;
XX
DT 10-FEB-2005 (first entry)

XX
DE Anti-CS1 mouse Luc63 light chain variable region.
XX
KW Antibody; CS1; SLAM family member 7; SLAMF7; immunoglobulin;
KW pharmaceutical; antibody-dependent cellular cytotoxicity;
KW FcgammaR receptor; cell proliferation; leukocyte; cancer;
KW multiple myeloma; multiple myeloma-related bone disorder; plasmacytoma;
KW macroglobulinemia; amyloidosis; chronic lymphocytic leukemia;
KW autoimmune disease; inflammatory bowel disease;
KW systemic lupus erythematosus; cytostatic; immunosuppressive;
KW antiinflammatory; gastrointestinal-gen.; dermatological; luc63;
KW light chain variable region.
XX
OS Mus sp.
XX
PN WO2004100898-A2.
XX
PD 25-NOV-2004.
XX
PF 10-MAY-2004; 2004WO-US014866.
XX
PR 08-MAY-2003; 2003US-0469211P.
PR 29-MAR-2004; 2004US-0557620P.
PR 29-MAR-2004; 2004US-0557621P.
PR 29-MAR-2004; 2004US-0557622P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Williams M, Tso YJ, Landolfi NF;
XX
DR WPI; 2004-821790/81.
XX
PT New anti-CS1 antibodies, useful for diagnosing, preventing or treating
PT cancer, myeloma, autoimmune disorder, inflammatory bowel disease, or
PT systemic lupus erythematosus.
XX
PS Claim 19; SEQ ID NO 28; 151pp; English.
XX
CC The invention relates to an antibody or its antigen-binding fragment,
CC which binds to CS1 (also known as SLAM family member 7, SLAMF7) and
CC inhibits immunoglobulin secretion, where the antibody binds to
CC substantially the same epitope as an antibody comprising an amino acid
CC sequence of any one of SEQ ID NOS: 3-26, the antibody comprises an amino
CC acid sequence of SEQ ID NOS: 27-44, and where the heavy chain variable
CC region comprises a complementarity determining region (CDR) of SEQ ID NO:
CC 33. Also disclosed are (i) a heavy chain CDR of an antibody comprising an
CC amino acid sequence of SEQ ID NOS: 9-11, 15-17, 21-23, 29-33, (ii) a
CC light chain CDR of an antibody comprising an amino acid sequence of SEQ
CC ID NOS: 12-14, 18-20, 24-26, 34-370, (iii) a pharmaceutical composition
CC comprising a pharmaceutical carrier and the antibody described above,
CC (iv) a method of inhibiting proliferation of CS1 expressing cells, (v)
CC inhibiting immunoglobulin secretion, and (vi) increasing antibody-
CC dependent cellular cytotoxicity (ADCC) activity of the antibody described
CC above, where the antibody has decreased levels of fucose or is mutated to
CC increase antibody affinity for a FcgammaR receptor. The antibody of the
CC invention inhibits the proliferation of leukocytes or cancer cells. The
CC antibody triggers cytotoxic effects on cells expressing CS1 or enhances
CC cytotoxicity mediated by immune cells, or triggers ADCC-mediated
CC cytotoxicity of cells expressing CS1. The antibody binds to substantially
CC the same epitope as the antibody produced by a hybridoma cell line having
CC ATCC accession number PTA-5091 or a Luc63 antibody. The antibody is
CC produced by a hybridoma cell line having ATCC accession number PTA-5091
CC or by a hybridoma cell line expressing Luc63 antibody. The antibody is a
CC monoclonal antibody, e.g. a chimeric antibody, a humanized antibody, or a
CC fully human antibody. The antibody is conjugated with a cytotoxic agent.
CC The antibody comprises a heavy chain variable region comprising amino
CC acid sequences of SEQ ID NOS: 3, 5, 7, or 27, and a light chain variable
CC region comprising amino acid sequences of SEQ ID NOS: 4, 6, 8, or 28. The
CC antibody, compositions, and methods are useful for diagnosing, preventing
CC or treating plasma cell cancer, e.g. myeloma, multiple myeloma, myeloma
CC of bone, extramedullary plasmacytoma, macroglobulinemia (including
CC Waldenstrom's macroglobulinemia), heavy-chain disease, primary
CC amyloidosis or monoclonal gammopathy of unknown significance, non-plasma
CC cell cancer (chronic lymphocytic leukemia), autoimmune disorder,
CC inflammatory bowel disease (IBD), or systemic lupus erythematosus (SLE).
CC This sequence represents an anti-CS1 antibody. Note: The present sequence
CC is referred to as SEQ ID No:28 on page 11 but is given as SEQ ID No:29 on
CC page 101 of the specification.
XX
SQ Sequence 127 AA;

Query Match 87.2%; Score 485.5; DB 8; Length 127;
Best Local Similarity 86.9%; Pred. No. 3.5e-34;
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

Qy 1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
:| :||||| |||||||||||||||||| :||||||:|||||||||| |||||||||
Db 21 DIVMTQSHKFMSTSVGDRVSITCKASQDVGIAVAWYQQKPGQSPKLLIYWASTRHTGVPD 80

Qy 61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
||||| |||||||||:|||||||||||||||| | :||||||||||
Db 81 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 127

RESULT 15
ABB07359
ID ABB07359 standard; protein; 115 AA.
XX
AC ABB07359;
XX
DT 09-APR-2002 (first entry)
XX
DE 22A5 IgM light chain variable region.
XX
KW Immunoglobulin; Ig; reperfusion; ischaemic injury; pathogenic;
KW vasotropic; antibody; 22A5; IgM.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Misc-difference 109
FT /note= "encoded by TGA"
XX
PN WO200193892-A1.
XX
PD 13-DEC-2001.
XX
PF 08-JUN-2001; 2001WO-US018510.
XX
PR 08-JUN-2000; 2000US-0210272P.
XX
PA (BLOO-) CENT BLOOD RES INC.
XX
PI Carroll MC, Moore FD, Hechtman HB;
XX
DR WPI; 2002-139643/18.
DR N-PSDB; ABA94516.
XX
PT Treating or preventing immunoglobulin-mediated reperfusion or ischemic
PT injury resulting from e.g. angioplasty or bypass surgery, by
PT administering an inhibitor of pathogenic immunoglobulin and ischemic
PT antigen interaction.
XX
PS Claim 50; Page 73-74; 77pp; English.
XX
CC The invention provides a method of treating or preventing immunoglobulin-
CC mediated reperfusion or ischemic injury in a subject. The method involves
CC administering an inhibitor of an interaction between a pathogenic
CC immunoglobulin, and an ischemic-specific antigen or a component of the
CC complement pathway. The method is useful for treating or preventing
CC immunoglobulin-mediated reperfusion or ischemic injury, in particular,
CC injury that results following a naturally occurring episode, a surgical
CC procedure (e.g. angioplasty, stenting procedure, atherectomy or bypass
CC surgery), or in an injury that occurs in a cardiovascular tissue. The
CC method is also useful for treating or preventing, in a subject, tissue
CC damage following reperfusion caused by a pathogenic immunoglobulin, e.g.

CC pathogenic IgMs. The present sequence represents the light chain variable
CC region of 22A5 IgM, a pathogenic immunoglobulin
XX
SQ Sequence 115 AA;

Query Match 86.8%; Score 483.5; DB 5; Length 115;
Best Local Similarity 87.7%; Pred. No. 4.7e-34;
Matches 93; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

```
Qy          2 IQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPDR 61
              | :||||| |||||||||||||||||||:||||||:|||||||||||| ||||||||||
Db          1 IVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPDR 60

Qy         62 FTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              |||| |||||||||:|||||||||||||||| |  :|| |||||||
Db         61 FTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPLTFGSGTKLEIK 106
```

Search completed: March 23, 2006, 00:51:37
Job time : 317.891 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 00:52:05 ; Search time 39.4419 Seconds
(without alignments)
258.583 Million cell updates/sec

Title: US-10-755-382-4
Perfect score: 557
Sequence: 1 EIQLTQSHKMMSTSVGDRVS.....FCQQYSLYRSFGGGTKLEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	491.5	88.2	117	2	S42466	Ig kappa chain V r
2	453.5	81.4	131	2	PL0207	anti-idiotypic ant
3	432.5	77.6	152	2	S30751	Ig kappa chain pre
4	428.5	76.9	107	2	A28195	Ig kappa chain V r
5	425.5	76.4	107	2	S32192	Ig kappa chain V r
6	425.5	76.4	149	1	KVMS11	Ig kappa chain pre
7	423.5	76.0	107	2	S32191	Ig kappa chain V r
8	422.5	75.9	108	2	PL0204	anti-DNA autoantib
9	419.5	75.3	119	2	PQ0265	Ig kappa chain V r
10	416.5	74.8	107	2	B28195	Ig kappa chain V r
11	414.5	74.4	100	2	H38601	Ig kappa chain V r
12	414.5	74.4	128	2	A47159	Ig lambda chain V
13	411	73.8	108	2	B44371	Ig kappa chain V r
14	390	70.0	90	2	S38561	Ig light chain V r
15	388	69.7	108	2	PL0083	Ig kappa chain V r
16	387.5	69.6	127	2	S04577	Ig kappa chain pre
17	387	69.5	94	2	F33730	Ig kappa chain V r
18	383	68.8	98	2	PH1072	Ig light chain V r
19	382.5	68.7	107	2	S09967	Ig kappa chain V-J
20	381	68.4	225	2	S37484	Ig kappa chain - m
21	380	68.2	93	2	S38559	Ig light chain V r
22	372	66.8	98	2	PH1073	Ig light chain V r
23	371.5	66.7	136	1	KVMS21	Ig kappa chain pre
24	369.5	66.3	107	2	S38713	Ig light chain V r
25	369	66.2	106	2	PL0088	Ig kappa chain V r
26	367.5	66.0	111	2	D37266	Ig kappa chain V r
27	361.5	64.9	107	2	S36268	Ig lambda chain V
28	360.5	64.7	107	2	S33132	Ig kappa chain V r
29	360.5	64.7	113	2	JC2270	PL7-6 antibody lig
30	360	64.6	138	2	S26040	Ig kappa chain pre
31	359	64.5	133	2	PS0023	Ig kappa chain pre
32	358	64.3	112	2	S41393	Ig kappa chain V r
33	357.5	64.2	214	2	S68212	Ig kappa chain (Ma
34	357	64.1	112	2	S43103	Ig kappa chain V-J
35	356.5	64.0	125	2	S40349	Ig kappa chain V-J
36	356	63.9	113	2	PT0407	Ig light chain V r
37	355.5	63.8	129	2	S40317	Ig kappa chain - h
38	355	63.7	133	1	K4HUJI	Ig kappa chain pre
39	354.5	63.6	90	2	I38601	Ig kappa chain V r
40	353.5	63.5	107	2	D53285	Ig kappa chain V a
41	353.5	63.5	107	2	S09964	Ig kappa chain V-J
42	353.5	63.5	132	2	S40334	Ig kappa chain - h
43	353	63.4	112	2	S09970	Ig kappa chain V-J
44	351.5	63.1	134	2	PC1214	Ig kappa chain pre
45	351	63.0	118	2	PT0356	Ig kappa chain V r

ALIGNMENTS

RESULT 1
S42466
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42466
R;Shiyanov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
submitted to the EMBL Data Library, March 1994
A;Reference number: S42466
A;Accession: S42466
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <SHI>
A;Cross-references: UNIPARC:UPI00001161DC; EMBL:X78108; NID:g460824; PIDN:CAA54998.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;26-100/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 491.5; DB 2; Length 117;
Best Local Similarity 87.9%; Pred. No. 2.1e-38;
Matches 94; Conservative 6; Mismatches 6; Indels 1; Gaps 1;

```
Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||:||||||:|||||||||||| |||||||||
Db         11 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 70

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
                ||||| |||||||||:|||||||||||||||| |  :||||||||||
Db         71 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 117
```

RESULT 2
PL0207
anti-idiotypic antibody E225, kappa chain V region precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: PL0207
R;Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.
Mol. Immunol. 27, 429-433, 1990
A;Title: Nucleotide sequence of the VH, VL regions of an anti-idiotopic antibody reacting
A;Reference number: PL0207; MUID:90309764; PMID:1973259
A;Accession: PL0207
A;Molecule type: mRNA
A;Residues: 1-131 <SOU>
A;Cross-references: UNIPARC:UPI000017678F
A;Note: This sequence corresponds to subgroup V mouse immunoglobulin light chain
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-20/Domain: signal sequence #status predicted <SIG>
F;36-110/Domain: immunoglobulin homology <IMM>
F;44-54/Region: complementarity-determining 1
F;70-76/Region: complementarity-determining 2
F;109-117/Region: complementarity-determining 3

```
F;116-127/Region: J region

  Query Match             81.4%;  Score 453.5;  DB 2;  Length 131;
  Best Local Similarity   82.2%;  Pred. No. 7.3e-35;
  Matches   88;  Conservative    6;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||  :||||||:||||||||||| |||||||||
Db         21 DIVMTQSHKFMSTSVGDRVSITCKASQDVRIAVAWYQQKPGQSPKLLIYWASTRHTGVPD 80

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYR-SFGGGTKLEIK 106
              ||||| |||||||||:||||||||||||     | :|| |||||||
Db         81 RFTGSGSGTDFTLTISNVQSEDLADYFCQHCGSYPFTFGSGTKLEIK 127


RESULT 3
S30751
Ig kappa chain precursor V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
C;Accession: S30751
R;Grant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.
Nucleic Acids Res. 15, 5496, 1987
A;Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.
A;Reference number: S30751; MUID:87260030; PMID:3601683
A;Accession: S30751
A;Molecule type: mRNA
A;Residues: 1-152 <GRA>
A;Cross-references: UNIPARC:UPI0000115D91; EMBL:X05877; NID:g52195; PIDN:CAA29301.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;45-119/Domain: immunoglobulin homology <IMM>
F;138-152/Domain: C region (C-kappa) (fragment) #status predicted <CRE>

  Query Match             77.6%;  Score 432.5;  DB 2;  Length 152;
  Best Local Similarity   76.6%;  Pred. No. 7.3e-33;
  Matches   82;  Conservative   14;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||: |||||||||||||||||| |:|:||||:|||||||||:| |||||||||
Db         30 DIVMTQSHRFMSTSVGDRVSITCKASQDVTTAVSWYQQKPGQSPKLLIFWASTRHTGVPD 89

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQ-YSLYRSFGGGTKLEIK 106
              ||||| ||||:||||::||:|||| |:||| ||   :|| |||||:|
Db         90 RFTGSGSGTDYTLTISSVQAEDLALYYCQQHYSTPLTFGAGTKLELK 136


RESULT 4
A28195
Ig kappa chain V region (anti-haloperidol antibody A) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jan-2000
C;Accession: A28195
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid s
A;Reference number: A28195; MUID:88153717; PMID:3267217
A;Accession: A28195
A;Molecule type: mRNA
A;Residues: 1-107 <SHE>
A;Cross-references: UNIPARC:UPI0000114D69; GB:M19766; NID:g197039; PIDN:AAA38891.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             76.9%;  Score 428.5;  DB 2;  Length 107;
  Best Local Similarity   77.6%;  Pred. No. 1.2e-32;
  Matches   83;  Conservative   12;  Mismatches   11;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||| | ||||||||||:||||||:|| :|||:||:|||||| |||  | |::||||
Db          1 DILMTQSQKFMSTSVGDRVSVTCKASQNVGNNVAWHQQKPGQSPKALIYSASYRYSGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||||||||||||||: |  :||||||||||
Db         61 RFTGSGSGTDFTLTITNVQSEDLAEYFCQQYNSYPYTFGGGTKLEIK 107


RESULT 5
S32192
Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S32192
R;Izui, S.
submitted to the EMBL Data Library, February 1993
A;Reference number: S32185
A;Accession: S32192
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <IZU>
A;Cross-references: UNIPARC:UPI0000116106; EMBL:X70097; NID:g288262; PIDN:CAA49701.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             76.4%;  Score 425.5;  DB 2;  Length 107;
  Best Local Similarity   78.5%;  Pred. No. 2.2e-32;
  Matches   84;  Conservative   10;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||| |:||||||:||||||||||  | |:|||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPGQSPKLLIYSASYRYTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQ-YSLYRSFGGGTKLEIK 106
              ||||| |||||| ||::||:|||| |:||| ||   :||||||||||
Db         61 RFTGSGSGTDFTFTISSVQAEDLAVYYCQQHYSTPYTFGGGTKLEIK 107


RESULT 6
KVMS11
Ig kappa chain precursor V region (MPC11) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
C;Accession: A90823; A90753; A90298; A01916
R;Kelley, D.E.; Coleclough, C.; Perry, R.P.
Cell 29, 681-689, 1982
A;Title: Functional significance and evolutionary development of the 5'-terminal regions
A;Reference number: A90823; MUID:83001944; PMID:6288267
A;Accession: A90823
A;Molecule type: DNA
A;Residues: 1-71 <KEL>
A;Cross-references: UNIPROT:P01633; UNIPARC:UPI0000173712
A;Note: the sequence was determined from the differentiated gene
R;Rabbitts, T.H.; Hamlyn, P.H.; Matthyssens, G.; Roe, B.A.
Can. J. Biochem. 58, 176-187, 1980
A;Title: The variability, arrangement, and rearrangement of immunoglobulin genes.
A;Reference number: A90753; MUID:80176554; PMID:6245773
A;Accession: A90753
A;Molecule type: mRNA
A;Residues: 41-149 <RAB>
A;Cross-references: UNIPARC:UPI0000173713
R;Smith, G.P.
Biochem. J. 171, 337-347, 1978
A;Title: Sequence of the full-length immunoglobulin kappa-chain of mouse myeloma MPC 11.
A;Reference number: A90298; MUID:78186617; PMID:418775
A;Contents: myeloma protein MPC11
A;Accession: A90298
A;Molecule type: protein
A;Residues: 30-149 <SMI>
A;Cross-references: UNIPARC:UPI0000173714
A;Note: the amidation states of residues 58, 69, 101, 111, 120, 122, and 123 were not det
C;Comment: The mature chain has 12 additional residues at its amino end, due to a tandem
 42 corresponds to the amino-terminal residue of typical kappa chains.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
```

```
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: duplication; heterotetramer; immunoglobulin
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-149/Product: Ig kappa chain V region (MPC11) #status experimental <MAT>
F;57-131/Domain: immunoglobulin homology <IMM>
F;64-129/Disulfide bonds: #status predicted

  Query Match             76.4%;  Score 425.5;  DB 1;  Length 149;
  Best Local Similarity   78.5%;  Pred. No. 3.1e-32;
  Matches   84;  Conservative   10;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||| |:||||||:||||||||||  | |:|||||
Db         42 DIVMTQSHKFMSTSVGDRVSITCKASQDVSTTVAWYQQKPGQSPKLLIYSASYRYTGVPD 101

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQ-YSLYRSFGGGTKLEIK 106
              ||||| |||||| ||::||:|||| |:||| ||   :||||||||||
Db        102 RFTGSGSGTDFTFTISSVQAEDLAVYYCQQHYSTPPTFGGGTKLEIK 148


RESULT 7
S32191
Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S32191
R;Izui, S.
submitted to the EMBL Data Library, February 1993
A;Reference number: S32185
A;Accession: S32191
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <IZU>
A;Cross-references: UNIPARC:UPI0000116105; EMBL:X70095; NID:g288260; PIDN:CAA49700.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             76.0%;  Score 423.5;  DB 2;  Length 107;
  Best Local Similarity   78.5%;  Pred. No. 3.4e-32;
  Matches   84;  Conservative    9;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||| |:||||||:||||||||||  | |:|||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPGQSPKLLIYSASYRYTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQ-YSLYRSFGGGTKLEIK 106
              ||||| |||||| ||::|| |||| |:||| ||   :||||||||||
Db         61 RFTGSGSGTDFTFTISSVQPEDLAVYYCQQHYSTPYTFGGGTKLEIK 107


RESULT 8
PL0204
anti-DNA autoantibody BV17-45, kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: PL0204
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N
A;Reference number: PL0198; MUID:90309768; PMID:2114528
A;Accession: PL0204
A;Molecule type: mRNA
A;Residues: 1-108 <SMI>
A;Cross-references: UNIPARC:UPI0000113787; GB:X53644; NID:g50198; PIDN:CAA37695.1; PID:g
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;50-56/Region: complementarity-determining 2
F;89-97/Region: complementarity-determining 3
F;96-108/Region: JH region

  Query Match             75.9%;  Score 422.5;  DB 2;  Length 108;
  Best Local Similarity   76.6%;  Pred. No. 4.3e-32;
  Matches   82;  Conservative   12;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||| | |||||||||:||||||:| | ||||||:|||||| |||  |:|:|||||
Db          1 DIVMTQSQKFMSTSVGDRVSVTCKASQNVNTYVAWYQQKPGQSPKALIYSASSRYTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| ||||||| |::|||||||:||||||: |  :||||||||||
Db         61 RFTGSGSGTDFTLAISSVQSEDLAEYFCQQYNSYPYTFGGGTKLEIK 107


RESULT 9
PQ0265
Ig kappa chain V region (MC1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PQ0265
R;Lohman, K.L.; Carrillo, M.A.; Kennedy, R.C.
Gene 105, 283-284, 1991
A;Title: Sequence analysis of the variable region of a mouse gene encoding a monoclonal a
A;Reference number: PQ0265; MUID:92039046; PMID:1937027
A;Accession: PQ0265
A;Molecule type: mRNA
A;Residues: 1-119 <LOH>
A;Cross-references: UNIPARC:UPI000017678E; GB:M59985
C;Comment: This protein recognizes a restricted idiotype associated with antibodies speci
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;28-102/Domain: immunoglobulin homology <IMM>
F;36-46/Region: complementarity-determining 1
F;62-68/Region: complementarity-determining 2
F;101-109/Region: complementarity-determining 3

  Query Match             75.3%;  Score 419.5;  DB 2;  Length 119;
  Best Local Similarity   77.6%;  Pred. No. 8.9e-32;
  Matches   83;  Conservative   10;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||| |:||||||:||||||||||  | |:|||||
Db         13 DIVMTQSHKFMSTSVGDRVSITCKASQDVSTTVAWYQQKPGQSPKLLIYSASYRYTGVPD 72

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQ-YSLYRSFGGGTKLEIK 106
              ||||| |||| | ||::||:|||| |:||| ||   :||||||||||
Db         73 RFTGSGSGTDLTFTISSVQAEDLAVYYCQQHYSTPPTFGGGTKLEIK 119


RESULT 10
B28195
Ig kappa chain V region (anti-haloperidol antibody B) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jan-2000
C;Accession: B28195
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid se
A;Reference number: A28195; MUID:88153717; PMID:3267217
A;Accession: B28195
A;Molecule type: mRNA
A;Residues: 1-107 <SHE>
A;Cross-references: UNIPARC:UPI0000114D6A; EMBL:M19767; NID:g197041; PIDN:AAA38892.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             74.8%;  Score 416.5;  DB 2;  Length 107;
  Best Local Similarity   75.7%;  Pred. No. 1.5e-31;
  Matches   81;  Conservative   11;  Mismatches   14;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||| | ||||||||||:||||||:| :|||:||:|||||| |||  | |::||||
Db          1 DILMTQSQKFMSTSVGDRVSVTCKASQNVGNNVAWHQQKPGQSPKALIYSASYRYSGVPD 60
```

```
Qy          61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
               ||||| |||||||||||||||| |:||||||: |   ||||| ||||
Db          61 RFTGSGSGTDFTLTITNVQSEDXAEYFCQQYNSYPYXFGGGTXLEIK 107


RESULT 11
H38601
Ig kappa chain V region (3A3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C;Accession: H38601
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same antigen
A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: H38601
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-100 <GOS>
A;Cross-references: UNIPARC:UPI000011517C; GB:M57985; NID:g196416; PIDN:AAA63366.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;8-82/Domain: immunoglobulin homology <IMM>

  Query Match             74.4%;  Score 414.5;  DB 2;  Length 100;
  Best Local Similarity   81.8%;  Pred. No. 2.1e-31;
  Matches   81;  Conservative    8;  Mismatches    9;  Indels    1;  Gaps    1;

Qy           9 KMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPDRFTGSVSG 68
               | |||:||||||||||||| | |:||||||:||||||||||  |:|:|||||||||| ||
Db           1 KFMSTTVGDRVSITCKASQTVDTAVAWYQQKPGQSPKLLIYSASSRYTGVPDRFTGSGSG 60

Qy          69 TDFTLTITNVQSEDLADYFCQQYSLYR-SFGGGTKLEIK 106
               ||||||| ::|||||||||||||| |  :|||||||||
Db          61 TDFTLTINSMQSEDLADYFCQQYSTYPCTFGGGTKLEIK 99


RESULT 12
A47159
Ig lambda chain V region (CEA-specific maId T84.66) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: A47159
R;Gaida, F.J.; Pieper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumaier, M.
J. Biol. Chem. 268, 14138-14145, 1993
A;Title: Molecular characterization of a cloned idiotypic cascade containing a network a
A;Reference number: A47159; MUID:93300804; PMID:7686150
A;Accession: A47159
A;Status: preliminary
A;Molecule type: DNA; protein
A;Residues: 1-128 <GAI>
A;Cross-references: UNIPARC:UPI00001767A5
A;Experimental source: hybridoma 6G6.C4
A;Note: sequence extracted from NCBI backbone (NCBIN:134419, NCBIP:134420)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

  Query Match             74.4%;  Score 414.5;  DB 2;  Length 128;
  Best Local Similarity   75.7%;  Pred. No. 2.8e-31;
  Matches   81;  Conservative   10;  Mismatches   15;  Indels    1;  Gaps    1;

Qy           1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
               :| : || | ||||||||||:|||||:|| :||||||:|||||| |||  | |::||||
Db          21 DIVMIQSQKFMSTSVGDRVSVTCKASQNVGNNVAWYQQKPGQSPKALIYSASYRYSGVPD 80

Qy          61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYR-SFGGGTKLEIK 106
               ||||| |||||||||:|||||||| ||| ||  |  :||||||||||
Db          81 RFTGSRSGTDFTLTISNVQSEDLAQYFCHQYDNYPWTFGGGTKLEIK 127


RESULT 13
B44371
```

```
Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Apr-1993 #sequence_revision 30-Apr-1993 #text_change 21-Jan-2000
C;Accession: B44371
R;Ayala, M.; Duenas, M.; Santos, A.; Vazquez, J.; Menendez, A.; Silva, A.; Gavilondo, J.V
BioTechniques 13, 790-799, 1992
A;Title: Bacterial single-chain antibody fragments, specific for carcinoembryonic antiger
A;Reference number: A44371; MUID:93040204; PMID:1418981
A;Accession: B44371
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <AYA>
A;Cross-references: UNIPARC:UPI0000176EB2; GB:S49457; NID:g259513; PIDN:AAB24087.1; PID:g
A;Note: This sequence is inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIP:119637)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             73.8%;  Score 411;  DB 2;  Length 108;
  Best Local Similarity   72.2%;  Pred. No. 4.8e-31;
  Matches   78;  Conservative   16;  Mismatches   12;  Indels    2;  Gaps    1;

Qy           1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
               :||:||| |  |||||||||:||||||: | :||||||:|||||| |||  |:|::||||
Db           1 DIQMTQSPKFSSTSVGDRVSVTCKASQNAGINVAWYQQKPGQSPKALIYSASSRNSGVPD 60

Qy          61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYR--SFGGGTKLEIK 106
               ||||| |||||||||:||||:|||:|||||||: |   :|| ||||::|
Db          61 RFTGSGSGTDFTLTISNVQSQDLAEYFCQQYNSYPLVTFGAGTKLQLK 108


RESULT 14
S38561
Ig light chain V region (ASWP1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38561
R;Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
submitted to the EMBL Data Library, September 1993
A;Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s Mu
A;Reference number: S38559
A;Accession: S38561
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-90 <MON>
A;Cross-references: UNIPARC:UPI00001161C8; EMBL:X75103; NID:g414155; PIDN:CAA52994.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             70.0%;  Score 390;  DB 2;  Length 90;
  Best Local Similarity   82.2%;  Pred. No. 3.4e-29;
  Matches   74;  Conservative    8;  Mismatches    8;  Indels    0;  Gaps    0;

Qy           1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
               :| :||| | ||||||||||||||||:|||:||||||:||||||||||  | |:|||||
Db           1 DIVMTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPD 60

Qy          61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQ 90
               ||||| |||||||||:|:| ||||||||||
Db          61 RFTGSGSGTDFTLTISNMQXEDLADYFCQQ 90


RESULT 15
PL0083
Ig kappa chain V region (E3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C;Accession: PL0083
R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Cap
J. Exp. Med. 169, 519-533, 1989
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are
A;Reference number: PL0080; MUID:89094248; PMID:2492056
```

A;Accession: PL0083
A;Molecule type: mRNA
A;Residues: 1-108 <MEE>
A;Cross-references: UNIPARC:UPI0000176CC1
A;Experimental source: strain BALB/c
A;Note: the sequence shown here is from the V kappa region of an antiidiotypic monoclona
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 69.7%; Score 388; DB 2; Length 108;
Best Local Similarity 73.1%; Pred. No. 6.3e-29;
Matches 79; Conservative 12; Mismatches 15; Indels 2; Gaps 2;

```
Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||: |||||||||||||||||| | |:|||||||:|||||||||  | |:|||||
Db          1 DIVMTQSHRFMSTSVGDRVSITCKASQAVSTAVAWYQQKPGQSPKLLIYSASYRYTGVPD 60

Qy         61 RFTGSVSGT-DFTLTITNVQSEDLADYFCQQ-YSLYRSFGGGTKLEIK 106
              ||||| ||| ||| ||::||:|| | |:||| |:   :|||||| ||
Db         61 RFTGSGSGTVDFTFTISSVQAEDQAVYYCQQHYTTPPTFGGGTKLGIK 108
```

Search completed: March 23, 2006, 00:57:30
Job time : 40.4419 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 00:45:29 ; Search time 242.403 Seconds
(without alignments)
308.519 Million cell updates/sec

Title: US-10-755-382-4
Perfect score: 557
Sequence: 1 EIQLTQSHKMMSTSVGDRVS.....FCQQYSLYRSFGGGTKLEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	468.5	84.1	238	2	Q58EU4_MOUSE	Q58eu4 mus musculu
2	425.5	76.4	149	1	KV5A_MOUSE	P01633 mus musculu
3	414.5	74.4	108	2	Q8VIJ0_MOUSE	Q8vij0 mus musculu
4	373.5	67.1	99	2	Q9JL74_MOUSE	Q9jl74 mus musculu
5	371.5	66.7	136	1	KV5B_MOUSE	P01634 mus musculu
6	355	63.7	133	1	KV4B_HUMAN	P06313 homo sapien
7	353.5	63.5	236	2	Q6GMX9_HUMAN	Q6gmx9 homo sapien
8	352.5	63.3	108	1	KV1Y_HUMAN	P80362 homo sapien
9	352.5	63.3	108	1	KV5M_MOUSE	P01646 mus musculu
10	348	62.5	243	2	Q7TQM2_MOUSE	Q7tqm2 mus musculu
11	345.5	62.0	108	1	KV5J_MOUSE	P01643 mus musculu
12	345.5	62.0	108	1	KV5K_MOUSE	P01644 mus musculu
13	344.5	61.8	108	2	Q9UL70_HUMAN	Q9ul70 homo sapien
14	344.5	61.8	114	1	KV4A_HUMAN	P01625 homo sapien
15	344	61.8	107	1	KV1D_HUMAN	P01596 homo sapien
16	343.5	61.7	108	1	KV1M_HUMAN	P01605 homo sapien
17	342.5	61.5	108	1	KV5N_MOUSE	P01647 mus musculu
18	342.5	61.5	234	2	Q7Z473_HUMAN	Q7z473 homo sapien
19	342	61.4	107	2	Q96SA9_HUMAN	Q96sa9 homo sapien
20	341.5	61.3	108	1	KV5L_MOUSE	P01645 mus musculu
21	340.5	61.1	236	2	Q6PIH7_HUMAN	Q6pih7 homo sapien
22	339.5	61.0	108	1	KV5P_MOUSE	P01649 mus musculu
23	338.5	60.8	134	1	KV4C_HUMAN	P06314 homo sapien
24	338.5	60.8	236	2	Q6PIT5_HUMAN	Q6pit5 homo sapien
25	338.5	60.8	244	2	Q65ZC8_HUMAN	Q65zc8 homo sapien
26	337	60.5	235	2	Q6GMW0_HUMAN	Q6gmw0 homo sapien
27	335.5	60.2	108	1	KV1L_HUMAN	P01604 homo sapien
28	335.5	60.2	108	1	KV1V_HUMAN	P04430 homo sapien
29	335.5	60.2	108	1	KV5O_MOUSE	P01648 mus musculu
30	335.5	60.2	236	2	Q6P5S8_HUMAN	Q6p5s8 homo sapien
31	335.5	60.2	240	2	Q65ZC9_HUMAN	Q65zc9 homo sapien
32	334.5	60.1	108	1	KV1F_HUMAN	P01598 homo sapien
33	334.5	60.1	240	2	Q52L64_MOUSE	Q52l64 mus musculu
34	333.5	59.9	108	2	Q9UL77_HUMAN	Q9ul77 homo sapien
35	333.5	59.9	236	2	Q6GMX8_HUMAN	Q6gmx8 homo sapien
36	333	59.8	109	2	Q9UL85_HUMAN	Q9ul85 homo sapien
37	332	59.6	109	2	Q9UL78_HUMAN	Q9ul78 homo sapien
38	331.5	59.5	108	1	KV1A_HUMAN	P01593 homo sapien
39	331.5	59.5	108	1	KV1P_HUMAN	P01608 homo sapien
40	331.5	59.5	108	1	KV1S_HUMAN	P01611 homo sapien
41	331.5	59.5	236	2	Q7Z3Y4_HUMAN	Q7z3y4 homo sapien
42	330	59.2	109	1	KV3E_HUMAN	P01623 homo sapien
43	330	59.2	129	1	KV3L_HUMAN	P18135 homo sapien
44	329.5	59.2	236	2	Q6GMW1_HUMAN	Q6gmw1 homo sapien
45	329.5	59.2	236	2	Q502W4_HUMAN	Q502w4 homo sapien

ALIGNMENTS

RESULT 1
Q58EU4_MOUSE
ID Q58EU4_MOUSE PRELIMINARY; PRT; 238 AA.
AC Q58EU4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Igk-C protein.
GN Name=Igk-C;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FVB/N; TISSUE=Colon;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC091754; AAH91754.1; -; mRNA.
DR SMR; Q58EU4; 25-238.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.

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DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   238 AA;  26440 MW;  AE2B2BA90B9F7D5D CRC64;

  Query Match             84.1%;  Score 468.5;  DB 2;  Length 238;
  Best Local Similarity   83.2%;  Pred. No. 1.5e-41;
  Matches   89;  Conservative    9;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||:|||||||||||||| |:||||||:|||||||:||:| |||||||||
Db         25 DIVMTQSHKFMSTSIGDRVSITCKASQDVTTAVAWYQQKPGQSPKVLIHWASTRHTGVPD 84

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||:|||||||||||||||| |  :|| |||||||
Db         85 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPLTFGSGTKLEIK 131


RESULT 2
KV5A_MOUSE
ID   KV5A_MOUSE     STANDARD;      PRT;   149 AA.
AC   P01633;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-V region MPC11 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE OF 1-71.
RX   MEDLINE=83001944; PubMed=6288267; DOI=10.1016/0092-8674(82)90184-2;
RA   Kelley D.E., Coleclough C., Perry R.P.;
RT   "Functional significance and evolutionary development of the 5'-
RT   terminal regions of immunoglobulin variable-region genes.";
RL   Cell 29:681-689(1982).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 41-149.
RX   MEDLINE=80176554; PubMed=6245773;
RA   Rabbitts T.H., Hamlyn P.H., Matthyssens G., Roe B.A.;
RT   "The variability, arrangement, and rearrangement of immunoglobulin
RT   genes.";
RL   Can. J. Biochem. 58:176-187(1980).
RN   [3]
RP   PROTEIN SEQUENCE OF 30-149.
RX   MEDLINE=78186617; PubMed=418775;
RA   Smith G.P.;
RT   "Sequence of the full-length immunoglobulin kappa-chain of mouse
RT   myeloma MPC 11.";
RL   Biochem. J. 171:337-347(1978).
CC   -!- MISCELLANEOUS: The mature chain has 12 additional residues at its
CC       amino end, due to a tandem duplication of 36 nucleotides after the
CC       codon for residue 36. Residue 42 corresponds to the N-terminal
CC       residue of typical kappa chains.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; J00561; AAA38776.1; -; Genomic_DNA.
DR   PIR; A90823; KVMS11.
DR   HSSP; P01634; 1IGC.
DR   SMR; P01633; 42-149.
DR   Ensembl; ENSMUSG00000061362; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Repeat; Signal.
FT   SIGNAL        1     29
FT   CHAIN        30    149       Ig kappa chain V-V region MPC11.
FT   REPEAT       26     35
FT   REPEAT       38     47
FT   REGION       42     64       Framework-1.
FT   REGION       65     75       Complementarity-determining-1.
FT   REGION       76     90       Framework-2.
FT   REGION       91     97       Complementarity-determining-2.
FT   REGION       98    129       Framework-3.
FT   REGION      130    138       Complementarity-determining-3.
FT   REGION      139    148       Framework-4.
FT   NON_TER     149    149
SQ   SEQUENCE   149 AA;  16434 MW;  B0480C87B682AC3E CRC64;

  Query Match             76.4%;  Score 425.5;  DB 1;  Length 149;
  Best Local Similarity   78.5%;  Pred. No. 3.4e-37;
  Matches   84;  Conservative   10;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||| |:||||||:||||||||||  | |:|||||
Db         42 DIVMTQSHKFMSTSVGDRVSITCKASQDVSTTVAWYQQKPGQSPKLLIYSASYRYTGVPD 101

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQ-YSLYRSFGGGTKLEIK 106
              ||||| |||||| ||::||:|||| |:||| ||   :||||||||||
Db        102 RFTGSGSGTDFTFTISSVQAEDLAVYYCQQHYSTPPTFGGGTKLEIK 148


RESULT 3
Q8VIJ0_MOUSE
ID   Q8VIJ0_MOUSE PRELIMINARY;      PRT;   108 AA.
AC   Q8VIJ0;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-DNA light chain (Fragment).
GN   Name=Igk-V19-14; Synonyms=Vk19;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C3H/HeJ-lpr/lpr;
RX   MEDLINE=96409289; PubMed=8814271;
RA   Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT   "Differences in V kappa gene utilization and VH CDR3 sequence among
RT   anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL   Eur. J. Immunol. 26:2225-2233(1996).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=2499887;
RA   Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT   "Two murine natural polyreactive autoantibodies are encoded by
RT   nonmutated germ-line genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
RA   Tillman D.M., Jou N.T., Hill R.J., Marion T.N.;
RT   "Both IgM and IgG anti-DNA antibodies are the products of clonally
RT   selective B cell stimulation in (NZB x NZW)F1 mice.";
RL   J. Exp. Med. 176:761-779(1992).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=91115823; PubMed=1703527;
RA   Goshorn S.C., Retzel E., Jemmerson R.;
RT   "Common structural features among monoclonal antibodies binding the
RT   same antigenic region of cytochrome c.";
RL   J. Biol. Chem. 266:2134-2142(1991).
DR   EMBL; U59155; AAB02917.1; -; mRNA.
DR   PIR; A33933; A33933.
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DR   PIR; A37262; A37262.
DR   PIR; PH1072; PH1072.
DR   HSSP; P01634; 1IGC.
DR   SMR; Q8VIJ0; 1-108.
DR   Ensembl; ENSMUSG00000053690; Mus musculus.
DR   MGI; MGI:1330830; Igk-V19-14.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11859 MW;  68506D75613DBFBE CRC64;

  Query Match             74.4%;  Score 414.5;  DB 2;  Length 108;
  Best Local Similarity   75.7%;  Pred. No. 3.5e-36;
  Matches   81;  Conservative   12;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :|||   ||||||||||:||||||:|||:||||||:|||||| |||  |  ::|||
Db          1 DIVMTQSQTFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKALIYSASYPYSGVPH 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||:||||||||:||||||: |  :||||||||||
Db         61 RFTGSGSGTDFTLTISNVQSEDLAEYFCQQYNSYPYTFGGGTKLEIK 107


RESULT 4
Q9JL74_MOUSE
ID   Q9JL74_MOUSE PRELIMINARY;      PRT;    99 AA.
AC   Q9JL74;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-myosin immunoglobulin light chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BALB/c;
RX   MEDLINE=20448942; PubMed=10992488;
RX   DOI=10.1128/IAI.68.10.5803-5808.2000;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "T-Cell-dependent antibody response to the dominant epitope of
RT   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT   with cardiac myosin.";
RL   Infect. Immun. 68:5803-5808(2000).
DR   EMBL; AF206032; AAF69330.1; -; mRNA.
DR   HSSP; P01634; 1IGC.
DR   SMR; Q9JL74; 1-99.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER      99     99
SQ   SEQUENCE   99 AA;  10939 MW;  3B25D0E784533324 CRC64;

  Query Match             67.1%;  Score 373.5;  DB 2;  Length 99;
  Best Local Similarity   73.7%;  Pred. No. 7.4e-32;
  Matches   73;  Conservative    8;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          9 KMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPDRFTGSVSG 68
              | :  | ||||:||||||| |   ||||||:||||||||||: | |:||||||||||  |
Db          1 KFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLIYYASNRYTGVPDRFTGSGYG 60

Qy         69 TDFTLTITNVQSEDLADYFCQQ-YSLYRSFGGGTKLEIK 106
              |||| ||: ||:|||| ||||| ||  |:||||||||||
Db         61 TDFTFTISTVQAEDLAVYFCQQDYSSPRTFGGGTKLEIK 99


RESULT 5
KV5B_MOUSE
ID   KV5B_MOUSE     STANDARD;      PRT;   136 AA.
AC   P01634;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-V region MOPC 21 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=82059477; PubMed=6170937;
RA   Hamlyn P.H., Gait M.J., Milstein C.;
RT   "Complete sequence of an immunoglobulin mRNA using specific priming
RT   and the dideoxynucleotide method of RNA sequencing.";
RL   Nucleic Acids Res. 9:4485-4494(1981).
RN   [2]
RP   PROTEIN SEQUENCE OF 30-136.
RX   MEDLINE=73053310; PubMed=4638343;
RA   Svasti J., Milstein C.;
RT   "The complete amino acid sequence of a mouse kappa light chain.";
RL   Biochem. J. 128:427-444(1972).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; V00810; CAA24192.1; ALT_TERM; mRNA.
DR   PIR; A93736; KVMS21.
DR   PDB; 1IGC; X-ray; L=30-136.
DR   Ensembl; ENSMUSG00000060300; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     29
FT   CHAIN        30    136       Ig kappa chain V-V region MOPC 21.
FT   REGION       30     52       Framework-1.
FT   REGION       53     63       Complementarity-determining-1.
FT   REGION       64     78       Framework-2.
FT   REGION       79     85       Complementarity-determining-2.
FT   REGION       86    117       Framework-3.
FT   REGION      118    126       Complementarity-determining-3.
FT   REGION      127    136       Framework-4.
FT   NON_TER     136    136
FT   STRAND       34     36
FT   STRAND       41     43
FT   TURN         44     45
FT   STRAND       48     53
FT   TURN         59     60
FT   STRAND       62     67
FT   TURN         69     70
FT   STRAND       74     78
FT   TURN         79     81
FT   STRAND       82     83
FT   TURN         85     86
FT   TURN         89     90
FT   STRAND       93     95
FT   STRAND       99    104
FT   TURN        110    111
FT   STRAND      113    119
FT   STRAND      126    127
FT   STRAND      132    136
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SQ   SEQUENCE   136 AA;  14902 MW;  8CDD85113996D1C2 CRC64;

  Query Match             66.7%;  Score 371.5;  DB 1;  Length 136;
  Best Local Similarity   70.8%;  Pred. No. 1.7e-31;
  Matches   75;  Conservative   13;  Mismatches   17;  Indels    1;  Gaps    1;

Qy          2 IQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPDR 61
              | :||| | || |||:||::||||||::| | |:||||:| |||||||| | |:||||||
Db         31 IVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPDR 90

Qy         62 FTGSVSGTDFTLTITNVQSEDLADYFC-QQYSLYRSFGGGTKLEIK 106
              |||| | |||||||::||:|||||| | | ||   :||||||||||
Db         91 FTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK 136


RESULT 6
KV4B_HUMAN
ID   KV4B_HUMAN     STANDARD;      PRT;   133 AA.
AC   P06313;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-IV region JI precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86041853; PubMed=2997712;
RA   Klobeck H.G., Bornkamm G.W., Combriato G., Mocikat R., Pohlenz H.D.,
RA   Zachau H.G.;
RT   "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT   single germline gene.";
RL   Nucleic Acids Res. 13:6515-6529(1985).
CC   ---------------------------------------------------------------------
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; Z00022; CAA77317.1; -; Genomic_DNA.
DR   PIR; A01904; K4HUJI.
DR   HSSP; P01625; 1LVE.
DR   SMR; P06313; 21-133.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    133       Ig kappa chain V-IV region JI.
FT   REGION       21     43       Framework-1.
FT   REGION       44     60       Complementarity-determining-1.
FT   REGION       61     75       Framework-2.
FT   REGION       76     82       Complementarity-determining-2.
FT   REGION       83    114       Framework-3.
FT   REGION      115    122       Complementarity-determining-3.
FT   REGION      123    132       Framework-4.
FT   DISULFID     43    114       By similarity.
FT   NON_TER     133    133
SQ   SEQUENCE   133 AA;  14633 MW;  5FB3953066744AF4 CRC64;

  Query Match             63.7%;  Score 355;  DB 1;  Length 133;
  Best Local Similarity   59.8%;  Pred. No. 9.7e-30;
  Matches   67;  Conservative   20;  Mismatches   19;  Indels    6;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTS------VAWYQQRPGQSPKLLIYWTSTR 54
                :| :|||   :: |:|:| :| ||:|| |  |      :|||||:||| ||||||| |||
Db         21 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASTR 80

Qy         55 HTGVPDRFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
                :||||||:|| |||||||||:::|:||:| |:||||    :||||||:|||
Db         81 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYDTIPTFGGGTKVEIK 132


RESULT 7
Q6GMX9_HUMAN
ID   Q6GMX9_HUMAN PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGKC protein.
GN   Name=IGKC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RG   NIH MGC Project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073763; AAH73763.1; -; mRNA.
DR   SMR; Q6GMX9; 23-236.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   236 AA;  25924 MW;  FDE2093DC560CFF7 CRC64;

  Query Match             63.5%;  Score 353.5;  DB 2;  Length 236;
  Best Local Similarity   63.6%;  Pred. No. 2.7e-29;
  Matches   68;  Conservative   19;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :||:|||   :| ||| ||:|||:|||:|   :|||||| ::|| ||| ||: |:|||
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Db         23 DIQMTQSPSSLSASVGHRVTITCRASQNVSRWLAWYQQRPEKAPKSLIYATSSLHSGVPS 82

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||:|| ||||||||||:::| || | |:||||: |  :||||||:|||
Db         83 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYNTYPLTFGGGTKVEIK 129


RESULT 8
KV1Y_HUMAN
ID   KV1Y_HUMAN     STANDARD;      PRT;   108 AA.
AC   P80362;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region WAT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=95086080; PubMed=7993911;
RA   Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA   Solomon A., Stevens F.J., Schiffer M.;
RT   "Comparison of crystal structures of two homologous proteins:
RT   structural origin of altered domain interactions in immunoglobulin
RT   light-chain dimers.";
RL   Biochemistry 33:14848-14857(1994).
RN   [2]
RP   PROTEIN SEQUENCE OF 1-35.
RX   MEDLINE=81267384; PubMed=6167731;
RA   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA   Popp R.A., Solomon A.;
RT   "Characterization and preliminary crystallographic data on the VL-
RT   related fragment of the human kI Bence Jones protein Wat.";
RL   J. Mol. Biol. 147:185-193(1981).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ----------------------------------------------------------------------
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CC   removed.
CC   ----------------------------------------------------------------------
DR   PDB; 1WTL; X-ray; A/B=1-108.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin domain; Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   CONFLICT     30     31       TN -> SD (in Ref. 2).
FT   NON_TER     108    108
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       45     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       84     90
FT   STRAND       98     98
FT   STRAND      102    106
SQ   SEQUENCE   108 AA;  11737 MW;  D9D941B3F0FAE697 CRC64;

  Query Match             63.3%;  Score 352.5;  DB 1;  Length 108;
  Best Local Similarity   62.6%;  Pred. No. 1.4e-29;
  Matches   67;  Conservative   19;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :||:|||   :| ||||||:|||:||||:   | |:|||||:||:|||  |   ||||
Db          1 DIQMTQSPSSLSASVGDRVTITCRASQDITNYVNWFQQRPGQAPKVLIYGASILETGVPS 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQY-SLYRSFGGGTKLEIK 106
              ||:|| |||||| ||:::| ||:| |:|||| :|  :||||||::||
Db         61 RFSGSGSGTDFTFTISSLQPEDIATYYCQQYDTLPLTFGGGTKVDIK 107


RESULT 9
KV5M_MOUSE
ID   KV5M_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01646;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-V region HP 123E6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=82150934; PubMed=6801658;
RA   Siegelman M., Capra J.D.;
RT   "Complete amino acid sequence of light chain variable regions derived
RT   from five monoclonal anti-p-azophenylarsonate antibodies differing
RT   with respect to a crossreactive idiotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC   -!- MISCELLANEOUS: Anti-arsonate hybridoma protein.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   HSSP; P01594; 1JV5.
DR   Ensembl; ENSMUSG00000029991; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
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SQ   SEQUENCE   108 AA;  11989 MW;  4C98599C08EBA09A CRC64;

  Query Match             63.3%;  Score 352.5;  DB 1;  Length 108;
  Best Local Similarity   61.7%;  Pred. No. 1.4e-29;
  Matches   66;  Conservative   21;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :||:|||   :| |:||||:|:|:||||:   : ||||:|  : |||||:||  |:|||
Db          1 DIQMTQSTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQ-YSLYRSFGGGTKLEIK 106
              ||:|| ||||::|||:|:: ||:| ||||| | | |:||||||||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGYMLPRTFGGGTKLEIK 107


RESULT 10
Q7TQM2_MOUSE
ID   Q7TQM2_MOUSE PRELIMINARY;      PRT;   243 AA.
AC   Q7TQM2;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ScFv 6H8 protein (Fragment).
GN   Name=scFv 6H8;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Balb/C;
RX   MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;
RA   Peter J.C., Eftekhari P., Billiald P., Wallukat G., Hoebeke J.;
RT   "scFv single chain antibody variable fragment as inverse agonist for
RT   the beta-2 adrenergic receptor.";
RL   J. Biol. Chem. 278:36740-36747(2003).
DR   EMBL; AJ574851; CAE00495.1; -; Genomic_DNA.
DR   HSSP; P01751; 1A6W.
DR   SMR; Q7TQM2; 1-236.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1       1
SQ   SEQUENCE   243 AA;  25976 MW;  BEFFF64D2DCF4F76 CRC64;

  Query Match             62.5%;  Score 348;  DB 2;  Length 243;
  Best Local Similarity   60.4%;  Pred. No. 1.1e-28;
  Matches   64;  Conservative   21;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :||:|||    | |:||||:||||||:|:   :|||||:|| :|:|||   ::  ||||
Db        132 DIQMTQSSSSFSVSLGDRVTITCKASEDIYNRLAWYQQKPGNAPRLLISGATSLETGVPS 191

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
              ||:|| || |:||:||::|:||:| |:||||   |:||||||||||
Db        192 RFSGSGSGKDYTLSITSLQTEDVATYYCQQYWSTRTFGGGTKLEIK 237


RESULT 11
KV5J_MOUSE
ID   KV5J_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01643;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-V region MOPC 173.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=76091934; PubMed=812696;
RA   Schiff C., Fougereau M.;
RT   "Determination of the primary structure of a mouse IgG2a
RT   immunoglobulin. Amino-acid sequence of the light chain.";
RL   Eur. J. Biochem. 59:525-537(1975).
CC   -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01926; KVMS73.
DR   HSSP; P01594; 1JV5.
DR   Ensembl; ENSMUSG00000058965; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11819 MW;  2AD29D92A72AA0A3 CRC64;

  Query Match             62.0%;  Score 345.5;  DB 1;  Length 108;
  Best Local Similarity   57.9%;  Pred. No. 7.9e-29;
  Matches   62;  Conservative   26;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :||:||:   :| |:||||:|:| ||| :|  : ||||:|  : |||||:||: |:|||
Db          1 DIQMTQTTSSLSASLGDRVTISCSASQSIGNYLBWYQQKPDGTVKLLIYYTSSLHSGVPS 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYS-LYRSFGGGTKLEIK 106
              ||:|| ||||::|||:::: :::| |:||||| | |:||||||||||
Db         61 RFSGSGSGTDYSLTISBLZPZBIATYYCQQYSKLPRTFGGGTKLEIK 107


RESULT 12
KV5K_MOUSE
ID   KV5K_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01644;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-V region HP R16.7.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RC   STRAIN=A/J;
RX   MEDLINE=82150934; PubMed=6801658;
RA   Siegelman M., Capra J.D.;
RT   "Complete amino acid sequence of light chain variable regions derived
RT   from five monoclonal anti-p-azophenylarsonate antibodies differing
RT   with respect to a crossreactive idiotype.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC   -!- MISCELLANEOUS: Anti-arsonate hybridoma protein.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------------
DR   PIR; A01927; KVMSAR.
DR   HSSP; P01594; 1JV5.
DR   SMR; P01644; 1-108.
DR   Ensembl; ENSMUSG00000029991; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11910 MW;  A554642C63EFF597 CRC64;

  Query Match             62.0%;  Score 345.5;  DB 1;  Length 108;
  Best Local Similarity   60.7%;  Pred. No. 7.9e-29;
  Matches   65;  Conservative   22;  Mismatches   19;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :||:||:   :| |:||||:|:|:||||:   : ||||:|  : |||||:||  |:|||
Db          1 DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPS 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQ-YSLYRSFGGGTKLEIK 106
              ||:|| ||||::|||:|:: ||:| |||||  || |:||||||||||
Db         61 RFSGSGSGTDYSLTISNLEQEDIATYFCQQGNSLPRTFGGGTKLEIK 107


RESULT 13
Q9UL70_HUMAN
ID   Q9UL70_HUMAN PRELIMINARY;      PRT;   108 AA.
AC   Q9UL70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1660528;
RA   Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA   Diamond B.;
RT   "Molecular characteristics of antibodies bearing an anti-DNA-
RT   associated idiotype.";
RL   J. Exp. Med. 174:1639-1652(1991).
DR   EMBL; AF035044; AAD56280.1; -; mRNA.
DR   PIR; PH0863; PH0863.
DR   HSSP; P01607; 1BWW.
DR   SMR; Q9UL70; 1-108.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11633 MW;  B7BEDC3E41FCCA37 CRC64;

  Query Match             61.8%;  Score 344.5;  DB 2;  Length 108;
  Best Local Similarity   62.6%;  Pred. No. 1e-28;
  Matches   67;  Conservative   18;  Mismatches   21;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
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Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQY-SLYRSFGGGTKLEIK 106
              ||:|| |||||||||:::| ||:| |:||:| |  |:|| |||||||
Db         61 RFSGSGSGTDFTLTISSLQPEDVATYYCQKYNSAPRTFGPGTKLEIK 107


RESULT 14
KV4A_HUMAN
ID   KV4A_HUMAN     STANDARD;      PRT;   114 AA.
AC   P01625;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-IV region Len.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=76004342; PubMed=50995;
RA   Schneider M., Hilschmann N.;
RT   "The primary structure of a monoclonic immunoglobulin-L-chain of
RT   subgroup IV of the kappa type (Bence-Jones protein Len).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
RN   [2]
RP   SEQUENCE REVISION TO 9.
RA   Salomon A.;
RL   Submitted (AUG-1996) to Swiss-Prot.
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ---------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------------
DR   PDB; 1EEQ; X-ray; A/B=1-114.
DR   PDB; 1EEU; X-ray; A/B=1-114.
DR   PDB; 1EFQ; X-ray; A=1-114.
DR   PDB; 1EK3; X-ray; A/B=1-114.
DR   PDB; 1LVE; X-ray; @=1-114.
DR   PDB; 2LVE; X-ray; @=1-114.
DR   PDB; 3LVE; X-ray; @=1-114.
DR   PDB; 4LVE; X-ray; A/B=1-114.
DR   PDB; 5LVE; X-ray; A=1-114.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin domain; Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
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FT   REGION       24     40       Complementarity-determining-1.
FT   REGION       41     55       Framework-2.
FT   REGION       56     62       Complementarity-determining-2.
FT   REGION       63     94       Framework-3.
FT   REGION       95    101       Complementarity-determining-3.
FT   REGION      102    113       Framework-4.
FT   DISULFID     23     94       By similarity.
FT   NON_TER     114    114
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
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FT   TURN         32     35
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FT   STRAND       68     73
FT   TURN         74     75
FT   STRAND       76     81
FT   HELIX        86     88
FT   STRAND       90     96
FT   STRAND      103    104
FT   STRAND      108    112
SQ   SEQUENCE   114 AA;  12640 MW;  0647F1D17F236485 CRC64;

  Query Match             61.8%;  Score 344.5;  DB 1;  Length 114;
  Best Local Similarity   61.1%;  Pred. No. 1.1e-28;
  Matches   69;  Conservative   18;  Mismatches   19;  Indels    7;  Gaps    2;

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Db          1 DIVMTQSPDSLAVSLGERATINCKSSQSVLYSSNSKNYLAWYQQKPGQPPKLLIYWASTR 60

Qy         55 HTGVPDRFTGSVSGTDFTLTITNVQSEDLADYFCQQ-YSLYRSFGGGTKLEIK 106
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Db         61 ESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPYSFGQGTKLEIK 113


RESULT 15
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ID   KV1D_HUMAN     STANDARD;      PRT;   107 AA.
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DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region CAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=75075135; PubMed=4216454;
RA   Milstein C.P., Deverson E.V.;
RT   "Primary structure of kappa light chain from a human myeloma
RT   protein.";
RL   Eur. J. Biochem. 49:377-391(1974).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC       marker.
CC   -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01864; K1HUAR.
DR   HSSP; P80362; 1WTL.
DR   SMR; P01596; 1-107.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   CARBOHYD     28     28       N-linked (GlcNAc. . .).
FT   NON_TER      107    107
SQ   SEQUENCE   107 AA;  11704 MW;  E1BF0DF9844C3346 CRC64;

  Query Match             61.8%;  Score 344;  DB 1;  Length 107;
  Best Local Similarity   56.6%;  Pred. No. 1.1e-28;
  Matches   60;  Conservative   29;  Mismatches   17;  Indels    0;  Gaps    0;

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Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
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Job time : 244.403 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 00:56:54 ; Search time 55.0543 Seconds
(without alignments)
159.182 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	557	100.0	106	1	US-08-318-157B-4	Sequence 4, Appli
2	557	100.0	106	2	US-09-253-794-4	Sequence 4, Appli
3	472.5	84.8	249	1	US-08-797-689-18	Sequence 18, Appl
4	472.5	84.8	249	2	US-09-984-186-18	Sequence 18, Appl
5	468.5	84.1	107	2	US-09-406-535-4	Sequence 4, Appli
6	463.5	83.2	107	1	US-07-634-278-50	Sequence 50, Appl
7	463.5	83.2	107	1	US-08-477-728-50	Sequence 50, Appl
8	463.5	83.2	107	1	US-08-474-040-50	Sequence 50, Appl
9	463.5	83.2	107	1	US-08-487-200-50	Sequence 50, Appl
10	463.5	83.2	107	2	US-08-838-682-19	Sequence 19, Appl
11	463.5	83.2	107	2	US-08-895-914-19	Sequence 19, Appl
12	463.5	83.2	107	2	US-08-484-537-50	Sequence 50, Appl
13	463.5	83.2	107	2	US-09-357-710A-19	Sequence 19, Appl
14	463.5	83.2	107	2	US-09-357-707-19	Sequence 19, Appl
15	463.5	83.2	107	2	US-09-357-708-19	Sequence 19, Appl
16	457.5	82.1	107	1	US-08-491-845-4	Sequence 4, Appli
17	451	81.0	106	1	US-08-318-157B-19	Sequence 19, Appl
18	451	81.0	106	2	US-09-253-794-19	Sequence 19, Appl
19	449.5	80.7	240	2	US-10-092-246-36	Sequence 36, Appl
20	449.5	80.7	240	2	US-10-096-246A-36	Sequence 36, Appl
21	449.5	80.7	240	2	US-10-096-246A-37	Sequence 37, Appl
22	447.5	80.3	127	2	US-08-646-265A-27	Sequence 27, Appl
23	444.5	79.8	240	2	US-10-096-246A-35	Sequence 35, Appl
24	441.5	79.3	240	2	US-10-092-246-37	Sequence 37, Appl
25	439.5	78.9	240	2	US-10-092-246-35	Sequence 35, Appl
26	437.5	78.5	145	2	US-10-226-795-17	Sequence 17, Appl
27	437	78.5	108	1	US-08-657-012-25	Sequence 25, Appl
28	437	78.5	108	2	US-09-013-872-25	Sequence 25, Appl
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34	435.5	78.2	250	1	US-08-464-589-8	Sequence 8, Appli
35	435.5	78.2	250	1	US-08-461-838-2	Sequence 2, Appli
36	435.5	78.2	250	1	US-08-461-386-2	Sequence 2, Appli
37	430.5	77.3	239	2	US-10-092-246-33	Sequence 33, Appl
38	430.5	77.3	239	2	US-10-096-246A-33	Sequence 33, Appl
39	428.5	76.9	106	2	US-09-189-129-4	Sequence 4, Appli
40	428.5	76.9	106	2	US-09-824-286-4	Sequence 4, Appli
41	428.5	76.9	123	1	US-08-398-613A-20	Sequence 20, Appl
42	428.5	76.9	123	1	US-08-398-612A-20	Sequence 20, Appl
43	428.5	76.9	123	1	US-08-398-611A-20	Sequence 20, Appl
44	428.5	76.9	123	1	US-08-491-334A-20	Sequence 20, Appl
45	428.5	76.9	123	2	US-09-027-449-17	Sequence 17, Appl

ALIGNMENTS

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RESULT 1
US-08-318-157B-4
; Sequence 4, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-4

  Query Match           100.0%;  Score 557;  DB 1;  Length 106;
  Best Local Similarity  100.0%;  Pred. No. 4e-48;
  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy          61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
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RESULT 2
US-09-253-794-4
; Sequence 4, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 106 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-253-794-4

  Query Match           100.0%;  Score 557;  DB 2;  Length 106;
  Best Local Similarity  100.0%;  Pred. No. 4e-48;
  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy          61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
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Db          61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106


RESULT 3
US-08-797-689-18
; Sequence 18, Application US/08797689
; Patent No. 5876969
;  GENERAL INFORMATION:
;    APPLICANT:  Fleer, Reinhard
;    APPLICANT:  Fournier, Alain
;    APPLICANT:  Guitton, Jean-Dominique
;    APPLICANT:  Jung, Gerard
;    APPLICANT:  Yeh, Patrice
;    TITLE OF INVENTION:  NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
;    TITLE OF INVENTION:  PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
;    TITLE OF INVENTION:  CONTAINING SAID POLYPEPTIDES
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  System 7.1
;      SOFTWARE:  Word 5.1 (PatentIn)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/797,689
;      FILING DATE:  31-JAN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/256,927
;      FILING DATE:  28-JUL-1994
;      APPLICATION NUMBER:  FR 92/01064
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/FR93/00085
;      FILING DATE:  28-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith Ph.D., Julie K.
;      REGISTRATION NUMBER:  P-38,619
;      REFERENCE/DOCKET NUMBER:  ST92006-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 454-3839
;      TELEFAX:  (610) 454-3808
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  249 amino acids
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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-797-689-18

  Query Match           84.8%;  Score 472.5;  DB 1;  Length 249;
  Best Local Similarity  87.7%;  Pred. No. 2.6e-39;
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RESULT 4
US-09-984-186-18
; Sequence 18, Application US/09984186
; Patent No. 6686179
;   GENERAL INFORMATION:
;        APPLICANT: Fleer, Reinhard
;                   Fournier, Alain
;                   Guitton, Jean-Dominique
;                   Jung, Gerard
;                   Yeh, Patrice
;        TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
;                            PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
;                            CONTAINING SAID POLYPEPTIDES
;        NUMBER OF SEQUENCES: 36
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Rhone-Poulenc Rorer Inc.
;
```

```
;             STREET: 500 Arcola Road, 3C43
;             CITY: Collegeville
;             STATE: PA
;             COUNTRY: USA
;             ZIP: 19426
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: Macintosh
;             OPERATING SYSTEM: System 7.1
;             SOFTWARE: Word 5.1 (PatentIn)
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/984,186
;             FILING DATE: 29-Oct-2001
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/797,689
;             FILING DATE: 31-JAN-1997
;             APPLICATION NUMBER: US 08/256,927
;             FILING DATE: 28-JUL-1994
;             APPLICATION NUMBER: FR 92/01064
;             FILING DATE: 31-JAN-1992
;             APPLICATION NUMBER: PCT/FR93/00085
;             FILING DATE: 28-JAN-1993
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Smith Ph.D., Julie K.
;             REGISTRATION NUMBER: P-38,619
;             REFERENCE/DOCKET NUMBER: ST92006-US
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (610) 454-3839
;             TELEFAX: (610) 454-3808
;   INFORMATION FOR SEQ ID NO: 18:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 249 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-984-186-18

  Query Match             84.8%;  Score 472.5;  DB 2;  Length 249;
  Best Local Similarity   87.7%;  Pred. No. 2.6e-39;
  Matches   93;  Conservative    3;  Mismatches    9;  Indels    1;  Gaps    1;

Qy          2 IQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPDR 61
              ||||||   |||||||||||||||||||| ||||||||:|||||||||||| ||||||||||
Db        144 IQLTQSPNSMSTSVGDRVSITCKASQDVDTSVAWYQQKPGQSPKLLIYWASTRHTGVPDR 203

Qy         62 FTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYR-SFGGGTKLEIK 106
              ||||  |||||||||:|||||| |||||||||  |  :||||||||||
Db        204 FTGSGSGTDFTLTISNVQSEDSADYFCQQYSSYPWTFGGGTKLEIK 249


RESULT 5
US-09-406-535-4
; Sequence 4, Application US/09406535
; Patent No. 6376653
; GENERAL INFORMATION:
;  APPLICANT: Connie L. Erickson-Miller
;  APPLICANT: Stephen D. Holmes
;  APPLICANT: James D. Winkler
;  TITLE OF INVENTION: Tie2 Antagonist Antibodies
;  FILE REFERENCE: P50844
;  CURRENT APPLICATION NUMBER: US/09/406,535
;  CURRENT FILING DATE: 1999-09-27
;  EARLIER APPLICATION NUMBER: 60/102,100
;  EARLIER FILING DATE: 1998-09-28
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-406-535-4

  Query Match             84.1%;  Score 468.5;  DB 2;  Length 107;
  Best Local Similarity   83.2%;  Pred. No. 2.5e-39;
  Matches   89;  Conservative    9;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||| |||||:|||:||||||:|||||||||| |:|||||||
Db          1 DIVMTQSHKFMSTSVGDRVSFTCKASQNVGTAVAWYQQKPGQSPKLLIYWASSRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||||||||||||||:|| |  :|| |||||:|
Db         61 RFTGSGSGTDFTLTITNVQSEDLADYFCQEYSSYPLTFGVGTKLELK 107


RESULT 6
US-07-634-278-50
; Sequence 50, Application US/07634278
; Patent No. 5530101
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COBLINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,278
;      FILING DATE:  19-DEC-1990
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-634-278-50

  Query Match             83.2%;  Score 463.5;  DB 1;  Length 107;
  Best Local Similarity   81.3%;  Pred. No. 7.7e-39;
  Matches   87;  Conservative   11;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
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              :| :||||| |||||||||||||||||||::| |:||: |||||||||| |||||||||
Db             1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGSAVVWHQQKSGQSPKLLIYWASTRHTGVPD 60

Qy            61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
                 ||||| |||||||||||||||||||||||::  :|| ||:||:|
Db            61 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYSIFPLTFGAGTRLELK 107


RESULT 7
US-08-477-728-50
; Sequence 50, Application US/08477728
; Patent No. 5585089
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,728
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-477-728-50

  Query Match             83.2%;  Score 463.5;  DB 1;  Length 107;
  Best Local Similarity   81.3%;  Pred. No. 7.7e-39;
  Matches   87;  Conservative   11;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||::| |:||: |||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGSAVVWHQQKSGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
                ||||| |||||||||||||||||||||||::  :|| ||:||:|
Db         61 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYSIFPLTFGAGTRLELK 107


RESULT 8
US-08-474-040-50
; Sequence 50, Application US/08474040
; Patent No. 5693761
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,040
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-474-040-50

  Query Match             83.2%;  Score 463.5;  DB 1;  Length 107;
  Best Local Similarity   81.3%;  Pred. No. 7.7e-39;
  Matches   87;  Conservative   11;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||::| |:||: |||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGSAVVWHQQKSGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
                ||||| |||||||||||||||||||||||::  :|| ||:||:|
Db         61 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYSIFPLTFGAGTRLELK 107


RESULT 9
US-08-487-200-50
```

```
; Sequence 50, Application US/08487200
; Patent No. 5693762
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,200
;      FILING DATE:  7-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002610
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-487-200-50

  Query Match             83.2%;  Score 463.5;  DB 1;  Length 107;
  Best Local Similarity   81.3%;  Pred. No. 7.7e-39;
  Matches   87;  Conservative   11;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||::| |:||: |||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGSAVVWHQQKSGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||||||||||||||::  :|| ||:||:|
Db         61 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYSIFPLTFGAGTRLELK 107


RESULT 10
US-08-838-682-19
; Sequence 19, Application US/08838682
; Patent No. 6107090
;  GENERAL INFORMATION:
;    APPLICANT:  Bander M.D., Neil H.
;    TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF PROSTATE
;    TITLE OF INVENTION:  CANCER
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle LLP
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  14603-1051
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/838,682
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/016,976
;      FILING DATE:  06-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/022,125
;      FILING DATE:  18-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldman, Michael L.
;      REGISTRATION NUMBER:  30,727
;      REFERENCE/DOCKET NUMBER:  19603/1172
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716) 263-1304
;      TELEFAX:  (716) 263-1600
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-838-682-19

  Query Match             83.2%;  Score 463.5;  DB 2;  Length 107;
  Best Local Similarity   82.2%;  Pred. No. 7.7e-39;
  Matches   88;  Conservative    8;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||| |||||||||:| ||||:|||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||||||||||||||||||: |  :|| || |::|
Db         61 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYNSYPLTFGAGTMLDLK 107


RESULT 11
US-08-895-914-19
; Sequence 19, Application US/08895914
; Patent No. 6136311
;  GENERAL INFORMATION:
;    APPLICANT:  Bander, Neil H.
;    TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF CANCER
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle LLP
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  14603-1051
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/895,914
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/016,976
;       FILING DATE:  06-MAY-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/022,125
;       FILING DATE:  18-JUL-1996
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/838,682
;       FILING DATE:  09-APR-1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Goldman, Michael L.
;       REGISTRATION NUMBER:  30,727
;       REFERENCE/DOCKET NUMBER:  19603/1173
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (716) 263-1304
;       TELEFAX:  (716) 263-1600
;   INFORMATION FOR SEQ ID NO:  19:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  107 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-895-914-19

  Query Match             83.2%;  Score 463.5;  DB 2;  Length 107;
  Best Local Similarity   82.2%;  Pred. No. 7.7e-39;
  Matches   88;  Conservative    8;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||| |||||||||:| |||||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||||||||||||||||: |  :|| || |::|
Db         61 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYNSYPLTFGAGTMLDLK 107


RESULT 12
US-08-484-537-50
; Sequence 50, Application US/08484537
; Patent No. 6180370
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,537
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,278
;      FILING DATE:  19-DEC-1990
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-484-537-50

  Query Match             83.2%;  Score 463.5;  DB 2;  Length 107;
  Best Local Similarity   81.3%;  Pred. No. 7.7e-39;
  Matches   87;  Conservative   11;  Mismatches    8;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
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Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGSAVVWHQQKSGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
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Db         61 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYSIFPLTFGAGTRLELK 107


RESULT 13
US-09-357-710A-19
; Sequence 19, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
;  APPLICANT:  Bander, Neil H.
;  TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  Lois M. Kwasigroch: BZL 242/025
;  CURRENT APPLICATION NUMBER: US/09/357,710A
;  CURRENT FILING DATE:  1999-07-20
;  PRIOR APPLICATION NUMBER:  US 08/838,682
;  PRIOR FILING DATE:  1997-04-09
;  PRIOR APPLICATION NUMBER:  US 60/016,976
;  PRIOR FILING DATE:  1996-05-06
;  PRIOR APPLICATION NUMBER:  US 60/022,125
;  PRIOR FILING DATE:  1996-07-18
;  NUMBER OF SEQ ID NOS:  21
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 19
;  LENGTH: 107
;  TYPE: PRT
;  ORGANISM: Mus sp.
US-09-357-710A-19

  Query Match             83.2%;  Score 463.5;  DB 2;  Length 107;
  Best Local Similarity   82.2%;  Pred. No. 7.7e-39;
  Matches   88;  Conservative    8;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
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Db          1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
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Db         61 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYNSYPLTFGAGTMLDLK 107


RESULT 14
US-09-357-707-19
; Sequence 19, Application US/09357707
; Patent No. 6649163
; GENERAL INFORMATION:
;  APPLICANT: Bander, Neil H.
;  TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
;  FILE REFERENCE: Lois M. Kwasigroch: BZL 242/078
;  CURRENT APPLICATION NUMBER: US/09/357,707
;  CURRENT FILING DATE:  1999-07-20
;  PRIOR APPLICATION NUMBER: US 08/895,914
;  PRIOR FILING DATE: 1997-07-17
;  PRIOR APPLICATION NUMBER: US 08/838,682
;  PRIOR FILING DATE: 1997-04-09
;  PRIOR APPLICATION NUMBER: US 60/016,976
;  PRIOR FILING DATE: 1996-05-06
;  PRIOR APPLICATION NUMBER: US 60/022,125
;  PRIOR FILING DATE: 1996-07-18
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-357-707-19

  Query Match             83.2%;  Score 463.5;  DB 2;  Length 107;
  Best Local Similarity   82.2%;  Pred. No. 7.7e-39;
  Matches   88;  Conservative    8;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||| |||||||||:| ||||:|||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||||||||||||||||||: |  :|| || |::|
Db         61 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYNSYPLTFGAGTMLDLK 107


RESULT 15
US-09-357-708-19
; Sequence 19, Application US/09357708
; Patent No. 6770450
; GENERAL INFORMATION:
;  APPLICANT: Bander, Neil H.
;  TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
;  FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
;  CURRENT APPLICATION NUMBER: US/09/357,708
;  CURRENT FILING DATE:  1999-07-20
;  PRIOR APPLICATION NUMBER: US 08/895,914
;  PRIOR FILING DATE: 1997-07-17
;  PRIOR APPLICATION NUMBER: US 08/838,682
;  PRIOR FILING DATE: 1997-04-09
;  PRIOR APPLICATION NUMBER: US 60/016,976
;  PRIOR FILING DATE: 1996-05-06
;  PRIOR APPLICATION NUMBER: US 60/022,125
;  PRIOR FILING DATE: 1996-07-18
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-357-708-19

  Query Match             83.2%;  Score 463.5;  DB 2;  Length 107;
  Best Local Similarity   82.2%;  Pred. No. 7.7e-39;
  Matches   88;  Conservative    8;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||| |||||||||:| ||||:|||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSIICKASQDVGTAVDWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||||||||||||||||||: |  :|| || |::|
Db         61 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYNSYPLTFGAGTMLDLK 107


Search completed: March 23, 2006, 00:58:42
Job time : 56.0543 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:12:29 ; Search time 186.527 Seconds
(without alignments)
237.445 Million cell updates/sec

Title: US-10-755-382-4
Perfect score: 557
Sequence: 1 EIQLTQSHKMMSTSVGDRVS.....FCQQYSLYRSFGGGTKLEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	557	100.0	106	3	US-09-253-794-4	Sequence 4, Appli
2	557	100.0	106	4	US-10-680-734-4	Sequence 4, Appli
3	557	100.0	106	5	US-10-755-382-4	Sequence 4, Appli
4	509	91.4	213	4	US-10-281-479A-76	Sequence 76, Appl
5	509	91.4	213	4	US-10-275-180A-76	Sequence 76, Appl
6	509	91.4	213	4	US-10-286-132A-76	Sequence 76, Appl
7	509	91.4	234	4	US-10-281-479A-24	Sequence 24, Appl
8	509	91.4	234	4	US-10-275-180A-24	Sequence 24, Appl
9	509	91.4	234	4	US-10-286-132A-24	Sequence 24, Appl
10	485.5	87.2	107	5	US-10-842-011-6	Sequence 6, Appli
11	485.5	87.2	107	5	US-10-842-011-42	Sequence 42, Appl
12	485.5	87.2	107	5	US-10-842-011-47	Sequence 47, Appl
13	485.5	87.2	127	5	US-10-842-011-28	Sequence 28, Appl
14	483.5	86.8	115	4	US-10-297-371A-8	Sequence 8, Appli
15	472.5	84.8	108	3	US-09-215-163-21	Sequence 21, Appl
16	472.5	84.8	249	3	US-09-984-186-18	Sequence 18, Appl
17	472.5	84.8	249	4	US-10-237-667-18	Sequence 18, Appl
18	472.5	84.8	249	4	US-10-237-708-18	Sequence 18, Appl
19	472.5	84.8	249	4	US-10-237-866-18	Sequence 18, Appl
20	472.5	84.8	249	4	US-10-237-871-18	Sequence 18, Appl
21	472.5	84.8	249	4	US-10-237-624-18	Sequence 18, Appl
22	472.5	84.8	249	4	US-10-702-536-18	Sequence 18, Appl
23	472.5	84.8	249	4	US-10-702-636-18	Sequence 18, Appl
24	472.5	84.8	249	6	US-11-146-077-18	Sequence 18, Appl
25	463.5	83.2	107	3	US-09-929-665-19	Sequence 19, Appl
26	463.5	83.2	107	3	US-09-929-546-19	Sequence 19, Appl
27	463.5	83.2	107	4	US-10-160-506-20	Sequence 20, Appl
28	463.5	83.2	107	4	US-10-389-155-9	Sequence 9, Appli
29	463.5	83.2	107	4	US-10-389-417-9	Sequence 9, Appli
30	463.5	83.2	107	4	US-10-452-357-52	Sequence 52, Appl
31	463.5	83.2	107	4	US-10-449-379-20	Sequence 20, Appl
32	463.5	83.2	107	4	US-10-688-015-20	Sequence 20, Appl
33	463.5	83.2	107	4	US-10-160-505-20	Sequence 20, Appl
34	455	81.7	213	4	US-10-281-479A-75	Sequence 75, Appl
35	455	81.7	213	4	US-10-275-180A-75	Sequence 75, Appl
36	455	81.7	213	4	US-10-286-132A-75	Sequence 75, Appl
37	451	81.0	106	3	US-09-253-794-19	Sequence 19, Appl
38	451	81.0	106	4	US-10-680-734-19	Sequence 19, Appl
39	451	81.0	106	5	US-10-755-382-19	Sequence 19, Appl
40	451	81.0	115	4	US-10-270-073-4	Sequence 4, Appli
41	451	81.0	232	4	US-10-006-771A-6	Sequence 6, Appli
42	451	81.0	232	4	US-10-377-109-4	Sequence 4, Appli
43	451	81.0	256	4	US-10-270-073-6	Sequence 6, Appli
44	451	81.0	257	4	US-10-270-073-8	Sequence 8, Appli
45	451	81.0	261	4	US-10-270-071-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-253-794-4
; Sequence 4, Application US/09253794
; Patent No. US20020018750A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 106 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-253-794-4

Query Match 100.0%; Score 557; DB 3; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.3e-46;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
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Db          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
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Db         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106


RESULT 2
US-10-680-734-4
; Sequence 4, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
;   LENGTH: 106
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-680-734-4

  Query Match             100.0%;  Score 557;  DB 4;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-46;
  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
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Db         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106


RESULT 3
US-10-755-382-4
; Sequence 4, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 106 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-755-382-4

  Query Match             100.0%;  Score 557;  DB 5;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-46;
  Matches  106;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
              ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106


RESULT 4
US-10-281-479A-76
; Sequence 76, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  Oshumi, Jun
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERA
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 21085.0029U6
;  CURRENT APPLICATION NUMBER: US/10/281,479A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 60/391,478
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 76
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthet
US-10-281-479A-76

  Query Match             91.4%;  Score 509;  DB 4;  Length 213;
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  Matches   95;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

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Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
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Db         61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYRTFGGGTKLEIK 106


RESULT 5
US-10-275-180A-76
; Sequence 76, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 76
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-275-180A-76

  Query Match             91.4%;  Score 509;  DB 4;  Length 213;
  Best Local Similarity   89.6%;  Pred. No. 3.9e-41;
  Matches   95;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||:||||||:|||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
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Db         61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYRTFGGGTKLEIK 106


RESULT 6
US-10-286-132A-76
; Sequence 76, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
;  APPLICANT: Zhou, Tong
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
;  TITLE OF INVENTION:  APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U7
;  CURRENT APPLICATION NUMBER: US/10/286,132A
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: US 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 76
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthet
US-10-286-132A-76

  Query Match             91.4%;  Score 509;  DB 4;  Length 213;
  Best Local Similarity   89.6%;  Pred. No. 3.9e-41;
  Matches   95;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||:||||||:|||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
              ||||| |||||||||:|||||||||||||||| ||:||||||||||
Db         61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYRTFGGGTKLEIK 106


RESULT 7
US-10-281-479A-24
; Sequence 24, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  Oshumi, Jun
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERA
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 21085.0029U6
;  CURRENT APPLICATION NUMBER: US/10/281,479A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 60/391,478
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthet
US-10-281-479A-24

  Query Match             91.4%;  Score 509;  DB 4;  Length 234;
  Best Local Similarity   89.6%;  Pred. No. 4.3e-41;
  Matches   95;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||:||||||:|||||||||| |||||||||
Db         22 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 81

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
              ||||| |||||||||:|||||||||||||||| ||:||||||||||
Db         82 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYRTFGGGTKLEIK 127


RESULT 8
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US-10-275-180A-24
; Sequence 24, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-275-180A-24

  Query Match             91.4%;  Score 509;  DB 4;  Length 234;
  Best Local Similarity   89.6%;  Pred. No. 4.3e-41;
  Matches   95;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||:||||||:|||||||||||| |||||||||
Db         22 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 81

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
              ||||| |||||||||:|||||||||||||||| ||:||||||||||
Db         82 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYRTFGGGTKLEIK 127


RESULT 9
US-10-286-132A-24
; Sequence 24, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
;  APPLICANT: Zhou, Tong
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
;  TITLE OF INVENTION:  APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U7
;  CURRENT APPLICATION NUMBER: US/10/286,132A
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: US 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-24

  Query Match             91.4%;  Score 509;  DB 4;  Length 234;
  Best Local Similarity   89.6%;  Pred. No. 4.3e-41;
  Matches   95;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||:||||||:|||||||||||| |||||||||
Db         22 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 81

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLYRSFGGGTKLEIK 106
              ||||| |||||||||:|||||||||||||||| ||:||||||||||
Db         82 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYRTFGGGTKLEIK 127


RESULT 10
US-10-842-011-6
; Sequence 6, Application US/10842011
; Publication No. US20050025763A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: 05882.0110.NPUS04
;  CURRENT APPLICATION NUMBER: US/10/842,011
;  CURRENT FILING DATE:  2004-05-07
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-842-011-6

  Query Match             87.2%;  Score 485.5;  DB 5;  Length 107;
  Best Local Similarity   86.9%;  Pred. No. 3.5e-39;
  Matches   93;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||| :||||||:|||||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGIAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||:|||||||||||||||| |  :||||||||||
Db         61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 107


RESULT 11
US-10-842-011-42
; Sequence 42, Application US/10842011
; Publication No. US20050025763A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: 05882.0110.NPUS04
;  CURRENT APPLICATION NUMBER: US/10/842,011
;  CURRENT FILING DATE:  2004-05-07
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-842-011-42

  Query Match             87.2%;  Score 485.5;  DB 5;  Length 107;
  Best Local Similarity   86.9%;  Pred. No. 3.5e-39;
  Matches   93;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||| :||||||:|||||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGIAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
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Db         61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 107


RESULT 12
US-10-842-011-47
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; Sequence 47, Application US/10842011
; Publication No. US20050025763A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: 05882.0110.NPUS04
;  CURRENT APPLICATION NUMBER: US/10/842,011
;  CURRENT FILING DATE:  2004-05-07
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-842-011-47

  Query Match             87.2%;  Score 485.5;  DB 5;  Length 107;
  Best Local Similarity   86.9%;  Pred. No. 3.5e-39;
  Matches   93;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||| :||||||:|||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGIAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
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Db         61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 107


RESULT 13
US-10-842-011-28
; Sequence 28, Application US/10842011
; Publication No. US20050025763A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: 05882.0110.NPUS04
;  CURRENT APPLICATION NUMBER: US/10/842,011
;  CURRENT FILING DATE:  2004-05-07
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-10-842-011-28

  Query Match             87.2%;  Score 485.5;  DB 5;  Length 127;
  Best Local Similarity   86.9%;  Pred. No. 4.2e-39;
  Matches   93;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||| :||||||:|||||||||| |||||||||
Db         21 DIVMTQSHKFMSTSVGDRVSITCKASQDVGIAVAWYQQKPGQSPKLLIYWASTRHTGVPD 80

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||:|||||||||||||||| |  :||||||||||
Db         81 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 127


RESULT 14
US-10-297-371A-8
; Sequence 8, Application US/10297371A
; Publication No. US20040131607A1
; GENERAL INFORMATION:
;  APPLICANT: Carroll, Michael C.
;  APPLICANT:  Moore, Jr., Francis D.
;  APPLICANT:  Hechtman, Herbert B.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
;  TITLE OF INVENTION:  IMMUNOGLOBULIN-MEDIATED REPERFUSION INJURY
;  FILE REFERENCE: 10861-024US1
;  CURRENT APPLICATION NUMBER: US/10/297,371A
;  CURRENT FILING DATE:  2004-01-02
;  PRIOR APPLICATION NUMBER: PCT/US01/18510
;  PRIOR FILING DATE: 2001-06-08
;  PRIOR APPLICATION NUMBER: US 60/210,272
;  PRIOR FILING DATE: 2000-06-08
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: 109
;   OTHER INFORMATION: Xaa = Unknown amino acid residue
US-10-297-371A-8

  Query Match             86.8%;  Score 483.5;  DB 4;  Length 115;
  Best Local Similarity   87.7%;  Pred. No. 5.8e-39;
  Matches   93;  Conservative    5;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          2 IQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPDR 61
              | :||||| |||||||||||||||||||:||||||:|||||||||| |||||||||
Db          1 IVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPDR 60

Qy         62 FTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
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Db         61 FTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPLTFGSGTKLEIK 106


RESULT 15
US-09-215-163-21
; Sequence 21, Application US/09215163
; Publication No. US20030170248A1
; GENERAL INFORMATION:
;  APPLICANT: STINSON, Jeffrey R.
;  APPLICANT: WONG, Hing
;  APPLICANT: O'BRIEN, ALISON
;  APPLICANT: SCHMITT, Clare K.
;  APPLICANT: MELTON-CELSA, Angela
;  TITLE OF INVENTION: HUMANIZED MONOCLONAL ANTIBODIES THAT PROTECT AGAINST
;  TITLE OF INVENTION: SHIGA TOXIN INDUCED DISEASE
;  FILE REFERENCE: 04995.0032-00000
;  CURRENT APPLICATION NUMBER: US/09/215,163
;  CURRENT FILING DATE: 1998-12-18
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: Shigella dysenteriae
US-09-215-163-21

  Query Match             84.8%;  Score 472.5;  DB 3;  Length 108;
  Best Local Similarity   84.1%;  Pred. No. 6.3e-38;
  Matches   90;  Conservative    6;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| ::|||| |||||||||||||||||:|||||| |||||| |||| |||||||||
Db          1 DIVMSQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQNPGQSPKFLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
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Db         61 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYSSYPLTFGAGTSLELK 107


Search completed: March 23, 2006, 01:17:10
Job time : 187.527 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:13:29 ; Search time 24.6512 Seconds
(without alignments)
123.078 Million cell updates/sec

Title: US-10-755-382-4
Perfect score: 557
Sequence: 1 EIQLTQSHKMMSTSVGDRVS.....FCQQYSLYRSFGGGTKLEIK 106

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	485.5	87.2	107	6	US-10-982-357-6	Sequence 6, Appli
2	485.5	87.2	107	6	US-10-982-357-42	Sequence 42, Appl
3	485.5	87.2	107	6	US-10-982-357-48	Sequence 48, Appl
4	485.5	87.2	127	6	US-10-982-357-28	Sequence 28, Appl
5	478.5	85.9	105	7	US-11-097-812-53	Sequence 53, Appl
6	467.5	83.9	108	7	US-11-097-812-45	Sequence 45, Appl
7	467.5	83.9	108	7	US-11-097-812-50	Sequence 50, Appl
8	462	82.9	108	7	US-11-097-812-52	Sequence 52, Appl
9	462	82.9	115	7	US-11-097-812-38	Sequence 38, Appl
10	447.5	80.3	127	6	US-10-839-799-27	Sequence 27, Appl
11	444.5	79.8	109	7	US-11-097-812-48	Sequence 48, Appl
12	442.5	79.4	109	7	US-11-097-812-37	Sequence 37, Appl
13	439.5	78.9	108	7	US-11-097-812-51	Sequence 51, Appl
14	438.5	78.7	109	7	US-11-097-812-42	Sequence 42, Appl
15	438.5	78.7	109	7	US-11-097-812-43	Sequence 43, Appl
16	438.5	78.7	109	7	US-11-097-812-54	Sequence 54, Appl
17	433.5	77.8	109	7	US-11-037-199-7	Sequence 7, Appli
18	427.5	76.8	110	7	US-11-195-095-2	Sequence 2, Appli
19	427	76.7	108	7	US-11-097-812-46	Sequence 46, Appl
20	426.5	76.6	112	7	US-11-173-071-4	Sequence 4, Appli
21	426.5	76.6	132	6	US-10-504-389A-53	Sequence 53, Appl
22	425.5	76.4	107	7	US-11-154-337-1	Sequence 1, Appli
23	425.5	76.4	107	7	US-11-182-908-1	Sequence 1, Appli
24	425.5	76.4	107	7	US-11-102-120-1	Sequence 1, Appli
25	425.5	76.4	107	7	US-11-223-361-1	Sequence 1, Appli
26	421.5	75.7	129	6	US-10-504-389A-47	Sequence 47, Appl
27	416	74.7	108	6	US-10-982-357-68	Sequence 68, Appl
28	414.5	74.4	107	6	US-10-982-357-44	Sequence 44, Appl
29	414.5	74.4	107	6	US-10-982-357-50	Sequence 50, Appl
30	413.5	74.2	107	7	US-11-226-325-130	Sequence 130, App
31	413.5	74.2	131	7	US-11-226-325-2	Sequence 2, Appli
32	409.5	73.5	109	7	US-11-097-812-113	Sequence 113, App
33	409	73.4	108	6	US-10-982-357-52	Sequence 52, Appl
34	408.5	73.3	107	6	US-10-982-357-4	Sequence 4, Appli
35	405.5	72.8	107	6	US-10-507-662-64	Sequence 64, Appl
36	405.5	72.8	107	7	US-11-226-325-134	Sequence 134, App
37	403.5	72.4	107	7	US-11-149-943-58	Sequence 58, Appl
38	401.5	72.1	107	6	US-10-507-662-63	Sequence 63, Appl
39	398.5	71.5	126	6	US-10-839-799-73	Sequence 73, Appl
40	398.5	71.5	126	6	US-10-839-799-75	Sequence 75, Appl
41	398	71.5	106	7	US-11-226-325-133	Sequence 133, App
42	391.5	70.3	126	6	US-10-839-799-63	Sequence 63, Appl
43	391.5	70.3	126	6	US-10-839-799-69	Sequence 69, Appl
44	390.5	70.1	126	6	US-10-839-799-81	Sequence 81, Appl
45	389.5	69.9	126	6	US-10-839-799-85	Sequence 85, Appl

ALIGNMENTS

RESULT 1
US-10-982-357-6
; Sequence 6, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/982,357
; CURRENT FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-982-357-6

Query Match 87.2%; Score 485.5; DB 6; Length 107;
Best Local Similarity 86.9%; Pred. No. 9.4e-39;
Matches 93; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

```
Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||| :||||||:|||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGIAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||:|||||||||||||||||  | :||||||||||
Db         61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 107
```

RESULT 2
US-10-982-357-42
; Sequence 42, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/982,357
; CURRENT FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-982-357-42

```
  Query Match             87.2%;  Score 485.5;  DB 6;  Length 107;
  Best Local Similarity   86.9%;  Pred. No. 9.4e-39;
  Matches   93;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||| :||||||:|||||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGIAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||:|||||||||||||||| |  :||||||||||
Db         61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 107


RESULT 3
US-10-982-357-48
; Sequence 48, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-48

  Query Match             87.2%;  Score 485.5;  DB 6;  Length 107;
  Best Local Similarity   86.9%;  Pred. No. 9.4e-39;
  Matches   93;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||| :||||||:|||||||||||| |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGIAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||:|||||||||||||||| |  :||||||||||
Db         61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 107


RESULT 4
US-10-982-357-28
; Sequence 28, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-28

  Query Match             87.2%;  Score 485.5;  DB 6;  Length 127;
  Best Local Similarity   86.9%;  Pred. No. 1.1e-38;
  Matches   93;  Conservative    6;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||| :||||||:|||||||||||| |||||||||
Db         21 DIVMTQSHKFMSTSVGDRVSITCKASQDVGIAVAWYQQKPGQSPKLLIYWASTRHTGVPD 80

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||:|||||||||||||||| |  :||||||||||
Db         81 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLEIK 127


RESULT 5
US-11-097-812-53
; Sequence 53, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
;   LENGTH: 105
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-53

  Query Match             85.9%;  Score 478.5;  DB 7;  Length 105;
  Best Local Similarity   85.7%;  Pred. No. 4.1e-38;
  Matches   90;  Conservative    8;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :: :||:|| |||||||||||||||||||:||||||:|||||||||||| |||||||||
Db          1 DVVMTQTHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLE 104
              ||||| |||||||||:|||||||||||||||| |  :||||||||
Db         61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPYTFGGGTKLE 105


RESULT 6
US-11-097-812-45
; Sequence 45, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
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;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-45

  Query Match             83.9%;  Score 467.5;  DB 7;  Length 108;
  Best Local Similarity   88.1%;  Pred. No. 4.5e-37;
  Matches   89;  Conservative    5;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          7 SHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPDRFTGSV 66
              ||| |||||||||||||||||||||:||||||:|||||||||||| ||||||||||||||
Db          6 SHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPDRFTGSG 65

Qy         67 SGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              |||||||||:||||||||||||||||| |  :|| |||||:|
Db         66 SGTDFTLTISNVQSEDLADYFCQQYSSYPLTFGAGTKLELK 106


RESULT 7
US-11-097-812-50
; Sequence 50, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-50

  Query Match             83.9%;  Score 467.5;  DB 7;  Length 108;
  Best Local Similarity   88.1%;  Pred. No. 4.5e-37;
  Matches   89;  Conservative    5;  Mismatches    6;  Indels    1;  Gaps    1;

Qy          7 SHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPDRFTGSV 66
              ||| |||||||||||||||||||||:||||||:|||||||||||| ||||||||||||||
Db          6 SHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPDRFTGSG 65

Qy         67 SGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              |||||||||:||||||||||||||||| |  :|| |||||:|
Db         66 SGTDFTLTISNVQSEDLADYFCQQYSSYPLTFGAGTKLELK 106


RESULT 8
US-11-097-812-52
; Sequence 52, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-52

  Query Match             82.9%;  Score 462;  DB 7;  Length 108;
  Best Local Similarity   85.0%;  Pred. No. 1.5e-36;
  Matches   91;  Conservative    7;  Mismatches    7;  Indels    2;  Gaps    2;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||:||||||:||||||||||  |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIY-ASTRHTGVPD 59

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||:||||||||||||||| |  :|| |||||:|
Db         60 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPLTFGAGTKLELK 106


RESULT 9
US-11-097-812-38
; Sequence 38, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-38

  Query Match             82.9%;  Score 462;  DB 7;  Length 115;
  Best Local Similarity   85.0%;  Pred. No. 1.6e-36;
  Matches   91;  Conservative    7;  Mismatches    7;  Indels    2;  Gaps    2;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||||| |||||||||||||||||||:||||||:||||||||||  |||||||||
Db          1 DIVMTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIY-ASTRHTGVPD 59

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
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                  ||||| |||||||||:|||||||||||||||| |  :|| |||||:|
Db          60 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPLTFGAGTKLELK 106


RESULT 10
US-10-839-799-27
; Sequence 27, Application US/10839799
; Publication No. US20050249726A1
;  GENERAL INFORMATION:
;       APPLICANT: OHTOMO, Toshihiko
;                  SATO, Koh
;                  TSUCHIYA, Masayuki
;       TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                           MEDULLOBLASTOMA CELLS
;       NUMBER OF SEQUENCES: 132
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/839,799
;            FILING DATE: 06-May-2004
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/646,265
;            FILING DATE: 09-SEP-1996
;            APPLICATION NUMBER: WO PCT/JP94/01763
;            FILING DATE: 19-OCT-1994
;            APPLICATION NUMBER: JP 5-291078
;            FILING DATE: 19-NOV-1993
;       ATTORNEY/AGENT INFORMATION:
;            NAME: WEGNER, Harold C.
;            REGISTRATION NUMBER: 25,258
;            REFERENCE/DOCKET NUMBER: 53466/184
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 27:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 127 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-839-799-27

  Query Match            80.3%;  Score 447.5;  DB 6;  Length 127;
  Best Local Similarity  81.3%;  Pred. No. 3.8e-35;
  Matches   87;  Conservative   10;  Mismatches    9;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| :||| | |||||||||:||||||:|||:||||||:|||||| |||  | |::||||
Db         21 DIVMTQSQKFMSTSVGDRVSVTCKASQNVGTNVAWYQQKPGQSPKPLIYSASYRYSGVPD 80

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||||||||||||||||: | |:||||||||||
Db         81 RFTGSGSGTDFTLTITNVQSEDLADYFCQQYNSYPRAFGGGTKLEIK 127


RESULT 11
US-11-097-812-48
; Sequence 48, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-48

  Query Match            79.8%;  Score 444.5;  DB 7;  Length 109;
  Best Local Similarity  81.3%;  Pred. No. 6.3e-35;
  Matches   87;  Conservative    9;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| |||| | |||||||||||||||||:|||:||||||:|||||||||  | |:|||||
Db          1 DIVLTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||:|:|||||||||||||| |  :|| |||||:|
Db         61 RFTGSGSGTDFTLTISNMQSEDLADYFCQQYSSYPLTFGAGTKLELK 107


RESULT 12
US-11-097-812-37
; Sequence 37, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: majority antibody sequence
US-11-097-812-37

  Query Match            79.4%;  Score 442.5;  DB 7;  Length 109;
```

```
  Best Local Similarity   82.2%;  Pred. No. 9.7e-35;
  Matches   88;  Conservative    6;  Mismatches   12;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :| |||| | |||||||||||||||| |||:||||||:||||||||||  | | |||||
Db          1 DIVLTQSPKFMSTSVGDRVSITCKASQSVGTAVAWYQQKPGQSPKLLIYSASNRETGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
              ||||| |||||||||:|||||||||||||||| |  :|| |||||:|
Db         61 RFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPLTFGAGTKLELK 107


RESULT 13
US-11-097-812-51
; Sequence 51, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-51

  Query Match             78.9%;  Score 439.5;  DB 7;  Length 108;
  Best Local Similarity   78.5%;  Pred. No. 1.8e-34;
  Matches   84;  Conservative   12;  Mismatches   10;  Indels    1;  Gaps    1;

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Db          1 DVAMTQTQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
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Db         61 RFTGSGSGTDFTLTISNMQSEDLADYFCQQYSSYPLTFGAGTKLELK 107


RESULT 14
US-11-097-812-42
; Sequence 42, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
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;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-42

  Query Match             78.7%;  Score 438.5;  DB 7;  Length 109;
  Best Local Similarity   78.5%;  Pred. No. 2.3e-34;
  Matches   84;  Conservative   12;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
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Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
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Db         61 RFTGSGSGTDFTLTISNMQSEDLADYFCQQYSSYPLTFGAGTKLELK 107


RESULT 15
US-11-097-812-43
; Sequence 43, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-43

  Query Match             78.7%;  Score 438.5;  DB 7;  Length 109;
  Best Local Similarity   78.5%;  Pred. No. 2.3e-34;
  Matches   84;  Conservative   12;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 EIQLTQSHKMMSTSVGDRVSITCKASQDVGTSVAWYQQRPGQSPKLLIYWTSTRHTGVPD 60
              :: :||: | |||||||||||||||:|||:||||||:||||||||||  | |:|||||
Db          1 DVVMTQTQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLLIYSASNRYTGVPD 60

Qy         61 RFTGSVSGTDFTLTITNVQSEDLADYFCQQYSLY-RSFGGGTKLEIK 106
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Search completed: March 23, 2006, 01:17:45
Job time : 25.6512 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:40:10 ; Search time 95.6849 Seconds
(without alignments)
50.511 Million cell updates/sec

Title: US-10-755-382-20
Perfect score: 51
Sequence: 1 KASQDVGTSVA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	51	100.0	11	4	AAB86084	Aab86084 H. pylori
3	51	100.0	11	4	AAB86052	Aab86052 H. pylori
4	51	100.0	11	8	ADM95102	Adm95102 Murine MN
5	51	100.0	11	8	ADM98311	Adm98311 Humanised
6	51	100.0	106	2	AAR97337	Aar97337 Humanised
7	51	100.0	106	2	AAR97335	Aar97335 Murine NE
8	51	100.0	106	4	AAB86108	Aab86108 H. pylori
9	51	100.0	106	4	AAB86070	Aab86070 H. pylori
10	51	100.0	106	8	ADM95097	Adm95097 Murine MN
11	51	100.0	106	8	ADM95100	Adm95100 Humanised
12	51	100.0	106	8	ADM98320	Adm98320 Murine MN
13	51	100.0	106	8	ADM98322	Adm98322 Humanised
14	51	100.0	115	6	ABR42756	Abr42756 Anti-CEA
15	51	100.0	232	6	ABG76490	Abg76490 Light cha
16	51	100.0	232	7	ADE64204	Ade64204 MN14LC pr
17	51	100.0	232	7	ADF60817	Adf60817 hMN-14 li
18	51	100.0	256	6	ABR42757	Abr42757 Anti-CEA
19	51	100.0	257	6	ABR42758	Abr42758 Anti-CEA
20	51	100.0	261	6	ABR42289	Abr42289 Diabody 6
21	51	100.0	261	6	ABR42754	Abr42754 Anti-CEA
22	51	100.0	261	6	ABR83645	Abr83645 hMN14-scF
23	51	100.0	262	6	ABR42295	Abr42295 Bispecifi
24	51	100.0	262	6	ABR42293	Abr42293 Bispecifi
25	51	100.0	262	6	ABR42298	Abr42298 Bispecifi
26	51	100.0	262	6	ABR42290	Abr42290 Diabody h
27	51	100.0	262	6	ABR42291	Abr42291 Bispecifi
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30	51	100.0	364	8	ADU26570	Adu26570 Chimeric
31	51	100.0	370	8	ADU26560	Adu26560 Chimeric
32	51	100.0	391	6	ABR83649	Abr83649 TS1 VL ch
33	51	100.0	443	6	ABG76488	Abg76488 Humanised
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35	51	100.0	669	9	ADY97271	Ady97271 Exemplary
36	48	94.1	11	5	AAU72806	Aau72806 TRA-8 lig
37	48	94.1	11	5	ABB07360	Abb07360 22A5 IgM
38	48	94.1	11	6	AAO29874	Aao29874 Mouse ant
39	48	94.1	11	7	ADJ79792	Adj79792 TRA-8 lig
40	48	94.1	11	9	ADZ45502	Adz45502 Murine fa
41	48	94.1	11	9	ADZ45548	Adz45548 Murine fa
42	48	94.1	105	8	ADT75007	Adt75007 Light cha
43	48	94.1	107	9	ADZ45501	Adz45501 Murine fa
44	48	94.1	108	2	AAY21817	Aay21817 Anti-STX1
45	48	94.1	108	8	ADT75006	Adt75006 Light cha
46	48	94.1	108	8	ADT75004	Adt75004 Light cha
47	48	94.1	108	8	ADT74999	Adt74999 Light cha
48	48	94.1	109	8	ADT75067	Adt75067 Light cha
49	48	94.1	115	5	ABB07359	Abb07359 22A5 IgM
50	48	94.1	115	8	ADT74992	Adt74992 Light cha
51	48	94.1	212	5	AAU72815	Aau72815 DNA encod
52	48	94.1	212	6	AAO29883	Aao29883 LM1 fusio
53	48	94.1	212	7	ADJ79836	Adj79836 LM1-type
54	48	94.1	213	5	AAU72810	Aau72810 TRA-8 lig
55	48	94.1	213	5	AAU72819	Aau72819 DNA encod
56	48	94.1	213	5	AAU72818	Aau72818 DNA encod
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61	48	94.1	213	6	AAO29884	Aao29884 LM3 fusio
62	48	94.1	213	6	AAO29887	Aao29887 LM6 fusio
63	48	94.1	213	6	AAO29885	Aao29885 LM4 fusio
64	48	94.1	213	7	ADJ79838	Adj79838 LM4-type
65	48	94.1	213	7	ADJ79837	Adj79837 LM3-type
66	48	94.1	213	7	ADJ79810	Adj79810 Humanized
67	48	94.1	213	7	ADJ79839	Adj79839 LM5-type
68	48	94.1	213	7	ADJ79840	Adj79840 LM6-type
69	48	94.1	234	5	AAU72802	Aau72802 TRA-8 lig
70	48	94.1	234	6	AAO29870	Aao29870 Mouse ant
71	48	94.1	234	7	ADJ79788	Adj79788 TRA-8 ant
72	48	94.1	238	5	AAE27930	Aae27930 Human C5E
73	48	94.1	238	6	ABB82839	Abb82839 Antibody
74	44	86.3	11	6	ABO10687	Abo10687 Murine J5
75	44	86.3	11	6	ABR44631	Abr44631 Murine J5
76	44	86.3	11	8	ADQ90755	Adq90755 Mouse com
77	44	86.3	11	8	ADU67883	Adu67883 Mouse ant
78	44	86.3	107	2	AAW47087	Aaw47087 Mouse J59
79	44	86.3	107	2	AAY90375	Aay90375 J591 mono
80	44	86.3	107	2	AAB36226	Aab36226 Monoclona
81	44	86.3	107	6	ABO10705	Abo10705 Variable
82	44	86.3	107	6	ABO10703	Abo10703 Variable
83	44	86.3	107	6	ABR44614	Abr44614 Murine de
84	44	86.3	107	6	ABR44647	Abr44647 Murine J5
85	44	86.3	107	6	ABR44649	Abr44649 Murine J5
86	44	86.3	107	6	ABR44616	Abr44616 Murine de
87	44	86.3	107	8	ADQ90771	Adq90771 Mouse J59
88	44	86.3	107	8	ADU67901	Adu67901 Mouse ant
89	44	86.3	107	8	ADU67899	Adu67899 Mouse ant
90	44	86.3	108	8	ADQ90773	Adq90773 Deimmunis
91	44	86.3	126	6	ABO10707	Abo10707 Variable
92	44	86.3	126	6	ABR44651	Abr44651 Murine J5
93	44	86.3	126	8	ADQ90779	Adq90779 Deimmunis
94	44	86.3	126	8	ADU67907	Adu67907 Mouse ant
95	44	86.3	233	8	ADU68009	Adu68009 Mouse ant
96	43	84.3	11	2	AAR85157	Aar85157 Human ONS
97	43	84.3	11	2	AAW59173	Aaw59173 Mouse PAF

98	43	84.3	11	2	AAW93477	Aaw93477 mAk TTC8
99	43	84.3	11	3	AAY79429	Aay79429 Tie2 rece
100	43	84.3	11	3	AAB19757	Aab19757 Erythropo
101	43	84.3	11	5	AAE19660	Aae19660 Human tum
102	43	84.3	11	5	AAE15816	Aae15816 Human mAb
103	43	84.3	11	8	ADL27477	Adl27477 CDR from
104	43	84.3	11	8	ADQ07649	Adq07649 Light cha
105	43	84.3	11	9	ADW47125	Adw47125 Anti-CD20
106	43	84.3	11	9	ADX26936	Adx26936 Murine mo
107	43	84.3	11	9	ADZ45506	Adz45506 Murine fa
108	43	84.3	11	9	ADZ45560	Adz45560 Murine fa
109	43	84.3	102	3	AAY56683	Aay56683 Humanized
110	43	84.3	104	2	AAW93481	Aaw93481 mAk TTC8
111	43	84.3	106	2	AAW85557	Aaw85557 Light cha
112	43	84.3	107	2	AAW01591	Aaw01591 Lead bind
113	43	84.3	107	2	AAW59168	Aaw59168 Mouse PAF
114	43	84.3	107	3	AAY79425	Aay79425 Tie2 rece
115	43	84.3	107	3	AAY56680	Aay56680 Anti-eryt
116	43	84.3	107	5	AAE19664	Aae19664 Human TNF
117	43	84.3	107	5	AAE19665	Aae19665 Human TNF
118	43	84.3	107	5	AAE15812	Aae15812 Human mAb
119	43	84.3	107	6	ABP97651	Abp97651 Amino aci
120	43	84.3	107	8	ADG25824	Adg25824 Anti-CD30
121	43	84.3	107	8	ADQ91074	Adq91074 Anti EpCA
122	43	84.3	107	9	ADX27047	Adx27047 Human gro
123	43	84.3	107	9	ADX27048	Adx27048 Human gro
124	43	84.3	108	2	AAW59169	Aaw59169 Mouse PAF
125	43	84.3	108	3	AAB19751	Aab19751 Erythropo
126	43	84.3	108	3	AAB19752	Aab19752 Erythropo
127	43	84.3	108	3	AAB19749	Aab19749 Erythropo
128	43	84.3	108	3	AAB19750	Aab19750 Erythropo
129	43	84.3	108	5	AAE19684	Aae19684 Mouse-hum
130	43	84.3	108	8	ADQ07679	Adq07679 Amino aci
131	43	84.3	108	8	ADT75005	Adt75005 Light cha
132	43	84.3	108	9	ADX27051	Adx27051 Murine hT
133	43	84.3	108	9	ADZ45505	Adz45505 Murine fa
134	43	84.3	109	2	AAR65164	Aar65164 Humanised
135	43	84.3	109	8	ADG25815	Adg25815 Anti-CD30
136	43	84.3	109	8	ADT75002	Adt75002 Light cha
137	43	84.3	109	8	ADT75008	Adt75008 Light cha
138	43	84.3	109	8	ADT74996	Adt74996 Light cha
139	43	84.3	109	8	ADT74997	Adt74997 Light cha
140	43	84.3	110	2	AAR65156	Aar65156 Murine PR
141	43	84.3	110	4	AAB49747	Aab49747 Anti-PF4/
142	43	84.3	112	3	AAB19746	Aab19746 Erythropo
143	43	84.3	118	2	AAR06253	Aar06253 Variable
144	43	84.3	123	2	AAR86317	Aar86317 Anti-IL-8
145	43	84.3	123	2	AAW23784	Aaw23784 Monoclona
146	43	84.3	123	2	AAW31574	Aaw31574 Anti IL-8
147	43	84.3	123	2	AAW42317	Aaw42317 Anti IL-8
148	43	84.3	123	2	AAW33739	Aaw33739 Anti IL-8
149	43	84.3	123	2	AAW69305	Aaw69305 Murine an
150	43	84.3	123	2	AAW40120	Aaw40120 Murine mo
151	43	84.3	123	2	AAY29437	Aay29437 Murine 5.
152	43	84.3	123	3	AAY77742	Aay77742 Murine an
153	43	84.3	123	3	AAB30299	Aab30299 Murine an
154	43	84.3	123	6	ABU13776	Abu13776 Mouse ant
155	43	84.3	123	6	ABU59489	Abu59489 Mouse ant
156	43	84.3	123	7	AAE39072	Aae39072 Murine 5.
157	43	84.3	126	2	AAR76667	Aar76667 Human/mur
158	43	84.3	126	2	AAR76670	Aar76670 Human/mur
159	43	84.3	126	2	AAR76671	Aar76671 Human/mur
160	43	84.3	126	2	AAR76673	Aar76673 Human/mur
161	43	84.3	126	2	AAR76675	Aar76675 Human/mur
162	43	84.3	126	2	AAR76679	Aar76679 Human/mur
163	43	84.3	126	2	AAR76680	Aar76680 Human/mur
164	43	84.3	126	2	AAR76678	Aar76678 Human/mur
165	43	84.3	126	2	AAR76666	Aar76666 Human/mur
166	43	84.3	126	2	AAR76665	Aar76665 Human/mur
167	43	84.3	126	2	AAR76668	Aar76668 Human/mur
168	43	84.3	126	2	AAR76672	Aar76672 Human/mur
169	43	84.3	126	2	AAR76674	Aar76674 Human/mur
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171	43	84.3	126	2	AAR76676	Aar76676 Human/mur
172	43	84.3	126	2	AAR76677	Aar76677 Human/mur
173	43	84.3	126	2	AAW04389	Aaw04389 Chimaeric
174	43	84.3	126	2	AAW04381	Aaw04381 Chimaeric
175	43	84.3	126	2	AAW04385	Aaw04385 Chimaeric
176	43	84.3	126	2	AAW04387	Aaw04387 Chimaeric
177	43	84.3	126	2	AAW04380	Aaw04380 Chimaeric
178	43	84.3	126	2	AAW04382	Aaw04382 Chimaeric
179	43	84.3	126	2	AAW04390	Aaw04390 Chimaeric
180	43	84.3	126	2	AAW04391	Aaw04391 Chimaeric
181	43	84.3	126	2	AAW04386	Aaw04386 Chimaeric
182	43	84.3	126	2	AAW04392	Aaw04392 Chimaeric
183	43	84.3	126	2	AAW04395	Aaw04395 Chimaeric
184	43	84.3	126	2	AAW04383	Aaw04383 Chimaeric
185	43	84.3	126	2	AAW04388	Aaw04388 Chimaeric
186	43	84.3	126	2	AAW04394	Aaw04394 Chimaeric
187	43	84.3	126	2	AAW04384	Aaw04384 Chimaeric
188	43	84.3	126	2	AAW04393	Aaw04393 Chimaeric
189	43	84.3	127	2	AAR76663	Aar76663 Murine ON
190	43	84.3	127	2	AAW04378	Aaw04378 Chimaeric
191	43	84.3	129	2	AAR27054	Aar27054 Anti-CEA
192	43	84.3	129	2	AAR30481	Aar30481 hCEA spec
193	43	84.3	129	7	ADC24962	Adc24962 Chimeric
194	43	84.3	129	7	ADK51717	Adk51717 Chimeric
195	43	84.3	132	2	AAR65169	Aar65169 PR1A3 ant
196	43	84.3	139	9	ADW47070	Adw47070 Light cha
197	43	84.3	139	9	ADW47076	Adw47076 Light cha
198	43	84.3	145	8	ADL27476	Adl27476 Amino aci
199	43	84.3	208	8	ADK90585	Adk90585 Grafted l
200	43	84.3	208	8	ADL13415	Adl13415 Mouse-der
201	43	84.3	214	5	AAE19696	Aae19696 Antibody
202	43	84.3	214	7	ADE01486	Ade01486 CDP870 li
203	43	84.3	214	8	ADF73140	Adf73140 Humanized
204	43	84.3	214	8	ADH34232	Adh34232 Anti-huma
205	43	84.3	214	8	ADQ07672	Adq07672 Amino aci
206	43	84.3	214	9	ADX27044	Adx27044 Murine hT
207	43	84.3	237	2	AAR86319	Aar86319 Anti-IL-8
208	43	84.3	237	2	AAW23786	Aaw23786 Chimeric
209	43	84.3	237	2	AAW31576	Aaw31576 Chimeric
210	43	84.3	237	2	AAW42319	Aaw42319 Murine va
211	43	84.3	237	2	AAW33741	Aaw33741 Chimeric
212	43	84.3	237	2	AAW69307	Aaw69307 Anti-IL-8
213	43	84.3	237	2	AAW40122	Aaw40122 Mab 5.12.
214	43	84.3	237	2	AAY29446	Aay29446 5.12.14 L
215	43	84.3	237	3	AAY77744	Aay77744 Chimeric
216	43	84.3	237	3	AAB30301	Aab30301 5-12-14 a
217	43	84.3	237	6	ABU13778	Abu13778 Mouse ant
218	43	84.3	237	6	ABU59491	Abu59491 Mouse ant
219	43	84.3	237	7	AAE39074	Aae39074 Murine 5.
220	43	84.3	241	2	AAW09435	Aaw09435 Anti-CD19
221	43	84.3	242	2	AAW09444	Aaw09444 Modified
222	43	84.3	248	2	AAW58826	Aaw58826 Human CD3
223	43	84.3	262	4	AAB70762	Aab70762 Single ch
224	43	84.3	267	8	ADR70320	Adr70320 Polioviru
225	43	84.3	268	8	ADR70385	Adr70385 Polioviru
226	43	84.3	268	8	ADR70386	Adr70386 Polioviru
227	43	84.3	269	2	AAR76682	Aar76682 Human ONS
228	43	84.3	269	2	AAW04397	Aaw04397 Chimaeric
229	43	84.3	450	3	AAY44991	Aay44991 M79scFv-i
230	43	84.3	451	8	ADR43339	Adr43339 scFv anti
231	43	84.3	456	3	AAY44992	Aay44992 M79scFv-i
232	43	84.3	492	8	ADQ91080	Adq91080 Antibody
233	43	84.3	492	8	ADQ91090	Adq91090 Antibody
234	43	84.3	492	8	ADQ91082	Adq91082 Antibody
235	43	84.3	492	8	ADQ91084	Adq91084 Antibody
236	43	84.3	492	8	ADQ91104	Adq91104 Antibody
237	43	84.3	492	8	ADQ91106	Adq91106 Antibody
238	43	84.3	492	8	ADQ91088	Adq91088 Antibody
239	43	84.3	492	8	ADQ91086	Adq91086 Antibody
240	43	84.3	492	8	ADQ91092	Adq91092 Antibody
241	43	84.3	492	8	ADQ91094	Adq91094 Antibody
242	43	84.3	492	8	ADQ91100	Adq91100 Antibody
243	43	84.3	492	8	ADQ91096	Adq91096 Antibody

244	43	84.3	492	8	ADQ91098	Adq91098	Antibody
245	43	84.3	492	8	ADQ91102	Adq91102	Antibody
246	43	84.3	492	8	ADQ91078	Adq91078	Bispecifi
247	42	82.4	11	2	AAR74946	Aar74946	L-CDR-1 o
248	42	82.4	11	2	AAW47101	Aaw47101	NMDA rece
249	42	82.4	11	2	AAW62189	Aaw62189	Mouse ant
250	42	82.4	11	2	AAW57577	Aaw57577	Chimeric
251	42	82.4	11	2	AAY02547	Aay02547	Artificia
252	42	82.4	11	2	AAW89629	Aaw89629	Mouse hum
253	42	82.4	11	3	AAY77515	Aay77515	Antibody
254	42	82.4	11	4	AAB76929	Aab76929	Human PTH
255	42	82.4	11	4	AAB76891	Aab76891	Human PTH
256	42	82.4	11	4	AAG67113	Aag67113	Amino aci
257	42	82.4	11	4	AAG64777	Aag64777	Anti-PTHr
258	42	82.4	11	4	AAG63395	Aag63395	Amino aci
259	42	82.4	11	4	AAB76910	Aab76910	Human PTH
260	42	82.4	11	5	AAE29174	Aae29174	Neuroacti
261	42	82.4	11	5	ABB95189	Abb95189	Human joi
262	42	82.4	11	5	AAM50680	Aam50680	Neuroacti
263	42	82.4	11	6	ABJ18539	Abj18539	Gangliosi
264	42	82.4	11	6	ABJ36660	Abj36660	Angiogene
265	42	82.4	11	7	ABU61656	Abu61656	Monoclona
266	42	82.4	11	8	ADO33856	Ado33856	Human par
267	42	82.4	11	8	ADU87705	Adu87705	Mouse Luc
268	42	82.4	11	8	ADU87721	Adu87721	Anti-CS1
269	42	82.4	12	5	AAE16427	Aae16427	Mouse ant
270	42	82.4	101	5	ABB07185	Abb07185	Mouse 04
271	42	82.4	101	8	ADI26686	Adi26686	Mouse ant
272	42	82.4	104	6	ABJ18565	Abj18565	Gangliosi
273	42	82.4	104	6	ABJ18568	Abj18568	Gangliosi
274	42	82.4	107	2	AAR55121	Aar55121	Mouse ant
275	42	82.4	107	2	AAR55125	Aar55125	Mouse-hum
276	42	82.4	107	2	AAR60300	Aar60300	Anti HIV
277	42	82.4	107	2	AAR60304	Aar60304	Chimeric
278	42	82.4	107	2	AAR74958	Aar74958	Immunoglo
279	42	82.4	107	8	ADU87730	Adu87730	Humanized
280	42	82.4	107	8	ADU87728	Adu87728	Light cha
281	42	82.4	107	8	ADU87734	Adu87734	VL region
282	42	82.4	107	8	ADU87693	Adu87693	Mouse Luc
283	42	82.4	107	8	ADU87736	Adu87736	Light cha
284	42	82.4	107	9	ADY52287	Ady52287	1H7 light
285	42	82.4	108	5	AAE16425	Aae16425	Mouse ant
286	42	82.4	108	8	ADG25826	Adg25826	Anti-CD30
287	42	82.4	108	8	ADI26698	Adi26698	Mouse ant
288	42	82.4	108	8	ADO57831	Ado57831	Human pro
289	42	82.4	108	8	ADQ76070	Adq76070	Heterorec
290	42	82.4	108	9	ADZ51185	Adz51185	Amino aci
291	42	82.4	108	9	ADZ42059	Adz42059	Human ant
292	42	82.4	108	9	AEB21880	Aeb21880	Human DC-
293	42	82.4	108	9	AEB21883	Aeb21883	Human DC-
294	42	82.4	108	9	AEB21886	Aeb21886	Human DC-
295	42	82.4	109	2	AAR30766	Aar30766	Light cha
296	42	82.4	109	8	ADG25817	Adg25817	Anti-CD30
297	42	82.4	109	8	ADI26471	Adi26471	Murine 14
298	42	82.4	109	8	ADT74991	Adt74991	Consensus
299	42	82.4	116	9	AEA88779	Aea88779	Murine SA
300	42	82.4	126	2	AAW65772	Aaw65772	Anti-huma
301	42	82.4	126	2	AAW62208	Aaw62208	Humanised
302	42	82.4	126	2	AAW62195	Aaw62195	Human ant
303	42	82.4	126	2	AAW77293	Aaw77293	HM1.24 an
304	42	82.4	126	2	AAY02553	Aay02553	Humanised
305	42	82.4	126	2	AAY02554	Aay02554	Humanised
306	42	82.4	126	2	AAY32769	Aay32769	Anti-HM1.
307	42	82.4	126	2	AAY05485	Aay05485	H chain V
308	42	82.4	126	5	AAM52353	Aam52353	L chain V
309	42	82.4	126	6	ABG71945	Abg71945	Human res
310	42	82.4	126	8	ADO60009	Ado60009	L chain V
311	42	82.4	127	8	ADU87781	Adu87781	Anti-CS1
312	42	82.4	128	8	ADI26718	Adi26718	Mouse ant
313	42	82.4	130	2	AAR74968	Aar74968	Anti-idio
314	42	82.4	131	2	AAW62187	Aaw62187	Mouse ant
315	42	82.4	131	2	AAY02545	Aay02545	L chain V
316	42	82.4	214	8	ADN97511	Adn97511	Artificia
317	42	82.4	223	1	AAP40031	Aap40031	Kappa ant
318	42	82.4	245	9	ADY52285	Ady52285	Single ch
319	42	82.4	247	1	AAP80155	Aap80155	FRs and C
320	42	82.4	247	1	AAP80156	Aap80156	Biosynthe
321	42	82.4	250	2	AAW02278	Aaw02278	741F8 ant
322	42	82.4	250	2	AAW29261	Aaw29261	Anti-c-er
323	42	82.4	250	2	AAW22400	Aaw22400	Single ch
324	42	82.4	250	2	AAW47012	Aaw47012	Single ch
325	42	82.4	250	2	AAW53168	Aaw53168	741F8 ant
326	42	82.4	250	2	AAW80422	Aaw80422	Anti-c-er
327	42	82.4	250	7	ABW00714	Abw00714	741F8 sFv
328	42	82.4	250	9	ADY60804	Ady60804	741F8 sFv
329	42	82.4	333	3	AAY70111	Aay70111	Anti-Her2
330	42	82.4	478	8	ADN97499	Adn97499	Artificia
331	42	82.4	509	8	ADN97517	Adn97517	Artificia
332	42	82.4	510	8	ADN97519	Adn97519	Artificia
333	42	82.4	510	8	ADN97501	Adn97501	Artificia
334	42	82.4	574	7	ADE52216	Ade52216	E3Bi prot
335	42	82.4	667	2	AAR39573	Aar39573	Sequence
336	42	82.4	700	8	ADN97521	Adn97521	Artificia
337	42	82.4	2606	7	ADE52217	Ade52217	pG1EN-EH3
338	42	82.4	2606	7	ADE52214	Ade52214	pG1EN-EH3
339	41	80.4	104	8	ADQ27999	Adq27999	Anti-DR5'
340	41	80.4	107	6	ABP58451	Abp58451	Humanised
341	41	80.4	107	6	ABP58449	Abp58449	Humanised
342	41	80.4	107	6	ABP58450	Abp58450	Humanised
343	41	80.4	108	7	ADD05266	Add05266	Female mo
344	41	80.4	108	8	ADM80357	Adm80357	Murine ho
345	41	80.4	109	8	ADQ27995	Adq27995	Anti-DR5
346	41	80.4	168	7	ABR84721	Abr84721	Vector pG
347	41	80.4	168	7	ABR84720	Abr84720	Vector pG
348	40	78.4	106	2	AAW31647	Aaw31647	Monoclona
349	40	78.4	107	2	AAR25723	Aar25723	Humanised
350	40	78.4	107	4	AAB69665	Aab69665	Murine Fd
351	40	78.4	107	4	AAB69666	Aab69666	Humanised
352	40	78.4	107	8	ADO47713	Ado47713	Humanised
353	40	78.4	107	8	ADO47768	Ado47768	Mouse Fd1
354	40	78.4	107	8	ADO47712	Ado47712	Mouse Fd1
355	40	78.4	107	8	ADO47769	Ado47769	Humanised
356	40	78.4	108	2	AAR82970	Aar82970	FB5 antib
357	40	78.4	108	2	AAR82975	Aar82975	FB5 human
358	40	78.4	108	2	AAR82976	Aar82976	FB5 human
359	40	78.4	109	2	AAY06382	Aay06382	Humanised
360	39	76.5	11	2	AAR85774	Aar85774	L-CDR-1 o
361	39	76.5	11	3	AAU78255	Aau78255	Mouse agg
362	39	76.5	11	7	ADD35391	Add35391	Human MAb
363	39	76.5	11	9	AEC20788	Aec20788	M-CSF spe
364	39	76.5	48	1	AAP60610	Aap60610	L-chain v
365	39	76.5	72	8	ADU04131	Adu04131	Human imm
366	39	76.5	103	7	ADF09997	Adf09997	Antibody
367	39	76.5	103	8	ADU04120	Adu04120	Human imm
368	39	76.5	107	2	AAR74959	Aar74959	Immunoglo
369	39	76.5	107	6	ABR55856	Abr55856	Anti-Her-
370	39	76.5	107	8	ADN49707	Adn49707	Light cha
371	39	76.5	107	8	ADU74383	Adu74383	Herceptin
372	39	76.5	109	2	AAR30762	Aar30762	Light cha
373	39	76.5	109	2	AAR47039	Aar47039	Sequence
374	39	76.5	109	7	ADD35373	Add35373	Human MAb
375	39	76.5	109	8	ADM46697	Adm46697	4D5 light
376	39	76.5	109	8	ADQ95004	Adq95004	Synthetic
377	39	76.5	109	9	ADX16938	Adx16938	Humanized
378	39	76.5	110	2	AAR93001	Aar93001	Humanised
379	39	76.5	110	2	AAR92999	Aar92999	Monoclona
380	39	76.5	120	2	AAR74969	Aar74969	Anti-idio
381	39	76.5	130	8	ADR10210	Adr10210	Human pro
382	39	76.5	130	9	ADV92508	Adv92508	Anti-her2
383	39	76.5	130	9	ADV98571	Adv98571	Novel chi
384	39	76.5	150	7	ADC24945	Adc24945	Mouse 19/
385	39	76.5	150	7	ADK51713	Adk51713	Murine 19
386	39	76.5	214	3	AAU78253	Aau78253	Mouse agg
387	39	76.5	214	3	AEA11265	Aea11265	Humanized
388	39	76.5	214	7	ADB85319	Adb85319	Light cha
389	39	76.5	214	7	ADC26166	Adc26166	Humanised

390	39	76.5	214	8	ADF11667	Adf11667 anti-HER2
391	39	76.5	214	8	ADH34510	Adh34510 Light cha
392	39	76.5	214	8	ADM31928	Adm31928 Humanised
393	39	76.5	214	9	ADX18554	Adx18554 VEGF-spec
394	39	76.5	214	9	ADX18559	Adx18559 VEGF-spec
395	39	76.5	214	9	ADX18555	Adx18555 VEGF-spec
396	39	76.5	214	9	ADX18562	Adx18562 VEGF-spec
397	39	76.5	214	9	ADX18553	Adx18553 VEGF-spec
398	39	76.5	214	9	ADX18557	Adx18557 VEGF-spec
399	39	76.5	214	9	ADX80641	Adx80641 Trastuzum
400	39	76.5	214	9	AEA13907	Aea13907 VEGF rela
401	39	76.5	214	9	AEA13911	Aea13911 VEGF rela
402	39	76.5	214	9	AEA13860	Aea13860 VEGF rela
403	39	76.5	214	9	AEA13915	Aea13915 VEGF rela
404	39	76.5	214	9	AEA13913	Aea13913 VEGF rela
405	39	76.5	214	9	AEA13909	Aea13909 VEGF rela
406	39	76.5	214	9	AEA13861	Aea13861 VEGF rela
407	39	76.5	214	9	AEA13912	Aea13912 VEGF rela
408	39	76.5	214	9	AEA13917	Aea13917 VEGF rela
409	39	76.5	214	9	AEC20772	Aec20772 M-CSF spe
410	39	76.5	232	7	ADF72730	Adf72730 Divalent
411	39	76.5	233	8	ADU23620	Adu23620 Human IgG
412	39	76.5	236	9	ADV92512	Adv92512 Anti-her2
413	39	76.5	236	9	ADV98575	Adv98575 Novel chi
414	39	76.5	237	2	AAR24047	Aar24047 Light cha
415	39	76.5	241	7	ADF72729	Adf72729 Monovalen
416	39	76.5	252	3	AAB28158	Aab28158 Human ant
417	39	76.5	255	7	ADF72734	Adf72734 His-tagge
418	39	76.5	255	8	ADM46842	Adm46842 Variant a
419	39	76.5	255	8	ADU23602	Adu23602 Phage dis
420	39	76.5	255	8	ADU23605	Adu23605 Phage dis
421	39	76.5	255	8	ADU23596	Adu23596 Phage dis
422	39	76.5	255	8	ADU23617	Adu23617 Human STO
423	39	76.5	256	8	ADM46844	Adm46844 Variant a
424	39	76.5	256	8	ADU23608	Adu23608 Phage dis
425	39	76.5	256	8	ADU23599	Adu23599 Phage dis
426	39	76.5	256	8	ADU23611	Adu23611 Phage dis
427	39	76.5	256	8	ADU23614	Adu23614 Phage dis
428	39	76.5	256	9	ADX16943	Adx16943 Light cha
429	39	76.5	513	4	AAB82924	Aab82924 Anti-HER2
430	39	76.5	665	9	ADV92518	Adv92518 FL/Fc/her
431	39	76.5	665	9	ADV98581	Adv98581 Novel chi
432	39	76.5	698	2	AAW83493	Aaw83493 4D5 Fab m
433	39	76.5	738	7	ADG87082	Adg87082 Fusion pr
434	39	76.5	739	7	ADG87089	Adg87089 Glucoamyl
435	39	76.5	739	7	ADG87090	Adg87090 Glucoamyl
436	39	76.5	740	7	ADG87091	Adg87091 Glucoamyl
437	39	76.5	741	7	ADG87093	Adg87093 Glucoamyl
438	39	76.5	742	7	ADG87092	Adg87092 Glucoamyl
439	39	76.5	743	7	ADG87072	Adg87072 Glucoamyl
440	39	76.5	743	7	ADG87094	Adg87094 Glucoamyl
441	38	74.5	11	6	ABO10767	Abo10767 Murine E9
442	38	74.5	11	6	ABP60556	Abp60556 Murine an
443	38	74.5	11	6	ABR44711	Abr44711 Murine E9
444	38	74.5	11	8	ADQ90853	Adq90853 Mouse com
445	38	74.5	11	8	ADU67981	Adu67981 Mouse ant
446	38	74.5	72	8	ADU04135	Adu04135 Murine im
447	38	74.5	107	6	ABO10753	Abo10753 Variable
448	38	74.5	107	6	ABR44697	Abr44697 Murine E9
449	38	74.5	107	8	ADQ90838	Adq90838 Mouse E99
450	38	74.5	107	8	ADU67966	Adu67966 Mouse ant
451	38	74.5	108	8	ADT75000	Adt75000 Light cha
452	38	74.5	109	8	ADO32156	Ado32156 Mouse ant
453	38	74.5	116	9	AEA88778	Aea88778 Murine SA
454	38	74.5	129	6	ABP60554	Abp60554 Murine an
455	38	74.5	214	3	AEA11267	Aea11267 Deamidate
456	37	72.5	11	5	ABB99229	Abb99229 CD45RO/RB
457	37	72.5	11	8	ADS52420	Ads52420 Fab targe
458	37	72.5	11	8	ADU87699	Adu87699 Mouse Luc
459	37	72.5	11	9	ADY80267	Ady80267 CDR1 from
460	37	72.5	11	9	AEB28745	Aeb28745 Human CDR
461	37	72.5	105	2	AAW00832	Aaw00832 Variable
462	37	72.5	105	2	AAW19018	Aaw19018 Anti-huma
463	37	72.5	106	9	AEA40019	Aea40019 Mouse ant
464	37	72.5	107	2	AAW86131	Aaw86131 Protein s
465	37	72.5	107	2	AAW86127	Aaw86127 Murine 70
466	37	72.5	107	2	AAW86129	Aaw86129 Protein s
467	37	72.5	107	5	ABB99226	Abb99226 Humanised
468	37	72.5	107	5	ABB99221	Abb99221 Part of c
469	37	72.5	107	5	ABB99225	Abb99225 Humanised
470	37	72.5	107	7	AAO24242	Aao24242 708 anti-
471	37	72.5	107	8	ADJ11300	Adj11300 Humanised
472	37	72.5	107	8	ADJ11298	Adj11298 Humanised
473	37	72.5	107	8	ADJ11296	Adj11296 Humanised
474	37	72.5	107	8	ADJ11293	Adj11293 Murine BH
475	37	72.5	107	8	ADU87691	Adu87691 Mouse Luc
476	37	72.5	107	9	ADY80256	Ady80256 Fragment
477	37	72.5	107	9	ADY80249	Ady80249 Fragment
478	37	72.5	107	9	ADY80255	Ady80255 Fragment
479	37	72.5	108	8	ADG25829	Adg25829 Anti-CD30
480	37	72.5	108	8	ADQ76072	Adq76072 Heterorec
481	37	72.5	108	9	ADZ51187	Adz51187 Amino aci
482	37	72.5	108	9	ADZ42061	Adz42061 Human ant
483	37	72.5	214	5	ABB99223	Abb99223 Chimeric
484	37	72.5	214	8	ADJ11307	Adj11307 BHA10 VL#
485	37	72.5	214	9	ADY80251	Ady80251 Amino aci
486	37	72.5	238	2	AAW14936	Aaw14936 2A2 Human
487	37	72.5	238	2	AAW14931	Aaw14931 Murine an
488	37	72.5	238	8	ADJ11352	Adj11352 BHA10 VL#
489	37	72.5	239	6	ABU07879	Abu07879 Venezuela
490	37	72.5	240	6	ABU07882	Abu07882 Venezuela
491	37	72.5	240	6	ABU07880	Abu07880 Venezuela
492	37	72.5	240	6	ABU07883	Abu07883 Venezuela
493	37	72.5	240	6	ABU07881	Abu07881 Venezuela
494	37	72.5	242	4	AAB31426	Aab31426 Protein u
495	37	72.5	244	2	AAY31610	Aay31610 Mucin Tn
496	37	72.5	244	4	AAB31425	Aab31425 Protein u
497	37	72.5	257	6	ABU07877	Abu07877 Anti-Vene
498	37	72.5	269	8	ADR28054	Adr28054 NPB polyp
499	37	72.5	296	8	ADS20752	Ads20752 SBP tagge
500	37	72.5	697	8	ADQ07403	Adq07403 hCBE11/hB
501	37	72.5	697	8	ADQ12180	Adq12180 Heavy cha
502	37	72.5	731	8	ADQ07407	Adq07407 hCBE11/hB
503	37	72.5	731	8	ADQ12184	Adq12184 huCBE11/h
504	36	70.6	11	2	AAW44178	Aaw44178 Monoclona
505	36	70.6	11	5	AAU72851	Aau72851 Anti-NKG2
506	36	70.6	11	6	ABJ26737	Abj26737 VEGF bind
507	36	70.6	11	7	ABR61514	Abr61514 Humanised
508	36	70.6	11	8	ADK18232	Adk18232 Mouse VEG
509	36	70.6	11	8	ADM78135	Adm78135 Human SJB
510	36	70.6	11	9	AEA39998	Aea39998 TNF resis
511	36	70.6	11	9	AEC07169	Aec07169 AF-20 ant
512	36	70.6	11	9	AEC20790	Aec20790 M-CSF spe
513	36	70.6	52	9	AEC20822	Aec20822 M-CSF spe
514	36	70.6	90	2	AAR80078	Aar80078 Mouse der
515	36	70.6	92	2	AAW95480	Aaw95480 Mouse der
516	36	70.6	92	2	AAW95476	Aaw95476 Mouse der
517	36	70.6	96	2	AAR54323	Aar54323 Anti-HIV
518	36	70.6	96	2	AAW01292	Aaw01292 VL region
519	36	70.6	96	3	AAY98253	Aay98253 Anti-gp12
520	36	70.6	96	3	AAY95144	Aay95144 Anti-gp12
521	36	70.6	99	9	AEC20815	Aec20815 M-CSF spe
522	36	70.6	107	2	AAR32129	Aar32129 Anti-IL2R
523	36	70.6	107	2	AAR78972	Aar78972 Light cha
524	36	70.6	107	2	AAR79247	Aar79247 Light cha
525	36	70.6	107	2	AAR79250	Aar79250 Light cha
526	36	70.6	107	2	AAW27121	Aaw27121 Murine an
527	36	70.6	107	5	AAU72850	Aau72850 Anti-NKG2
528	36	70.6	107	7	ADJ80369	Adj80369 Antibody
529	36	70.6	107	7	ADJ80370	Adj80370 FR homolo
530	36	70.6	107	9	AEA39996	Aea39996 TNF resis
531	36	70.6	107	9	AEC07207	Aec07207 Variant N
532	36	70.6	107	9	AEC07208	Aec07208 Variant N
533	36	70.6	107	9	AEC07209	Aec07209 Variant N
534	36	70.6	107	9	AEC07204	Aec07204 Murine NY
535	36	70.6	107	9	AEC07206	Aec07206 Variant N

536	36	70.6	108	2	AAR21310	Aar21310	Light cha
537	36	70.6	108	7	ABR61524	Abr61524	Humanised
538	36	70.6	108	7	ABR61520	Abr61520	Murine RS
539	36	70.6	108	8	ADI26702	Adi26702	Mouse ant
540	36	70.6	109	2	AAW18271	Aaw18271	PrP 37 li
541	36	70.6	109	2	AAW85910	Aaw85910	PrP 37 li
542	36	70.6	109	4	AAG65862	Aag65862	Anti-PrP
543	36	70.6	109	5	ABP51796	Abp51796	Anti-prio
544	36	70.6	109	6	ABJ26741	Abj26741	VEGF bind
545	36	70.6	109	6	ABU58877	Abu58877	Anti-prio
546	36	70.6	109	8	ADK18236	Adk18236	Mouse VEG
547	36	70.6	109	8	ADJ10235	Adj10235	Murine an
548	36	70.6	109	9	AEB92150	Aeb92150	Murine pr
549	36	70.6	109	9	AEC20891	Aec20891	M-CSF spe
550	36	70.6	109	9	AEC20808	Aec20808	Low+ mod
551	36	70.6	109	9	AEC20766	Aec20766	M-CSF spe
552	36	70.6	109	9	AEC20806	Aec20806	Low risk
553	36	70.6	109	9	AEC20897	Aec20897	Low+ mod
554	36	70.6	109	9	AEC20809	Aec20809	Low risk
555	36	70.6	109	9	AEC20892	Aec20892	M-CSF spe
556	36	70.6	109	9	AEC20893	Aec20893	M-CSF spe
557	36	70.6	117	2	AAW47582	Aaw47582	Human mon
558	36	70.6	117	9	AEB15493	Aeb15493	Anti-teta
559	36	70.6	124	9	AEC07178	Aec07178	NYR-1002
560	36	70.6	127	2	AAW44176	Aaw44176	Monoclona
561	36	70.6	130	8	ADI26651	Adi26651	Human ant
562	36	70.6	143	2	AAW19580	Aaw19580	Mouse ant
563	36	70.6	144	8	ADJ57086	Adj57086	3G4 antib
564	36	70.6	153	8	ADJ57089	Adj57089	3G4-2BVL-
565	36	70.6	201	8	ADN19871	Adn19871	Bacterial
566	36	70.6	214	6	ABP96757	Abp96757	TSH recep
567	36	70.6	214	6	ABP96766	Abp96766	TSH recep
568	36	70.6	214	6	ABP96758	Abp96758	TSH recep
569	36	70.6	214	6	ABP96762	Abp96762	TSH recep
570	36	70.6	214	6	ABP96761	Abp96761	TSH recep
571	36	70.6	214	6	ABP96765	Abp96765	TSH recep
572	36	70.6	214	9	AEC20765	Aec20765	M-CSF spe
573	36	70.6	214	9	AEC20776	Aec20776	M-CSF spe
574	36	70.6	233	7	ABR61526	Abr61526	Humanised
575	36	70.6	233	7	ABR61528	Abr61528	Humanised
576	36	70.6	240	6	ABJ26742	Abj26742	VEGF bind
577	36	70.6	240	8	ADK18245	Adk18245	Mouse VEG
578	36	70.6	252	5	AAU72863	Aau72863	P4-14 sin
579	36	70.6	257	5	AAU72869	Aau72869	P5-11 sin
580	36	70.6	283	8	ADF85426	Adf85426	V122scFv
581	36	70.6	480	7	ADH26642	Adh26642	Granzyme
582	36	70.6	499	5	AAU72872	Aau72872	3B10xP4-1
583	36	70.6	507	5	ABG71552	Abg71552	Murine sc
584	36	70.6	510	5	AAU72860	Aau72860	Human p53
585	36	70.6	572	2	AAR06023	Aar06023	Viral hae
586	36	70.6	572	5	AAU74678	Aau74678	Parainflu
587	36	70.6	737	8	ADS27986	Ads27986	Bacterial
588	36	70.6	938	8	ADR10306	Adr10306	Human pro
589	36	70.6	1604	4	AAB47327	Aab47327	FCTR4. 8/
590	35	68.6	11	2	AAR37602	Aar37602	hIL2R Ab
591	35	68.6	11	4	AAB60405	Aab60405	ErbB2-rea
592	35	68.6	11	4	AAB61590	Aab61590	Humanised
593	35	68.6	11	5	AAU72843	Aau72843	Anti-NKG2
594	35	68.6	11	8	ADE71459	Ade71459	Variable
595	35	68.6	11	8	ADJ88013	Adj88013	Murine VL
596	35	68.6	11	8	ADN12059	Adn12059	Humanised
597	35	68.6	11	8	ADP43334	Adp43334	Humanised
598	35	68.6	11	8	ADU07229	Adu07229	Human 4D4
599	35	68.6	11	8	ADT88296	Adt88296	Human IL-
600	35	68.6	11	9	AEA40603	Aea40603	Anti-VEGF
601	35	68.6	105	8	ADU07255	Adu07255	Human 7F3
602	35	68.6	105	8	ADT88322	Adt88322	Human IL-
603	35	68.6	107	2	AAR37610	Aar37610	B-B10 MAb
604	35	68.6	107	2	AAR37612	Aar37612	hIL2R Ab
605	35	68.6	107	2	AAR88845	Aar88845	Murine an
606	35	68.6	107	3	AAY90824	Aay90824	520C9 hyb
607	35	68.6	107	4	AAB62083	Aab62083	Murine MA
608	35	68.6	107	4	AAB62085	Aab62085	Humanised
609	35	68.6	107	4	AAB60398	Aab60398	Humanised
610	35	68.6	107	4	AAB60396	Aab60396	Mouse ant
611	35	68.6	107	4	AAB61583	Aab61583	Humanised
612	35	68.6	107	4	AAB61581	Aab61581	Murine 2C
613	35	68.6	107	5	AAU72842	Aau72842	Anti-NKG2
614	35	68.6	107	7	ADG75548	Adg75548	Human L1
615	35	68.6	107	7	ADG75554	Adg75554	Humanised
616	35	68.6	107	7	ADG75557	Adg75557	Humanised
617	35	68.6	107	7	ADG75555	Adg75555	Humanised
618	35	68.6	107	7	ADG75558	Adg75558	Humanised
619	35	68.6	107	7	ADG75561	Adg75561	Humanised
620	35	68.6	107	7	ADG75562	Adg75562	Humanised
621	35	68.6	107	7	ADG75559	Adg75559	Humanised
622	35	68.6	107	7	ADG75556	Adg75556	Humanised
623	35	68.6	107	7	ADG75560	Adg75560	Humanised
624	35	68.6	107	8	ADE71452	Ade71452	Humanise
625	35	68.6	107	8	ADE71450	Ade71450	Murine mo
626	35	68.6	107	8	ADJ88004	Adj88004	Murine mo
627	35	68.6	107	8	ADJ88006	Adj88006	Humanised
628	35	68.6	107	8	ADN12050	Adn12050	Variable
629	35	68.6	107	8	ADN12052	Adn12052	Variable
630	35	68.6	107	8	ADP43326	Adp43326	Humanised
631	35	68.6	107	8	ADP43324	Adp43324	Murine an
632	35	68.6	107	8	ADU07233	Adu07233	Human 4D4
633	35	68.6	107	8	ADU07249	Adu07249	Human 71A
634	35	68.6	107	8	ADU07243	Adu07243	Human 4D4
635	35	68.6	107	8	ADU07247	Adu07247	Human 7F3
636	35	68.6	107	8	ADT88314	Adt88314	Human IL-
637	35	68.6	107	8	ADT88316	Adt88316	Human IL-
638	35	68.6	107	8	ADT88310	Adt88310	Human IL-
639	35	68.6	107	8	ADT88300	Adt88300	Human IL-
640	35	68.6	107	9	ADX80643	Adx80643	Humanized
641	35	68.6	107	9	AEA40462	Aea40462	Anti-VEGF
642	35	68.6	107	9	AEA40457	Aea40457	Anti-VEGF
643	35	68.6	107	9	AEA40461	Aea40461	Anti-VEGF
644	35	68.6	108	1	AAP91381	Aap91381	Antibody
645	35	68.6	108	2	AAR04936	Aar04936	Sequence
646	35	68.6	108	3	AAB11392	Aab11392	Murine II
647	35	68.6	109	2	AAR37349	Aar37349	Sequence
648	35	68.6	109	2	AAY06388	Aay06388	Humanised
649	35	68.6	109	5	AAU74542	Aau74542	Human ant
650	35	68.6	109	5	AAU74543	Aau74543	Human ant
651	35	68.6	109	9	AEC20814	Aec20814	Low+ mod
652	35	68.6	109	9	AEC20812	Aec20812	Low risk
653	35	68.6	120	7	ADG75542	Adg75542	Humanised
654	35	68.6	127	2	AAW06447	Aaw06447	HuMc3 VL
655	35	68.6	127	2	AAW06443	Aaw06443	HuMc3 VL
656	35	68.6	147	2	AAW19576	Aaw19576	Mouse ant
657	35	68.6	165	6	ABU44442	Abu44442	Protein e
658	35	68.6	215	5	AAO22340	Aao22340	Anti-CD14
659	35	68.6	234	2	AAR47452	Aar47452	chiT84.12
660	35	68.6	235	2	AAR47449	Aar47449	T84.12 li
661	35	68.6	235	2	AAR47451	Aar47451	T84.12 L4
662	35	68.6	239	2	AAR34511	Aar34511	Fv(TU25).
663	35	68.6	240	2	AAR34510	Aar34510	Fv(TU27).
664	35	68.6	243	2	AAW02280	Aaw02280	520C9 ant
665	35	68.6	243	2	AAW53170	Aaw53170	520C9 ant
666	35	68.6	243	2	AAW80424	Aaw80424	520C9 sFv
667	35	68.6	243	7	ABW00716	Abw00716	520C9 sFv
668	35	68.6	243	9	ADY60808	Ady60808	520C9 sFv
669	35	68.6	246	2	AAR39569	Aar39569	Sequence
670	35	68.6	260	8	ADL65425	Adl65425	DNA gyras
671	35	68.6	267	4	AAU04944	Aau04944	Humanised
672	35	68.6	355	2	AAW35133	Aaw35133	R. pipien
673	35	68.6	374	4	AAG82285	Aag82285	S. epider
674	35	68.6	389	5	ABP38316	Abp38316	Staphyloc
675	35	68.6	389	8	ADS04809	Ads04809	Staphyloc
676	35	68.6	409	4	AAU04945	Aau04945	Humanised
677	35	68.6	510	5	AAU72859	Aau72859	6E5A7x4-7
678	35	68.6	534	2	AAR39571	Aar39571	Sequence
679	35	68.6	801	4	AAG81498	Aag81498	S. epider
680	35	68.6	801	6	ABU42839	Abu42839	Protein e
681	35	68.6	802	5	ABP38896	Abp38896	Staphyloc

682	35	68.6	802	8	ADS05509	Ads05509 Staphyloc
683	34	66.7	9	9	ADY52290	Ady52290 SP-3b1 li
684	34	66.7	11	2	AAR85502	Aar85502 ScFv(FRP)
685	34	66.7	11	6	ABO10711	Abo10711 Murine J4
686	34	66.7	11	6	ABR44655	Abr44655 Murine J4
687	34	66.7	11	8	ADE25849	Ade25849 Anti-alph
688	34	66.7	11	8	ADQ90783	Adq90783 Mouse com
689	34	66.7	11	8	ADU67911	Adu67911 Mouse ant
690	34	66.7	11	9	AEA44046	Aea44046 Anti-TPO
691	34	66.7	93	4	AAM99650	Aam99650 Human exc
692	34	66.7	93	4	AAM42465	Aam42465 Human kid
693	34	66.7	104	2	AAW26795	Aaw26795 Anti-gp54
694	34	66.7	106	2	AAR41234	Aar41234 Monoclona
695	34	66.7	106	8	ADQ90799	Adq90799 Mouse J41
696	34	66.7	106	8	ADQ90817	Adq90817 Deimmunis
697	34	66.7	107	6	ABO10737	Abo10737 Variable
698	34	66.7	107	6	ABO10727	Abo10727 Variable
699	34	66.7	107	6	ABO10739	Abo10739 Variable
700	34	66.7	107	6	ABO10741	Abo10741 Consensus
701	34	66.7	107	6	ABO10729	Abo10729 Variable
702	34	66.7	107	6	ABO10735	Abo10735 Variable
703	34	66.7	107	6	ABO10738	Abo10738 Variable
704	34	66.7	107	6	ABO10736	Abo10736 Variable
705	34	66.7	107	6	ABR44682	Abr44682 Murine J4
706	34	66.7	107	6	ABR44618	Abr44618 Murine J4
707	34	66.7	107	6	ABR44624	Abr44624 Murine J4
708	34	66.7	107	6	ABR44680	Abr44680 Murine J4
709	34	66.7	107	6	ABR44620	Abr44620 Murine J4
710	34	66.7	107	6	ABR44622	Abr44622 Murine J4
711	34	66.7	107	6	ABR44623	Abr44623 Murine J4
712	34	66.7	107	6	ABR44625	Abr44625 Murine J4
713	34	66.7	107	6	ABR44685	Abr44685 Murine J4
714	34	66.7	107	6	ABR44617	Abr44617 Murine J4
715	34	66.7	107	6	ABR44673	Abr44673 Murine J4
716	34	66.7	107	6	ABR44683	Abr44683 Murine J4
717	34	66.7	107	6	ABR44621	Abr44621 Murine J4
718	34	66.7	107	6	ABR44679	Abr44679 Murine J4
719	34	66.7	107	6	ABR44681	Abr44681 Murine J4
720	34	66.7	107	6	ABR44671	Abr44671 Murine J4
721	34	66.7	107	7	ADC27435	Adc27435 TMEFF2#19
722	34	66.7	107	8	ADE25857	Ade25857 Anti-alph
723	34	66.7	107	8	ADQ90815	Adq90815 Deimmunis
724	34	66.7	107	8	ADQ90801	Adq90801 Deimmunis
725	34	66.7	107	8	ADQ90819	Adq90819 Deimmunis
726	34	66.7	107	8	ADQ90813	Adq90813 Deimmunis
727	34	66.7	107	8	ADQ90814	Adq90814 Deimmunis
728	34	66.7	107	8	ADQ90816	Adq90816 Deimmunis
729	34	66.7	107	8	ADU67941	Adu67941 Mouse ant
730	34	66.7	107	8	ADU67942	Adu67942 Mouse ant
731	34	66.7	107	8	ADU67944	Adu67944 Mouse ant
732	34	66.7	107	8	ADU67929	Adu67929 Mouse ant
733	34	66.7	107	8	ADU67947	Adu67947 Mouse ant
734	34	66.7	107	8	ADU67943	Adu67943 Mouse ant
735	34	66.7	107	8	ADU67945	Adu67945 Mouse ant
736	34	66.7	107	8	ADU67927	Adu67927 Mouse ant
737	34	66.7	108	7	ADC27461	Adc27461 Humanised
738	34	66.7	108	7	ADC27465	Adc27465 Humanised
739	34	66.7	108	7	ADC27463	Adc27463 Humanised
740	34	66.7	108	9	AEB21882	Aeb21882 Human DC-
741	34	66.7	109	9	AEC20890	Aec20890 M-CSF spe
742	34	66.7	115	9	AEA44096	Aea44096 Anti-TPO
743	34	66.7	126	1	AAP90479	Aap90479 Chimeric
744	34	66.7	126	2	AAR04388	Aar04388 Colon Can
745	34	66.7	126	3	AAY57053	Aay57053 Antibody
746	34	66.7	126	3	AAY90721	Aay90721 CC92 VL r
747	34	66.7	126	4	AAU02140	Aau02140 Mouse DNA
748	34	66.7	126	7	ADK66840	Adk66840 Mouse CC9
749	34	66.7	240	2	AAR85494	Aar85494 ErbB-2-sp
750	34	66.7	240	2	AAW05134	Aaw05134 Single ch
751	34	66.7	240	2	AAW26799	Aaw26799 Anti-gp54
752	34	66.7	241	2	AAR26979	Aar26979 Fv heavy
753	34	66.7	330	7	ADC23777	Adc23777 Protein s
754	34	66.7	330	8	ADH35878	Adh35878 Chemical
755	34	66.7	330	8	ADG93579	Adg93579 Nitrilase
756	34	66.7	330	8	ADI62176	Adi62176 Nitrilase
757	34	66.7	330	8	ADI64297	Adi64297 Nitrilase
758	34	66.7	344	5	ABP74124	Abp74124 Human TRI
759	34	66.7	461	2	AAR85508	Aar85508 Leader-sc
760	34	66.7	530	2	AAR95053	Aar95053 scFv(FRP5
761	34	66.7	565	4	AAU36274	Aau36274 Pseudomon
762	34	66.7	565	6	ABU38443	Abu38443 Protein e
763	34	66.7	581	9	ADV11594	Adv11594 CD46/FRP5
764	34	66.7	593	7	ABO76528	Abo76528 Pseudomon
765	34	66.7	615	2	AAR95056	Aar95056 GAL4-DT-s
766	34	66.7	617	2	AAR95057	Aar95057 GAL4-DT-s
767	34	66.7	637	2	AAR26982	Aar26982 (FRP5)-ET
768	34	66.7	651	2	AAW05136	Aaw05136 scFv(FRP5
769	34	66.7	698	4	AAB65702	Aab65702 Novel pro
770	34	66.7	698	8	ADI29311	Adi29311 Human MAR
771	34	66.7	699	2	AAW05138	Aaw05138 scFv(FRP5
772	34	66.7	711	2	AAR26980	Aar26980 Fv(FRP5)-
773	34	66.7	892	2	AAW05140	Aaw05140 scFv2(225
774	34	66.7	892	2	AAW05143	Aaw05143 scFv2(FRP
775	34	66.7	892	2	AAW05139	Aaw05139 scFv2(FRP
776	34	66.7	895	2	AAW05142	Aaw05142 scFv2(FRP
777	34	66.7	899	2	AAW05144	Aaw05144 scFv2(FRP
778	34	66.7	911	5	ABP29744	Abp29744 Streptoco
779	34	66.7	911	5	ABP26657	Abp26657 Streptoco
780	34	66.7	975	4	AAE07144	Aae07144 Murine Ki
781	34	66.7	975	4	AAE07148	Aae07148 Mutant mu
782	34	66.7	975	9	AEA19289	Aea19289 Mouse c-k
783	34	66.7	975	9	AEA80342	Aea80342 Mouse KIT
784	34	66.7	1020	2	AAW05141	Aaw05141 scFv2(FRP
785	34	66.7	2406	4	ABB64198	Abb64198 Drosophil
786	33	64.7	11	2	AAY26990	Aay26990 CDR1 doma
787	33	64.7	11	3	AAY59314	Aay59314 Light cha
788	33	64.7	11	4	AAB37955	Aab37955 Anti-EGFR
789	33	64.7	11	5	AAU77787	Aau77787 Mouse lig
790	33	64.7	11	8	ADE25848	Ade25848 Anti-alph
791	33	64.7	11	8	ADR15158	Adr15158 Mouse ant
792	33	64.7	11	8	ADR15177	Adr15177 Anti-prot
793	33	64.7	11	8	ADQ80414	Adq80414 Murine an
794	33	64.7	11	8	ADR43405	Adr43405 CDR with
795	33	64.7	11	8	ADR31550	Adr31550 Murine TE
796	33	64.7	11	9	AEC08126	Aec08126 Murine mA
797	33	64.7	89	2	AAW90047	Aaw90047 B. stearo
798	33	64.7	106	2	AAW71241	Aaw71241 Light cha
799	33	64.7	107	2	AAR50190	Aar50190 Light cha
800	33	64.7	107	2	AAW08949	Aaw08949 Kappa lig
801	33	64.7	107	2	AAW08948	Aaw08948 Kappa lig
802	33	64.7	107	2	AAW21938	Aaw21938 Variable
803	33	64.7	107	2	AAW21939	Aaw21939 Variable
804	33	64.7	107	2	AAY05268	Aay05268 Antibody
805	33	64.7	107	2	AAY05270	Aay05270 Antibody
806	33	64.7	107	2	AAY05271	Aay05271 Antibody
807	33	64.7	107	2	AAY05269	Aay05269 Antibody
808	33	64.7	107	2	AAY26979	Aay26979 Light cha
809	33	64.7	107	3	AAY70604	Aay70604 Vkappa re
810	33	64.7	107	5	ABG98273	Abg98273 Murine an
811	33	64.7	107	5	ABG98281	Abg98281 Murine an
812	33	64.7	107	5	ABG98274	Abg98274 Murine an
813	33	64.7	107	5	ABG98275	Abg98275 Murine an
814	33	64.7	107	5	ABG98276	Abg98276 Murine an
815	33	64.7	107	6	ABR54894	Abr54894 Light cha
816	33	64.7	107	7	ADG75549	Adg75549 Human L1
817	33	64.7	107	7	AAO24247	Aao24247 708 anti-
818	33	64.7	107	8	ADE25856	Ade25856 Anti-alph
819	33	64.7	107	8	ADR43467	Adr43467 Light cha
820	33	64.7	107	8	ADR43401	Adr43401 Murine an
821	33	64.7	107	8	ADR43469	Adr43469 Light cha
822	33	64.7	107	8	ADR43465	Adr43465 Light cha
823	33	64.7	107	8	ADR43461	Adr43461 Light cha
824	33	64.7	107	8	ADR43457	Adr43457 Light cha
825	33	64.7	107	8	ADR43463	Adr43463 Heavy cha
826	33	64.7	107	8	ADR31610	Adr31610 Murine TE
827	33	64.7	107	8	ADR31608	Adr31608 Murine TE

828	33	64.7	107	8	ADR31546	Adr31546	Murine TE
829	33	64.7	107	8	ADR31602	Adr31602	Murine TE
830	33	64.7	107	8	ADR31612	Adr31612	Murine TE
831	33	64.7	107	8	ADR31614	Adr31614	Murine TE
832	33	64.7	107	8	ADR31606	Adr31606	Murine TE
833	33	64.7	107	8	ADR87520	Adr87520	Mouse ant
834	33	64.7	107	9	ADY31687	Ady31687	Anti-IL9
835	33	64.7	107	9	ADY31675	Ady31675	Anti-IL9
836	33	64.7	107	9	AEA48149	Aea48149	Mouse ant
837	33	64.7	107	9	AEA48156	Aea48156	Mouse ant
838	33	64.7	107	9	AEA48154	Aea48154	Mouse ant
839	33	64.7	107	9	AEA48155	Aea48155	Mouse ant
840	33	64.7	107	9	AEB13698	Aeb13698	Human ant
841	33	64.7	107	9	AEB13703	Aeb13703	Human ant
842	33	64.7	107	9	AEB13704	Aeb13704	Human ant
843	33	64.7	107	9	AEB13702	Aeb13702	Human ant
844	33	64.7	107	9	AEB19270	Aeb19270	IgG kappa
845	33	64.7	107	9	AEC07205	Aec07205	Variant N
846	33	64.7	107	9	AEC08122	Aec08122	Murine mA
847	33	64.7	107	9	AEC08190	Aec08190	Anti-IgE
848	33	64.7	107	9	AEC08184	Aec08184	Anti-IgE
849	33	64.7	107	9	AEC08182	Aec08182	Anti-IgE
850	33	64.7	107	9	AEC08186	Aec08186	Anti-IgE
851	33	64.7	107	9	AEC08188	Aec08188	Anti-IgE
852	33	64.7	107	9	AEC08178	Aec08178	Anti-IgE
853	33	64.7	108	7	ADG75665	Adg75665	Humanised
854	33	64.7	108	7	ADG75543	Adg75543	Humanised
855	33	64.7	108	8	ADR15138	Adr15138	Mouse ant
856	33	64.7	110	2	AAR93005	Aar93005	Monoclona
857	33	64.7	110	2	AAR93007	Aar93007	Humanised
858	33	64.7	112	2	AAR43688	Aar43688	PB1.3 lig
859	33	64.7	124	2	AAR33307	Aar33307	MaE13 lig
860	33	64.7	124	3	AAY85195	Aay85195	Light cha
861	33	64.7	124	9	AEC07213	Aec07213	NYDIVK1 a
862	33	64.7	126	2	AAR43691	Aar43691	PB1.3/Hum
863	33	64.7	126	2	AAR43692	Aar43692	PB1.3/Hum
864	33	64.7	126	2	AAR62675	Aar62675	CY1748RLB
865	33	64.7	126	2	AAR62676	Aar62676	CY1748RLC
866	33	64.7	126	2	AAR62677	Aar62677	CY1748RLD
867	33	64.7	126	2	AAR62674	Aar62674	CY1748RLA
868	33	64.7	127	2	AAR50192	Aar50192	Light cha
869	33	64.7	127	2	AAR50187	Aar50187	Light cha
870	33	64.7	127	2	AAR50191	Aar50191	Light cha
871	33	64.7	127	2	AAW08945	Aaw08945	Kappa lig
872	33	64.7	127	2	AAW08941	Aaw08941	Kappa lig
873	33	64.7	127	2	AAW08946	Aaw08946	Kappa lig
874	33	64.7	127	2	AAW08943	Aaw08943	Kappa lig
875	33	64.7	127	2	AAY26981	Aay26981	Light cha
876	33	64.7	127	2	AAY26980	Aay26980	Light cha
877	33	64.7	127	2	AAY26982	Aay26982	Light cha
878	33	64.7	127	8	ADR87522	Adr87522	Humanised
879	33	64.7	127	8	ADR87524	Adr87524	Humanised
880	33	64.7	127	8	ADR87526	Adr87526	Humanised
881	33	64.7	131	2	AAR04387	Aar04387	Colon Can
882	33	64.7	131	3	AAY57052	Aay57052	Amino aci
883	33	64.7	131	3	AAY90720	Aay90720	CC83 VL r
884	33	64.7	131	4	AAU02139	Aau02139	Mouse par
885	33	64.7	131	7	ADK66826	Adk66826	Mouse CC8
886	33	64.7	133	2	AAW21936	Aaw21936	Variable
887	33	64.7	133	2	AAW21934	Aaw21934	Variable
888	33	64.7	133	2	AAW21933	Aaw21933	Variable
889	33	64.7	133	2	AAY05266	Aay05266	Antibody
890	33	64.7	133	2	AAY05264	Aay05264	Antibody
891	33	64.7	133	2	AAY05263	Aay05263	Antibody
892	33	64.7	133	5	ABG98315	Abg98315	Murine hu
893	33	64.7	133	5	ABG98314	Abg98314	Murine hu
894	33	64.7	133	5	ABG98317	Abg98317	Murine wi
895	33	64.7	144	8	ADU02979	Adu02979	Novel hum
896	33	64.7	165	7	ADG76341	Adg76341	Human Inc
897	33	64.7	214	8	ADT55440	Adt55440	Anti IgE
898	33	64.7	214	9	AEA48169	Aea48169	Mouse ant
899	33	64.7	214	9	AEA48166	Aea48166	Mouse ant
900	33	64.7	214	9	AEB56306	Aeb56306	Anti-IgE
901	33	64.7	234	4	AAB36208	Aab36208	Human imm
902	33	64.7	234	8	ADS14301	Ads14301	EGFR ligh
903	33	64.7	236	8	ADP44635	Adp44635	Murine an
904	33	64.7	236	9	AEA60461	Aea60461	Mouse ant
905	33	64.7	240	2	AAW05133	Aaw05133	Single ch
906	33	64.7	240	2	AAW71243	Aaw71243	scFv comp
907	33	64.7	245	3	AAY70605	Aay70605	scFv frag
908	33	64.7	254	6	ABU41359	Abu41359	Protein e
909	33	64.7	256	8	ADN47469	Adn47469	Thermococ
910	33	64.7	268	8	ADR70319	Adr70319	Polioviru
911	33	64.7	283	5	ABB78313	Abb78313	Amino aci
912	33	64.7	307	8	ADX88979	Adx88979	Plant ful
913	33	64.7	310	8	ADN99728	Adn99728	Novel hum
914	33	64.7	310	8	ADN99620	Adn99620	Novel hum
915	33	64.7	315	8	ADT60896	Adt60896	Plant pol
916	33	64.7	386	3	AAY58170	Aay58170	Human hyd
917	33	64.7	415	6	ABM71060	Abm71060	Staphyloc
918	33	64.7	488	4	AAG78335	Aag78335	Maize def
919	33	64.7	502	3	AAY97031	Aay97031	N-acetylg
920	33	64.7	545	8	ADX90096	Adx90096	Plant ful
921	33	64.7	558	1	AAP50501	Aap50501	Sequence
922	33	64.7	572	1	AAP94799	Aap94799	Perdue st
923	33	64.7	572	1	AAP94800	Aap94800	Parainflu
924	33	64.7	572	2	AAR31957	Aar31957	Sequence
925	33	64.7	572	2	AAR79037	Aar79037	PI-3 haem
926	33	64.7	609	2	AAR21414	Aar21414	Vibrolysi
927	33	64.7	609	2	AAW86187	Aaw86187	Vibriolys
928	33	64.7	609	6	AAO16252	Aao16252	Vibrio pr
929	33	64.7	609	8	ADM66774	Adm66774	Vibrio sp
930	33	64.7	610	1	AAP93578	Aap93578	Extracell
931	33	64.7	651	2	AAW05135	Aaw05135	scFv(225)
932	33	64.7	730	9	AEC08410	Aec08410	ScFv-B2-F
933	33	64.7	730	9	AEC08411	Aec08411	ScFv-B2-F
934	33	64.7	735	8	ADS42152	Ads42152	Bacterial
935	33	64.7	761	9	AEC08409	Aec08409	ScFv-A12A
936	33	64.7	762	9	AEC08408	Aec08408	ScFv-B2-F
937	33	64.7	792	2	AAR59765	Aar59765	Extracell
938	33	64.7	962	7	ABW02045	Abw02045	Maize pul
939	32	62.7	11	2	AAY05011	Aay05011	Tumour an
940	32	62.7	11	2	AAY05009	Aay05009	Tumour an
941	32	62.7	11	3	AAY44589	Aay44589	Mouse ant
942	32	62.7	11	7	ADC82740	Adc82740	CDR regio
943	32	62.7	11	7	ADC82736	Adc82736	CDR regio
944	32	62.7	11	8	ADR15159	Adr15159	Mouse ant
945	32	62.7	11	9	AEA46174	Aea46174	Apolipopr
946	32	62.7	11	9	AEA45349	Aea45349	Apolipopr
947	32	62.7	13	2	AAW86053	Aaw86053	Peptide f
948	32	62.7	13	2	AAW86067	Aaw86067	Peptide f
949	32	62.7	14	2	AAR75031	Aar75031	Replaceme
950	32	62.7	71	9	ABM92278	Abm92278	M. xanthu
951	32	62.7	95	2	AAW18269	Aaw18269	PrP 81 li
952	32	62.7	95	2	AAW85908	Aaw85908	PrP 81 li
953	32	62.7	95	4	AAG65860	Aag65860	Anti-PrP
954	32	62.7	95	5	ABP51794	Abp51794	Anti-prio
955	32	62.7	95	6	ABU58875	Abu58875	Anti-prio
956	32	62.7	95	8	ADJ10233	Adj10233	Murine an
957	32	62.7	95	9	AEB92148	Aeb92148	Murine pr
958	32	62.7	106	5	ABG76546	Abg76546	HCV E1 an
959	32	62.7	107	2	AAW86138	Aaw86138	Protein s
960	32	62.7	107	2	AAW86142	Aaw86142	Protein s
961	32	62.7	107	2	AAW86136	Aaw86136	Protein s
962	32	62.7	107	2	AAW86140	Aaw86140	Protein s
963	32	62.7	108	2	AAW48863	Aaw48863	Murine mo
964	32	62.7	108	2	AAW48864	Aaw48864	Chimeric
965	32	62.7	108	3	AAY44587	Aay44587	Mouse ant
966	32	62.7	108	8	ADR15139	Adr15139	Mouse ant
967	32	62.7	108	9	AEA37669	Aea37669	Mouse CD4
968	32	62.7	109	2	AAR13658	Aar13658	Murine OK
969	32	62.7	109	2	AAW18270	Aaw18270	PrP 28 li
970	32	62.7	109	2	AAW26797	Aaw26797	Anti-gp54
971	32	62.7	109	2	AAW85909	Aaw85909	PrP 28 li
972	32	62.7	109	4	AAG65861	Aag65861	Anti-PrP
973	32	62.7	109	5	ABP51795	Abp51795	Anti-prio

974	32	62.7	109	6	ABU58876	Abu58876 Anti-prio
975	32	62.7	109	8	ABG75337	Abg75337 Antibody
976	32	62.7	109	8	ADJ10234	Adj10234 Murine an
977	32	62.7	109	9	AEB92149	Aeb92149 Murine pr
978	32	62.7	110	6	ADA89264	Ada89264 Human ant
979	32	62.7	110	7	ADD28335	Add28335 Human het
980	32	62.7	110	9	ADV86848	Adv86848 Venezuela
981	32	62.7	112	5	AAM50879	Aam50879 Anti-bovi
982	32	62.7	129	2	AAW09815	Aaw09815 PelB-VL34
983	32	62.7	132	2	AAR56961	Aar56961 MAb A33 l
984	32	62.7	135	3	AAY44599	Aay44599 Mouse lig
985	32	62.7	140	8	ADG32252	Adg32252 Mutant B_
986	32	62.7	191	7	ABO64839	Abo64839 Klebsiell
987	32	62.7	212	7	ADB64360	Adb64360 Human pro
988	32	62.7	236	9	ADW95680	Adw95680 Mouse ant
989	32	62.7	236	9	ADX15685	Adx15685 Mouse ant
990	32	62.7	237	2	AAW95440	Aaw95440 A33/212 s
991	32	62.7	237	3	AAY44595	Aay44595 EscFv#125
992	32	62.7	237	3	AAY54836	Aay54836 Linked fu
993	32	62.7	241	2	AAW95441	Aaw95441 A33/218 s
994	32	62.7	241	3	AAY54837	Aay54837 Linked fu
995	32	62.7	243	3	AAY44596	Aay44596 EscFv#125
996	32	62.7	245	2	AAW26800	Aaw26800 Anti-gp54
997	32	62.7	245	2	AAW97891	Aaw97891 A33/218 s
998	32	62.7	246	2	AAR58612	Aar58612 Il-6 bind
999	32	62.7	258	2	AAW09820	Aaw09820 VL3418-li
1000	32	62.7	264	2	AAW35562	Aaw35562 HindIII-E

ALIGNMENTS

RESULT 1
AAR97313
ID AAR97313 standard; peptide; 11 AA.
XX
AC AAR97313;
XX
DT 15-OCT-1996 (first entry)
XX
DE Humanised monoclonal antibody light chain CDR.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Mus musculus.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Claim 5; Page 38; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. This sequence is a murine derived CDR region which corresponds
CC to CDR 1 in the light chain of the humanised MAb. See AAR97313-97333
XX
SQ Sequence 11 AA;

Query Match 100.0%; Score 51; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||||||
Db 1 KASQDVGTSVA 11

RESULT 2
AAB86084
ID AAB86084 standard; peptide; 11 AA.
XX
AC AAB86084;
XX
DT 17-JUL-2001 (first entry)
XX
DE H. pylori catalase derived antibody HP25/6m/1B5 light chain CDR1.
XX
KW Catalase; beta-urease; antibody; antigen; detection; infection; epitope;
KW acid-resistant microorganism; complementarity determining region; CDR;
KW feces; heavy chain; light chain.
XX
OS Unidentified.
XX
PN WO200127612-A2.
XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-EP010057.
XX
PR 12-OCT-1999; 99EP-00120351.
PR 16-MAR-2000; 2000EP-00105592.
PR 31-MAR-2000; 2000EP-00107028.
PR 10-MAY-2000; 2000EP-00110110.
XX
PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
XX
PI Reiter C, Cullmann G, Lakner M, Truee A, Dehnert S, Schwartz G;
XX
DR WPI; 2001-282086/29.
DR N-PSDB; AAF88111.
XX
PT Detecting infections by acid-resistant microorganisms, particularly for
PT diagnosing Helicobacter pylori, comprises immunochromatographic detection
PT of antigen in feces.
XX
PS Claim 26; Page 26; 90pp; German.
XX
CC This invention describes a novel method for detecting infection by an
CC acid-resistant microorganism (A), in a mammal, using
CC immunochromatography. The method is used to diagnose infection by an acid
CC -resistant microorganism (A), in a mammal, such as Helicobacter,
CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
CC H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,
CC inexpensive and non-invasive, and may indicate the stage of infection. A
CC test strip used in the method may include a filter to eliminate particles
CC present in the sample and only a single receptor provides a reasonably
CC secure diagnosis, with specificity and selectivity improved by detecting
CC several epitopes (of catalase) or different antigens (catalase and beta-
CC urease). The method can be automated. This sequence represents a
CC complementarity determining region (CDR) from an antibody raised against
CC the H. pylori catalase or beta-urease antigen which is used to illustrate
CC the method of the invention

```
XX
SQ   Sequence 11 AA;

  Query Match             100.0%;  Score 51;  DB 4;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.0034;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db          1 KASQDVGTSVA 11


RESULT 3
AAB86052
ID   AAB86052 standard; peptide; 11 AA.
XX
AC   AAB86052;
XX
DT   17-JUL-2001  (first entry)
XX
DE   H. pylori catalase derived antibody HP25/6m/1B5 light chain CDR1.
XX
KW   Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;
KW   infection; acid-resistant microorganism; fecal; antibody; diagnosis;
KW   antibacterial; complementarity determining region.
XX
OS   Unidentified.
XX
PN   WO200127613-A2.
XX
PD   19-APR-2001.
XX
PF   12-OCT-2000; 2000WO-EP010058.
XX
PR   12-OCT-1999;   99EP-00120351.
PR   16-MAR-2000; 2000EP-00105592.
PR   31-MAR-2000; 2000EP-00107028.
PR   10-MAY-2000; 2000EP-00110110.
XX
PA   (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
XX
PI   Reiter C,  Cullmann G,  Heppner P,  Ringeis A,  Mueller H,  Haindl E;
XX
DR   WPI; 2001-282087/29.
DR   N-PSDB; AAF88054.
XX
PT   Detecting infections by acid-resistant microorganisms, particularly for
PT   diagnosing Helicobacter pylori, comprises an immunoassay on a fecal
PT   sample.
XX
PS   Claim 21; Page 16; 89pp; German.
XX
CC   This invention describes a novel method for detecting, in a mammal,
CC   infection by an acid-resistant microorganism (A) which comprises reacting
CC   a fecal sample with: (i) a receptor (R) such that a complex is formed
CC   with an antigen (Ag) of (A); or (ii) two different R so that a three-part
CC   complex is formed with Ag, and the formation of a complex detected. R are
CC   specific for an Ag which, after passage through the intestines, at least
CC   in some mammals, retains a native (or corresponding) structure against
CC   which the mammal produces antibodies (when immunized or infected with
CC   (A), or its extracts, lysates or derived proteins (or fragments) or
CC   synthetic peptides). The products of the invention have antibacterial
CC   activity. The method is used to diagnose infection by Helicobacter,
CC   Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
CC   H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the
CC   progress of treatment. Receptors, particularly antibodies, directed
CC   against Ag can be used therapeutically for treatment of infections. The
CC   method requires only one R to provide a reasonably secure diagnosis
CC   (although use of two R improves sensitivity), so is relatively
CC   inexpensive and more easily standardized. Also it is direct, non-
CC   invasive, suitable for automation and may indicate the stage of an
CC   infection. This sequence represents a complementarity determining region
CC   (CDR) from an antibody generated against a Helicobacter pylori antigen
CC   (catalase or beta-urease) which is used to illustrate the method of the
CC   invention
XX
SQ   Sequence 11 AA;

  Query Match             100.0%;  Score 51;  DB 4;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.0034;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db          1 KASQDVGTSVA 11


RESULT 4
ADM95102
ID   ADM95102 standard; peptide; 11 AA.
XX
AC   ADM95102;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Murine MN-14 MAb light chain variable region CDR1.
XX
KW   non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW   complementarity determining region; pancreatic cancer; breast cancer;
KW   ovarian cancer.
XX
OS   Mus sp.
XX
PN   WO2004032962-A1.
XX
PD   22-APR-2004.
XX
PF   11-OCT-2002; 2002WO-US032307.
XX
PR   08-OCT-2002; 2002US-0416531P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-364813/34.
XX
PT   Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT   comprises administering, either concurrently or sequentially, Class III
PT   anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT   therapeutic agent(s).
XX
PS   Claim 6; SEQ ID NO 20; 88pp; English.
XX
CC   The invention relates to a method of treating a non-medullary thyroid
CC   carcinoma or treating medullary thyroid carcinoma involves administering
CC   to a subject, either concurrently or sequentially, a Class III anti-CEA
CC   (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC   least one therapeutic agent. The antibody or its fragment comprises the
CC   complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC   antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC   medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC   ovarian cancer, in a subject. This sequence corresponds to the CDR1 of
CC   the murine MN-14 antibody light chain variable region and used to
CC   generate the humanised/chimeric antibody of the invention.
XX
SQ   Sequence 11 AA;

  Query Match             100.0%;  Score 51;  DB 8;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.0034;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db          1 KASQDVGTSVA 11
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RESULT 5
ADM98311
ID   ADM98311 standard; peptide; 11 AA.
XX
AC   ADM98311;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 antibody light chain variable region CDR1 peptide.
XX
KW   carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; humanised;
KW   murine; mouse; antibody; MN-14; non-medullary thyroid carcinoma;
KW   medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW   hepatocellular carcinoma; breast cancer; lung cancer;
KW   antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW   apoptosis.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   WO2004032857-A2.
XX
PD   22-APR-2004.
XX
PF   08-OCT-2003; 2003WO-US031801.
XX
PR   08-OCT-2002; 2002US-0416531P.
PR   11-OCT-2002; 2002WO-US032307.
PR   02-MAY-2003; 2003US-0467161P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-340797/31.
XX
PT   Treating non-medullary or medullary thyroid carcinoma, involves
PT   administering to subject, either concurrently or sequentially, anti-
PT   carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS   Claim 8; Page 76; 122pp; English.
XX
CC   This invention relates to methods for treating cancers that express
CC   carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC   therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC   antibodies that can be used following administration of an agent that
CC   will increase antibody effector functions or following administration of
CC   an amount of interferon effective to upregulate CEA expression in tumour
CC   cells. The present invention describes the anti-CEA antibody as a class
CC   III humanised murine monoclonal antibody that retains specificity for CEA
CC   binding and is preferably an MN-14 antibody or fragment thereof.
CC   Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC   composition useful for the treatment of non-medullary or medullary
CC   thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC   carcinoma, as well as breast or lung cancer. Furthermore, it can
CC   stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC   mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC   cell growth and angiogenesis. This peptide sequence is a CDR region of
CC   the humanised murine MN-14 antibody of the invention.
XX
SQ   Sequence 11 AA;

  Query Match             100.0%;  Score 51;  DB 8;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.0034;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db          1 KASQDVGTSVA 11


RESULT 6
AAR97337
ID   AAR97337 standard; protein; 106 AA.
XX
AC   AAR97337;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Humanised antibody variable light chain (MN14HuVK).
XX
KW   Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW   complementary determining region; anti-carcinoembryonic antigen; CEA;
KW   diagnosis; imaging; therapy; immune response.
XX
OS   Mus musculus.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    24. .34
FT                   /label= CDR 1.
FT   Binding-site    50. .56
FT                   /label= CDR 2.
FT   Binding-site    89. .96
FT                   /label= CDR 3.
XX
PN   WO9611013-A1.
XX
PD   18-APR-1996.
XX
PF   28-SEP-1995;   95WO-US011964.
XX
PR   05-OCT-1994;   94US-00318157.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Hansen HJ,  Armour KL;
XX
DR   WPI; 1996-209653/21.
DR   N-PSDB; AAT29013.
XX
PT   New humanised anti-CEA monoclonal antibody - having engrafted murine
PT   CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS   Disclosure; Fig 8; 62pp; English.
XX
CC   New humanised monoclonal antibodies (MAbs) comprising the complementary
CC   determining regions (CDRs) of a parental murine class III anti-
CC   carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC   heterologous antibody which can be derived from any species including
CC   human, retain the anti-CEA binding specificity of the parental murine MAb
CC   but are less immunogenic in a human subject than the parental MAb. The
CC   humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC   -producing cancers and patients receiving the humanised antibodies and
CC   conjugates show improved therapeutic results, decreased immune responses
CC   and decreased immune-mediated adverse effects compared to the parent
CC   antibody. See AAR97313-97333 for the CDR sequence and framework regions
CC   of the humanised MAbs
XX
SQ   Sequence 106 AA;

  Query Match             100.0%;  Score 51;  DB 2;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.038;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db         24 KASQDVGTSVA 34


RESULT 7
AAR97335
ID   AAR97335 standard; protein; 106 AA.
XX
AC   AAR97335;
```

```
XX
DT   15-OCT-1996  (first entry)
XX
DE   Murine NEWM MN-14 variable region light chain.
XX
KW   Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW   complementary determining region; anti-carcinoembryonic antigen; CEA;
KW   diagnosis; imaging; therapy; immune response.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    24. .34
FT                   /label= CDR 1.
FT   Binding-site    50. .56
FT                   /label= CDR 2.
FT   Binding-site    89. .96
FT                   /label= CDR 3.
XX
PN   WO9611013-A1.
XX
PD   18-APR-1996.
XX
PF   28-SEP-1995;   95WO-US011964.
XX
PR   05-OCT-1994;   94US-00318157.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Hansen HJ,  Armour KL;
XX
DR   WPI; 1996-209653/21.
DR   N-PSDB; AAT29011.
XX
PT   New humanised anti-CEA monoclonal antibody - having engrafted murine
PT   CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS   Example 7; Fig 2; 62pp; English.
XX
CC   New humanised monoclonal antibodies (MAbs) comprising the complementary
CC   determining regions (CDRs) of a parental murine class III anti-
CC   carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC   heterologous antibody which can be derived from any species including
CC   human, retain the anti-CEA binding specificity of the parental murine MAb
CC   but are less immunogenic in a human subject than the parental MAb. The
CC   humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC   -producing cancers and patients receiving the humanised antibodies and
CC   conjugates show improved therapeutic results, decreased immune responses
CC   and decreased immune-mediated adverse effects compared to the parent
CC   antibody. See AAR97313-97333 for the CDR sequence and framework regions
CC   of the humanised MAbs
XX
SQ   Sequence 106 AA;

  Query Match             100.0%;  Score 51;  DB 2;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.038;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db         24 KASQDVGTSVA 34


RESULT 8
AAB86108
ID   AAB86108 standard; protein; 106 AA.
XX
AC   AAB86108;
XX
DT   17-JUL-2001  (first entry)
XX
DE   H. pylori catalase antibody HP25/2m/1BS V region light chain.
XX
KW   Catalase; beta-urease; antibody; antigen; detection; infection; epitope;
KW   acid-resistant microorganism; complementarity determining region; CDR;
KW   feces; heavy chain; light chain.
XX
OS   Unidentified.
XX
PN   WO200127612-A2.
XX
PD   19-APR-2001.
XX
PF   12-OCT-2000; 2000WO-EP010057.
XX
PR   12-OCT-1999;   99EP-00120351.
PR   16-MAR-2000; 2000EP-00105592.
PR   31-MAR-2000; 2000EP-00107028.
PR   10-MAY-2000; 2000EP-00110110.
XX
PA   (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
XX
PI   Reiter C,  Cullmann G,  Lakner M,  Truee A,  Dehnert S,  Schwartz G;
XX
DR   WPI; 2001-282086/29.
DR   N-PSDB; AAF88154.
XX
PT   Detecting infections by acid-resistant microorganisms, particularly for
PT   diagnosing Helicobacter pylori, comprises immunochromatographic detection
PT   of antigen in feces.
XX
PS   Claim 31; Fig 4; 90pp; German.
XX
CC   This invention describes a novel method for detecting infection by an
CC   acid-resistant microorganism (A), in a mammal, using
CC   immunochromatography. The method is used to diagnose infection by an acid
CC   -resistant microorganism (A), in a mammal, such as Helicobacter,
CC   Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
CC   H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,
CC   inexpensive and non-invasive, and may indicate the stage of infection. A
CC   test strip used in the method may include a filter to eliminate particles
CC   present in the sample and only a single receptor provides a reasonably
CC   secure diagnosis, with specificity and selectivity improved by detecting
CC   several epitopes (of catalase) or different antigens (catalase and beta-
CC   urease). The method can be automated. This sequence represents a
CC   Helicobacter pylori catalase derived antibody V-region light chain
CC   fragment used to illustrate the method of the invention
XX
SQ   Sequence 106 AA;

  Query Match             100.0%;  Score 51;  DB 4;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.038;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db         24 KASQDVGTSVA 34


RESULT 9
AAB86070
ID   AAB86070 standard; protein; 106 AA.
XX
AC   AAB86070;
XX
DT   17-JUL-2001  (first entry)
XX
DE   H. pylori catalase antibody HP25/6m/1B5 V-region light chain.
XX
KW   Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;
KW   infection; acid-resistant microorganism; fecal; antibody; diagnosis;
KW   antibacterial; complementarity determining region; V-region.
XX
OS   Unidentified.
XX
PN   WO200127613-A2.
```

XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-EP010058.
XX
PR 12-OCT-1999; 99EP-00120351.
PR 16-MAR-2000; 2000EP-00105592.
PR 31-MAR-2000; 2000EP-00107028.
PR 10-MAY-2000; 2000EP-00110110.
XX
PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
XX
PI Reiter C, Cullmann G, Heppner P, Ringeis A, Mueller H, Haindl E;
XX
DR WPI; 2001-282087/29.
DR N-PSDB; AAF88097.
XX
PT Detecting infections by acid-resistant microorganisms, particularly for
PT diagnosing Helicobacter pylori, comprises an immunoassay on a fecal
PT sample.
XX
PS Claim 27; Fig 4; 89pp; German.
XX
CC This invention describes a novel method for detecting, in a mammal,
CC infection by an acid-resistant microorganism (A) which comprises reacting
CC a fecal sample with: (i) a receptor (R) such that a complex is formed
CC with an antigen (Ag) of (A); or (ii) two different R so that a three-part
CC complex is formed with Ag, and the formation of a complex detected. R are
CC specific for an Ag which, after passage through the intestines, at least
CC in some mammals, retains a native (or corresponding) structure against
CC which the mammal produces antibodies (when immunized or infected with
CC (A), or its extracts, lysates or derived proteins (or fragments) or
CC synthetic peptides). The products of the invention have antibacterial
CC activity. The method is used to diagnose infection by Helicobacter,
CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
CC H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the
CC progress of treatment. Receptors, particularly antibodies, directed
CC against Ag can be used therapeutically for treatment of infections. The
CC method requires only one R to provide a reasonably secure diagnosis
CC (although use of two R improves sensitivity), so is relatively
CC inexpensive and more easily standardized. Also it is direct, non-
CC invasive, suitable for automation and may indicate the stage of an
CC infection. This sequence represents a Helicobacter pylori anti-catalase
CC derived antibody HP25/6m/1BM V-region light chain fragment which is
CC described in the method of the invention
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 51; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||||||
Db 24 KASQDVGTSVA 34

RESULT 10
ADM95097
ID ADM95097 standard; protein; 106 AA.
XX
AC ADM95097;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 MAb light chain variable region.
XX
KW non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW complementarity determining region; pancreatic cancer; breast cancer;
KW ovarian cancer.
XX
OS Mus sp.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-364813/34.
DR N-PSDB; ADM95096.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Disclosure; Fig 12A-B; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the murine MN-
CC 14 antibody light chain variable region.
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 51; DB 8; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||||||
Db 24 KASQDVGTSVA 34

RESULT 11
ADM95100
ID ADM95100 standard; protein; 106 AA.
XX
AC ADM95100;
XX
DT 15-JUL-2004 (first entry)
XX
DE Humanised murine MN-14 MAb light chain variable region.
XX
KW non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW complementarity determining region; pancreatic cancer; breast cancer;
KW ovarian cancer.
XX
OS Mus sp.
OS Homo sapiens.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX

DR WPI; 2004-364813/34.
DR N-PSDB; ADM95098.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Claim 14; Fig 16A; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the humanised
CC murine MN-14 antibody light chain variable region.
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 51; DB 8; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||||
Db 24 KASQDVGTSVA 34

RESULT 12
ADM98320
ID ADM98320 standard; protein; 106 AA.
XX
AC ADM98320;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 antibody light chain variable region protein.
XX
KW carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW antibody; MN-14; non-medullary thyroid carcinoma;
KW medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW hepatocellular carcinoma; breast cancer; lung cancer;
KW antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW apoptosis.
XX
OS Mus sp.
XX
PN WO2004032857-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031801.
XX
PR 08-OCT-2002; 2002US-0416531P.
PR 11-OCT-2002; 2002WO-US032307.
PR 02-MAY-2003; 2003US-0467161P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-340797/31.
DR N-PSDB; ADM98319.
XX
PT Treating non-medullary or medullary thyroid carcinoma, involves
PT administering to subject, either concurrently or sequentially, anti-
PT carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS Disclosure; Fig 12; 122pp; English.
XX
CC This invention relates to methods for treating cancers that express
CC carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC antibodies that can be used following administration of an agent that
CC will increase antibody effector functions or following administration of
CC an amount of interferon effective to upregulate CEA expression in tumour
CC cells. The present invention describes the anti-CEA antibody as a class
CC III humanised murine monoclonal antibody that retains specificity for CEA
CC binding and is preferably an MN-14 antibody or fragment thereof.
CC Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC composition useful for the treatment of non-medullary or medullary
CC thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC carcinoma, as well as breast or lung cancer. Furthermore, it can
CC stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC cell growth and angiogenesis. This polypeptide sequence is murine MN-14
CC antibody light chain variable region protein of the invention.
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 51; DB 8; Length 106;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||||
Db 24 KASQDVGTSVA 34

RESULT 13
ADM98322
ID ADM98322 standard; protein; 106 AA.
XX
AC ADM98322;
XX
DT 15-JUL-2004 (first entry)
XX
DE Humanised murine MN-14 antibody light chain variable region protein.
XX
KW carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW antibody; MN-14; non-medullary thyroid carcinoma;
KW medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW hepatocellular carcinoma; breast cancer; lung cancer;
KW antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW apoptosis; humanised.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO2004032857-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031801.
XX
PR 08-OCT-2002; 2002US-0416531P.
PR 11-OCT-2002; 2002WO-US032307.
PR 02-MAY-2003; 2003US-0467161P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-340797/31.
DR N-PSDB; ADM98321.
XX
PT Treating non-medullary or medullary thyroid carcinoma, involves
PT administering to subject, either concurrently or sequentially, anti-
PT carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS Disclosure; Fig 23a; 122pp; English.
XX

```
CC   This invention relates to methods for treating cancers that express
CC   carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC   therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC   antibodies that can be used following administration of an agent that
CC   will increase antibody effector functions or following administration of
CC   an amount of interferon effective to upregulate CEA expression in tumour
CC   cells. The present invention describes the anti-CEA antibody as a class
CC   III humanised murine monoclonal antibody that retains specificity for CEA
CC   binding and is preferably an MN-14 antibody or fragment thereof.
CC   Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC   composition useful for the treatment of non-medullary or medullary
CC   thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC   carcinoma, as well as breast or lung cancer. Furthermore, it can
CC   stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC   mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC   cell growth and angiogenesis. This polypeptide sequence is the humanised
CC   murine MN-14 antibody light chain variable region protein of the
CC   invention.
XX
SQ   Sequence 106 AA;

  Query Match             100.0%;  Score 51;  DB 8;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.038;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db         24 KASQDVGTSVA 34


RESULT 14
ABR42756
ID   ABR42756 standard; protein; 115 AA.
XX
AC   ABR42756;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14 Vkappa region.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Disclosure; Fig 12; 62pp; English.
XX
CC   The present sequence is the protein sequence of the light chain variable
CC   region of anti-carcinoembryonic antigen (CEA) humanized monoclonal
CC   antibody hMN-14. scFv constructs comprising the hMN-14 Vkappa and VH
CC   regions are used in novel multivalent, monospecific binding proteins
CC   (diabody, triabody and tetrabody) of the invention (see also ABR42754,
CC   ABR42757 and ABR42758). Claimed binding proteins are specific for a
CC   tumour-associated antigen, and are used in the diagnosis and treatment of
CC   a tumour, carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma,
CC   lymphoma or myeloma, or a cancer selected from acute lymphoblastic
CC   leukaemia, acute myelogenous leukaemia, biliary, breast, cervical,
CC   chronic lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 115 AA;

  Query Match             100.0%;  Score 51;  DB 6;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 0.042;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db         24 KASQDVGTSVA 34


RESULT 15
ABG76490
ID   ABG76490 standard; protein; 232 AA.
XX
AC   ABG76490;
XX
DT   13-MAY-2003  (first entry)
XX
DE   Light chain variable, VL, region of antibody hMN14.
XX
KW   CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW   colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW   human; zeta signalling chain; CD8alpha hinge; humanised antibody;
KW   light chain variable region; VL.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT   Protein         20. .232
FT                   /label= Mature_VL_of_hMN14
XX
PN   US2002165360-A1.
XX
PD   07-NOV-2002.
XX
PF   10-DEC-2001; 2001US-00006771.
XX
PR   30-NOV-2000; 2000US-0250087P.
PR   30-NOV-2000; 2000US-0250090P.
XX
PA   (JUNG/) JUNGHANS R P.
XX
PI   Junghans RP;
XX
DR   WPI; 2003-298705/29.
DR   N-PSDB; ABX13170.
XX
PT   New chimeric molecule from humanized antibody against carcinoembryonic
PT   antigen and having signaling molecules of T cells and other effector
PT   cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS   Disclosure; Page 10-11; 20pp; English.
XX
CC   The invention relates to a chimaeric molecule comprising the
CC   carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
```

CC as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC which the cysteine residues have been mutated, with the IgTCR molecule
CC occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC NK (not defined) or other effector cells are useful in treating patients
CC with cancers expressing the CEA antigen, together with other or with
CC heterologous constructs to engage additional stimulatory and functional
CC properties of the effector cells to enhance the anti-tumour therapeutic
CC efficacy. The cancer disorder includes colorectal, breast and lung
CC cancers. The present sequence represents the light chain variable, VL,
CC region of antibody hMN14. The VL protein is humanised (complementarity
CC determining region-grafted) and has a leader peptide
XX
SQ Sequence 232 AA;

Query Match 100.0%; Score 51; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||||||
Db 43 KASQDVGTSVA 53

RESULT 16
ADE64204
ID ADE64204 standard; protein; 232 AA.
XX
AC ADE64204;
XX
DT 29-JAN-2004 (first entry)
XX
DE MN14LC protein related to a novel antibody library.
XX
KW antibody library; retroviral vector; antibody light chain;
KW antibody heavy chain; human therapy; multiplicity of infection; MOI;
KW plasmid; GATEWAY vector; MN14LC.
XX
OS Unidentified.
XX
PN WO2003083077-A2.
XX
PD 09-OCT-2003.
XX
PF 28-MAR-2003; 2003WO-US009662.
XX
PR 28-MAR-2002; 2002US-0368808P.
PR 10-APR-2002; 2002US-0371299P.
PR 28-MAR-2003; 2003US-00371299.
XX
PA (GALA-) GALA DESIGN INC.
XX
PI Bremel RD, Eakle K, Imboden M;
XX
DR WPI; 2003-804051/75.
DR N-PSDB; ADE64208.
XX
PT New antibody library comprising cells comprising at least one integrated
PT retroviral vector expressing an antibody light or heavy chain, useful in
PT preparing a composition for diagnosing or treating disorders.
XX
PS Disclosure; Fig 8; 57pp; English.
XX
CC This invention relates to a new antibody library which comprises at least
CC 100 cells, each of which comprises at least one integrated retroviral
CC vector expressing an antibody light or heavy chain. Antibodies are of
CC increasing importance in human therapy, assay procedures and diagnostic
CC methods and a need exists for efficient methods of generating and
CC screening antibody libraries containing large numbers of antibodies. The
CC antibody library of the invention addresses this need, with the
CC additional advantage of strict control over multiplicity of infection
CC (MOI), and is useful in preparing a composition for diagnosing or
CC treating a wide variety of disorders. The present sequence is the amino
CC acid sequence of the MN14LC protein, which was encoded by the Gateway
CC retroviral vectors used in the exemplification of the invention.
XX
SQ Sequence 232 AA;

Query Match 100.0%; Score 51; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||||||
Db 43 KASQDVGTSVA 53

RESULT 17
ADF60817
ID ADF60817 standard; protein; 232 AA.
XX
AC ADF60817;
XX
DT 12-FEB-2004 (first entry)
XX
DE hMN-14 light chain amino acid sequence.
XX
KW Immunomodulatory; antidiabetic; immunosuppressive; cardiovascular;
KW neuroprotective; nootropic; fungicide; virucide; antimalarial;
KW antihelmintic; antiparasitic; haemostatic; muscular; antiinflammatory;
KW dermatological; antipyretic; antirheumatic; cytostatic; mutant;
KW bispecific antibody; immunoglobulin G; IgG; scFvs; Fvs; CH2 domain;
KW immune; autoimmune; disease; organ graft rejection; cardiovascular;
KW neurological; Alzheimer's disease; graft vs host disease;
KW systemic lupus erythematosus; diabetes mellitus.
XX
OS Homo sapiens.
XX
PN WO2003074569-A2.
XX
PD 12-SEP-2003.
XX
PF 03-MAR-2003; 2003WO-GB000871.
XX
PR 01-MAR-2002; 2002US-0361037P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (MCCA/) MCCALL J D.
XX
PI Qu Z, Hansen H, Goldenberg DM;
XX
DR WPI; 2003-902725/82.
DR N-PSDB; ADF60816.
XX
PT Mutant bispecific antibody which is rapidly cleared from a patient's
PT body, useful as a pretargeting agent in methods for diagnosing or
PT treating diseases, such as autoimmune disease, and disease caused by
PT infectious agents.
XX
PS Example; Fig 2; 68pp; English.
XX
CC The invention relates to a mutant bispecific antibody (mbAb1) comprising
CC at least a human hinge constant region from immunoglobulin G (IgG), two
CC single chain variable fragments (scFvs), and two variable fragments
CC (Fvs), where the constant region contains one or more amino acid
CC mutations in the heavy chain 2 (CH2) domain. The methods and antibody of
CC the invention are used to diagnose or treat an immune dysregulation
CC disease, an autoimmune disease, organ graft rejection, cardiovascular
CC disease, neurological disease (Alzheimer's disease) or graft vs. host
CC disease. The methods are also useful for treating a disease caused by a
CC fungus, virus, parasite, or bacterium. The methods may also be used for
CC intraoperative or endoscopic diagnosis to identify diseased tissue. The
CC autoimmune diseases that may be diagnosed or treated include acute or
CC chronic idiopathic thrombocytopenic purpura, dermatomyositis, Sydenham's
CC chorea, myasthenia gravis, systemic lupus erythematosus, lupus nephritis,

```
CC   rheumatic fever, polyglandular syndromes and diabetes mellitus. The
CC   current sequence represents the hMN-14 light chain amino acid sequence.
XX
SQ   Sequence 232 AA;

  Query Match             100.0%;  Score 51;  DB 7;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 0.089;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db         43 KASQDVGTSVA 53


RESULT 18
ABR42757
ID   ABR42757 standard; protein; 256 AA.
XX
AC   ABR42757;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-0.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-0;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; triabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .256
FT                   /label= hMN-14-0
FT   Region          142. .250
FT                   /label= hMN-14Vkappa
FT   Region          251. .256
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
DR   N-PSDB; ACC58722.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 39; Fig 13; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-0, which is
CC   designed to form an hMN-14 triabody. The hMN-14-0 polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa without a peptide linker. The use of the zero linker enables the
CC   secreted polypeptide to form a triabody, forming 3 binding sites for CEA.
CC   The polypeptide also includes a pelB signal peptide, which precedes the
CC   VH moiety to facilitate synthesis of the polypeptide in the periplasmic
CC   space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific triabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 256 AA;

  Query Match             100.0%;  Score 51;  DB 6;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 0.099;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db        165 KASQDVGTSVA 175


RESULT 19
ABR42758
ID   ABR42758 standard; protein; 257 AA.
XX
AC   ABR42758;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-1G.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-1G;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; tetrabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .257
FT                   /label= hMN-14-0
FT   Region          142
FT                   /label= 1G_linker
FT   Region          143. .251
FT                   /label= hMN-14Vkappa
FT   Region          252. .257
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
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```
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 48; Fig 14; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-1G, which is
CC   designed to form an hMN-14 tetrabody. The hMN-14-1G polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa via a single glycine residues. Use of the 1G linker enables some
CC   of the the secreted polypeptide to form a tetrabody with 4 binding sites
CC   for CEA. The polypeptide also includes a pelB signal peptide, which
CC   precedes the VH moiety to facilitate synthesis of the polypeptide in the
CC   periplasmic space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific tetrabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 257 AA;

  Query Match             100.0%;  Score 51;  DB 6;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 0.099;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db        166 KASQDVGTSVA 176


RESULT 20
ABR42289
ID   ABR42289 standard; protein; 261 AA.
XX
AC   ABR42289;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Diabody 679-scFv-L5 polypeptide (VH-I3Q/C101S mutant).
XX
KW   Diabody; antibody; 679-scFv-L5; histamine-succinyl-glycyl; HSG;
KW   affinity enhancement system; tumour; targeting; mutant; mutein.
XX
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB signal peptide"
FT   Misc-difference 3
FT                   /note= "wild-type Ile substituted by Gln"
FT   Protein         23. .268
FT                   /label= 679-scFv-L5
FT   Region          23. .142
FT                   /label= 679VH(I3Q/C101S)
FT   Misc-difference 101
FT                   /note= "wild-type Cys substituted by Ser"
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .260
FT                   /label= 679Vk
FT   Region          261. .268
FT                   /label= 6His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57803.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Disclosure; Fig 28; 87pp; English.
XX
CC   The present sequence is the protein sequence of a 679 mutant diabody in
CC   which antibody 679 VH has a Gln for Ile amino acid substitution at
CC   position 3 and a Ser for Gln amino acid substitution at position 101.
CC   Murine monoclonal antibody 679 binds with high affinity to molecules
CC   containing the moiety histamine-succinyl-glycyl (HSG). The present
CC   polypeptide comprises: 679 VH(I3Q) linked to 679 Vk via a peptide linker
CC   (enables the secreted polypeptide to dimerise into a diabody, forming 2
CC   sites for HSG); a pelB leader signal peptide (facilitates transport of
CC   the polypeptide into the periplasmic space of Escherichia coli); and 6
CC   His residues (allows purification by IMAC). The 679 diabody was expressed
CC   in E. coli at a level of 10 ug/l of culture, compared with 1 ug/l for the
CC   non-mutant polypeptide. The invention provides a bispecific diabody
CC   comprising an HSG binding site and a carcinoembryonic antigen (CEA)
CC   binding site. The HSG antigen binding site may comprise the VH and Vk
CC   polypeptides of 679 MAb. These diabodies are produced via recombinant DNA
CC   technology and create a novel affinity enhancement system that shows
CC   specific affinity for HSG and CEA. They pre-target CEA positive tumours
CC   for subsequent specific delivery of therapeutic radioisotopes carried by
CC   HSG-carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 261 AA;

  Query Match             100.0%;  Score 51;  DB 6;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db        170 KASQDVGTSVA 180


RESULT 21
ABR42754
ID   ABR42754 standard; protein; 261 AA.
XX
AC   ABR42754;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-scFv-L5.
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```
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-scFv-15;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .261
FT                   /label= hMN-14-scFv-L5
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .255
FT                   /label= hMN-14Vkappa
FT   Region          256. .261
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
DR   N-PSDB; ACC58721.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 31; Fig 11; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-scFv-L5, which was
CC   designed to form an hMN-14 diabody. The hMN-14-scFv-L5 polypeptide
CC   comprises the C-terminal end of anti-carcinoembryonic antigen (CEA)
CC   humanized monoclonal antibody hMN-14 VH linked to the N-terminal part of
CC   hMN-14 Vkappa by a peptide linker that enables the secreted polypeptide
CC   to dimerize into a diabody, forming 2 binding sites for CEA. The
CC   polypeptide also includes a pelB signal peptide, which precedes the VH
CC   moiety to facilitate synthesis of the polypeptide in the periplasmic
CC   space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. In the claimed monospecific diabody, each scFv comprises
CC   the present sequence. The diabody is an example of claimed multivalent
CC   binding proteins specific for a tumour-associated antigen. The binding
CC   proteins are used in the diagnosis and treatment of a tumour, carcinoma,
CC   melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma or myeloma,
CC   or a cancer selected from acute lymphoblastic leukaemia, acute
CC   myelogenous leukaemia, biliary, breast, cervical, chronic lymphocytic
CC   leukaemia, chronic myelogenous leukaemia, colorectal, endometrial,
CC   oesophageal, gastric, head and neck, Hodgkin's lymphoma, lung, medullary
CC   thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic, prostate and
CC   bladder
XX
SQ   Sequence 261 AA;

  Query Match             100.0%;  Score 51;  DB 6;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db        170 KASQDVGTSVA 180


RESULT 22
ABR83645
ID   ABR83645 standard; protein; 261 AA.
XX
AC   ABR83645;
XX
DT   16-OCT-2003  (first entry)
XX
DE   hMN14-scFv-L5 amino acid sequence.
XX
KW   Multispecific binding protein; multivalent; target antigen; cytostatic;
KW   immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW   immunotherapy; autoimmune disease; infectious disease;
KW   cardiovascular disease; inflammatory disease.
XX
OS   Escherichia coli.
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003057829-A2.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-US038985.
XX
PR   26-DEC-2001; 2001US-0342103P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg D;
XX
DR   WPI; 2003-607997/57.
DR   N-PSDB; ACF57430.
XX
PT   Novel multivalent, multi-specific binding protein useful for treating
PT   cancer, has first binding site having affinity towards hapten group and
PT   second and third binding sites each having affinity towards target
PT   antigen.
XX
PS   Claim 11; Fig 6; 43pp; English.
XX
CC   The present invention describes a multivalent, multi-specific binding
CC   protein (I) comprising a first binding site having an affinity towards a
CC   hapten group and a second and a third binding sites each having affinity
CC   towards a target antigen, which may be the same or a different target
CC   antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC   and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC   useful for delivering a diagnostic agent, a therapeutic agent, or its
CC   combination to a target, which involves administering (I) to a subject,
CC   waiting for a sufficient amount of time for an amount of the non-binding
CC   protein to clear the subject's blood stream, and administering to the
CC   subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC   agent, or its combination, that binds to a binding site of the binding
CC   protein. (I) is also useful for detecting or treating a human disorder,
CC   preferably cancer, autoimmune diseases, infectious diseases,
CC   cardiovascular diseases and inflammatory diseases. The present sequence
CC   represents a hMN14-scFv-L5 amino acid sequence, which is used in the
CC   exemplification of the present invention
XX
SQ   Sequence 261 AA;

  Query Match             100.0%;  Score 51;  DB 6;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 KASQDVGTSVA 11
              ||||||||||
Db        170 KASQDVGTSVA 180


RESULT 23
ABR42295
ID   ABR42295 standard; protein; 262 AA.
XX
AC   ABR42295;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS2 polypeptide #1.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BS2_polypeptide#1
FT   Region          24. .142
FT                   /label= 679_VH(I3Q)
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
FT                   /label= hMN14_VH
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57809.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 34; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #1 of novel
CC   bispecific diabody BS2 comprising the VH region of monoclonal antibody
CC   679 and the Vk region of monoclonal antibody hMN14. The 679VH moiety
CC   includes I3Q and C101S mutations, which improve solubility. Mouse
CC   antibody 679 binds with high affinity to molecules containing the moiety
CC   histamine-succinyl-glycyl (HSG). Humanised antibody hMN14 binds
CC   specifically to carcinoembryonic antigen (CEA). The bispecific diabody
CC   can be produced using recombinant DNA methods, e.g. in Escherichia coli
CC   host cells. It provides a novel affinity enhancement system that shows
CC   specific affinity for HSG and CEA. Such bispecific diabodies pre-target
CC   CEA positive tumours for subsequent specific delivery of therapeutic
CC   radioisotopes carried by HSG-carrying peptides. Cancer, autoimmune
CC   diseases, infectious disease, cardiovascular diseases and inflammatory
CC   diseases can be detected or treated using the methods of the invention
XX
SQ   Sequence 262 AA;

  Query Match             100.0%;  Score 51;  DB 6;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db        171 KASQDVGTSVA 181


RESULT 24
ABR42293
ID   ABR42293 standard; protein; 262 AA.
XX
AC   ABR42293;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS1.5 polypeptide #1.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BS1.5_polypeptide#1
FT   Region          24. .142
FT                   /label= 679_VH(I3Q)
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
FT                   /label= hMN14_VH
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
```

PS Claim 14; Fig 32; 87pp; English.
XX
CC The present sequence is the protein sequence for polypeptide #1 of a
CC novel bispecific diabody comprising the VH region of monoclonal antibody
CC 679 and the Vk region of monoclonal antibody hMN14. The 679VH region
CC includes an I3Q mutation which improves solubility. Mouse antibody 679
CC binds with high affinity to molecules containing the moiety histamine-
CC succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC carcinoembryonic antigen. The bispecific diabody can be produced using
CC recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC a novel affinity enhancement system that shows specific affinity for HSG
CC and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC cardiovascular diseases and inflammatory diseases can be detected or
CC treated using the methods of the invention
XX
SQ Sequence 262 AA;

Query Match 100.0%; Score 51; DB 6; Length 262;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||||
Db 171 KASQDVGTSVA 181

RESULT 25
ABR42298
ID ABR42298 standard; protein; 262 AA.
XX
AC ABR42298;
XX
DT 11-AUG-2003 (first entry)
XX
DE Bispecific diabody BS1.5H polypeptide #1.
XX
KW Diabody; antibody; carcinoembryonic antigen; CEA;
KW histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW targeting; mutant; mutein.
XX
OS Homo sapiens.
OS Mus sp.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1. .22
FT /label= Signal_peptide
FT /note= "pelB leader peptide"
FT Protein 23. .262
FT /label= BS1.5H_polypeptide#1
FT Region 24. .142
FT /label= 679_VH(I3Q)
FT Region 143. .147
FT /label= Linker
FT Region 148. .254
FT /label= hMN14_VH
FT Region 257. .262
FT /label= His_tag
XX
PN WO2003033653-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032717.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (IBCP-) IBC PHARM.
XX
PI Chang CK, Rossi E;
XX
DR WPI; 2003-393513/37.
DR N-PSDB; ACC57812.
XX
PT New kit comprising a multivalent, multi-specific binding protein and a
PT carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT for treating cancer, and cardiovascular, immune, inflammatory, or
PT infectious diseases.
XX
PS Claim 14; Fig 37; 87pp; English.
XX
CC The present sequence is the protein sequence for polypeptide #1 of novel
CC bispecific diabody BS1.5H comprising the VH region of monoclonal antibody
CC 679 and the Vk region of monoclonal antibody hMN14. The 679VH moiety
CC includes an I3Q mutation, which improves solubility. Mouse antibody 679
CC binds with high affinity to molecules containing the moiety histamine-
CC succinyl-glycyl (HSG). A humanised version of its VH and Vk sequences
CC have been used in BS1.5H. Humanised antibody hMN14 binds specifically to
CC carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC provides a novel affinity enhancement system that shows specific affinity
CC for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC tumours for subsequent specific delivery of therapeutic radioisotopes
CC carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC disease, cardiovascular diseases and inflammatory diseases can be
CC detected or treated using the methods of the invention
XX
SQ Sequence 262 AA;

Query Match 100.0%; Score 51; DB 6; Length 262;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||||
Db 171 KASQDVGTSVA 181

RESULT 26
ABR42290
ID ABR42290 standard; protein; 262 AA.
XX
AC ABR42290;
XX
DT 11-AUG-2003 (first entry)
XX
DE Diabody hMN14-scFv-L5 polypeptide.
XX
KW Diabody; antibody; hMN14-scFv-L5; carcinoembryonic antigen; CEA;
KW affinity enhancement system; tumour; targeting.
XX
OS Homo sapiens.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1. .22
FT /label= Signal_peptide
FT /note= "pelB signal peptide"
FT Protein 23. .262
FT /label= hMN14-scFv-L5
FT Region 23. .141
FT /label= hMN14VH
FT Region 142. .146
FT /label= Linker
FT Region 147. .253
FT /label= 679Vk
FT Region 257. .262
FT /label= 6His_tag

```
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 10; Fig 29; 87pp; English.
XX
CC   The present sequence is the protein sequence of a hMN14 diabody,
CC   designated hMN14-scFv-L5. Humanised monoclonal antibody hMN14 binds
CC   specifically to carcinoembryonic antigen (CEA). hMN14-scFv-L5 comprises:
CC   hMN14 VH linked to 679 Vk via a peptide linker (enables the secreted
CC   polypeptide to dimerise into a diabody, forming 2 sites for HSG); a pelB
CC   leader signal peptide (facilitates transport of the polypeptide into the
CC   periplasmic space of Escherichia coli); and 6 His residues (allows
CC   purification by IMAC). The invention provides a bispecific diabody
CC   comprising a histamine-succinyl-glycyl (HSG) binding site and a CEA
CC   binding site. The CEA binding site may comprise the VH and Vk
CC   polypeptides of hMN14 MAb. These diabodies are produced via recombinant
CC   DNA technology and create a novel affinity enhancement system that shows
CC   specific affinity for HSG and CEA. They pre-target CEA positive tumours
CC   for subsequent specific delivery of therapeutic radioisotopes carried by
CC   HSG-carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 262 AA;

  Query Match             100.0%;  Score 51;  DB 6;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db        171 KASQDVGTSVA 181


RESULT 27
ABR42291
ID   ABR42291 standard; protein; 262 AA.
XX
AC   ABR42291;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody polypeptide #1.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BSI_polypeptide#1
FT   Region          24. .142
FT                   /label= 679_VH
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
FT                   /label= hMN14_VH
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57805.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 30; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #1 of a
CC   novel bispecific diabody comprising the VH region of monoclonal antibody
CC   679 and the Vk region of monoclonal antibody hMN14. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen. The bispecific diabody can be produced using
CC   recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC   a novel affinity enhancement system that shows specific affinity for HSG
CC   and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC   subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC   carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 262 AA;

  Query Match             100.0%;  Score 51;  DB 6;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 0.1;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db        171 KASQDVGTSVA 181


RESULT 28
ADU26571
ID   ADU26571 standard; protein; 358 AA.
XX
AC   ADU26571;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric hBS14 polypeptide 2.
```

```
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26573.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 2; SEQ ID NO 12; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
CC   activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC   site of inflammation (caused by infectious agent). (I) is useful in
CC   antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric hBS14 polypeptide 2 containing heavy and light chain variable
CC   regions.
XX
SQ   Sequence 358 AA;

  Query Match             100.0%;  Score 51;  DB 8;  Length 358;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
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```
Db         25 KASQDVGTSVA 35


RESULT 29
ADU26561
ID   ADU26561 standard; protein; 363 AA.
XX
AC   ADU26561;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric BS14hp polypeptide 2.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .6
FT                   /note= "signal peptide"
FT   Protein         7. .363
FT                   /note= "mature protein"
FT   Region          30. .40
FT                   /note= "CDR1hMN14Vk"
FT   Region          56. .62
FT                   /note= "CDR2hMN14Vk"
FT   Region          95. .102
FT                   /note= "CDR3hMN14Vk"
FT   Region          114. .119
FT                   /note= "linker region"
FT   Region          150. .154
FT                   /note= "CDR1hMN14Vh"
FT   Region          169. .185
FT                   /note= "CDR2hMN14Vh"
FT   Region          218. .227
FT                   /note= "CDR3hMN14Vh"
FT   Region          238. .242
FT                   /note= "linker region"
FT   Region          266. .282
FT                   /note= "CDR1h679Vk"
FT   Region          298. .304
FT                   /note= "CDR2h679Vk"
FT   Region          337. .344
FT                   /note= "CDR3h679Vk"
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
```

```
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26569.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 1; SEQ ID NO 2; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
CC   activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC   site of inflammation (caused by infectious agent). (I) is useful in
CC   antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric BS14HP polypeptide 2 containing heavy and light chain variable
CC   regions. The encoded polypeptide is designated alpha-factor-hMN-14Vk-
CC   GGGGS-hMN-14Vh-LEGGGS-h679Vk-6-His where the hMN14 is from a humanized
CC   antibody that binds specifically to the carcinoembryonic antigen and the
CC   h679 is a monoclonal antibody that binds the tri-peptide moiety histamine
CC   -succinyl-glycyl (HSG).
XX
SQ   Sequence 363 AA;

  Query Match            100.0%;  Score 51;  DB 8;  Length 363;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db         30 KASQDVGTSVA 40


RESULT 30
ADU26570
ID   ADU26570 standard; protein; 364 AA.
XX
AC   ADU26570;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric hBS14 polypeptide 1.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26572.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 2; SEQ ID NO 11; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
CC   activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC   site of inflammation (caused by infectious agent). (I) is useful in
CC   antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric hBS14 polypeptide 1 containing heavy and light chain variable
CC   regions.
XX
SQ   Sequence 364 AA;

  Query Match            100.0%;  Score 51;  DB 8;  Length 364;
  Best Local Similarity  100.0%;  Pred. No. 0.14;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db        149 KASQDVGTSVA 159


RESULT 31
ADU26560
ID   ADU26560 standard; protein; 370 AA.
XX
AC   ADU26560;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric  BS14HP polypeptide 1.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
```

KW nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW neoplasm; fungal infection; viral infection; bacterial infection;
KW mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW autoimmune disease; myocardial infarction; ischemic heart disease;
KW atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .7
FT		/note= "signal peptide"
FT	Protein	8. .370
FT		/note= "mature protein"
FT	Region	38. .42
FT		/note= "CDR1h679Vh"
FT	Region	57. .68
FT		/note= "CDR2h679Vh"
FT	Region	106. .115
FT		/note= "CDR3h679Vh"
FT	Region	127. .131
FT		/note= "linker region"
FT	Region	155. .165
FT		/note= "CDR1hMN14Vk"
FT	Region	181. .187
FT		/note= "CDR2hMN14Vk"
FT	Region	220. .227
FT		/note= "CDR3hMN14Vk"
FT	Region	239. .244
FT		/note= "linker region"
FT	Region	275. .279
FT		/note= "CDR1hMN14Vh"
FT	Region	294. .310
FT		/note= "CDR2hMN14Vh"
FT	Region	343. .352
FT		/note= "CDR3hMN14Vh"

XX
PN WO2004094613-A2.
XX
PD 04-NOV-2004.
XX
PF 22-APR-2004; 2004WO-US012662.
XX
PR 22-APR-2003; 2003US-0464532P.
PR 24-NOV-2003; 2003US-0525391P.
XX
PA (IBCP-) IBC PHARM.
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Rossi EA, Chang C, Mcbride WJ;
XX
DR WPI; 2004-795560/78.
DR N-PSDB; ADU26568.
XX
PT Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT chains having immunoglobulin variable domains, to form complex having
PT three antigen binding sites.
XX
PS Example 1; SEQ ID NO 1; 148pp; English.
XX
CC The invention relates to a polyvalent protein complex (PPC) (I),
CC comprising a first and second polypeptide chains having immunoglobulin
CC variable domains, where the first and second polypeptide chains form a
CC complex having three antigen binding sites, and where each binding site
CC comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC useful in pretargeting method of treating or diagnosing, or treating and
CC diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC also useful for diagnosing a non-neoplastic disease or disorder where the
CC disease or disorder is caused by a fungus, a virus, a bacterium, a
CC mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC infarction, ischemic heart disease, atherosclerotic plaques, graft
CC rejection, Alzheimer's disease or inflammation caused by accretion of
CC activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC site of inflammation (caused by infectious agent). (I) is useful in
CC antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC molecule, and immunostaining technique. This sequence corresponds to the
CC chimeric BS14HP polypeptide 1 containing heavy and light chain variable
CC regions. The encoded polypeptide is designated alpha-factor-h679Vh-GGGGS-
CC hMN-14Vk-LEGGGS-hMN-14Vh-6-His where the hMN14 is from a humanized
CC antibody that binds specifically to the carcinoembryonic antigen and the
CC h679 is a monoclonal antibody that binds the tri-peptide moiety histamine
CC -succinyl-glycyl (HSG).
XX
SQ Sequence 370 AA;

Query Match 100.0%; Score 51; DB 8; Length 370;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 KASQDVGTSVA 11
              ||||||||||
Db        155 KASQDVGTSVA 165
```

RESULT 32
ABR83649
ID ABR83649 standard; protein; 391 AA.
XX
AC ABR83649;
XX
DT 16-OCT-2003 (first entry)
XX
DE TS1 VL chain amino acid sequence.
XX
KW Multispecific binding protein; multivalent; target antigen; cytostatic;
KW immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW immunotherapy; autoimmune disease; infectious disease;
KW cardiovascular disease; inflammatory disease.
XX
OS Escherichia coli.
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003057829-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US038985.
XX
PR 26-DEC-2001; 2001US-0342103P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg D;
XX
DR WPI; 2003-607997/57.
DR N-PSDB; ACF57434.
XX
PT Novel multivalent, multi-specific binding protein useful for treating
PT cancer, has first binding site having affinity towards hapten group and
PT second and third binding sites each having affinity towards target
PT antigen.
XX
PS Claim 48; Fig 9A-B; 43pp; English.
XX
CC The present invention describes a multivalent, multi-specific binding
CC protein (I) comprising a first binding site having an affinity towards a

CC hapten group and a second and a third binding sites each having affinity
CC towards a target antigen, which may be the same or a different target
CC antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC useful for delivering a diagnostic agent, a therapeutic agent, or its
CC combination to a target, which involves administering (I) to a subject,
CC waiting for a sufficient amount of time for an amount of the non-binding
CC protein to clear the subject's blood stream, and administering to the
CC subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC agent, or its combination, that binds to a binding site of the binding
CC protein. (I) is also useful for detecting or treating a human disorder,
CC preferably cancer, autoimmune diseases, infectious diseases,
CC cardiovascular diseases and inflammatory diseases. The present sequence
CC represents the TS1 VL chain amino acid sequence, which is used in the
CC exemplification of the present invention
XX
SQ Sequence 391 AA;

Query Match 100.0%; Score 51; DB 6; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||||
Db 300 KASQDVGTSVA 310

RESULT 33
ABG76488
ID ABG76488 standard; protein; 443 AA.
XX
AC ABG76488;
XX
DT 13-MAY-2003 (first entry)
XX
DE Humanised anti-CEA antibody, hMN14.
XX
KW CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW human; zeta signalling chain; CD8alpha hinge; humanised antibody.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
PN US2002165360-A1.
XX
PD 07-NOV-2002.
XX
PF 10-DEC-2001; 2001US-00006771.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250090P.
XX
PA (JUNG/) JUNGHANS R P.
XX
PI Junghans RP;
XX
DR WPI; 2003-298705/29.
DR N-PSDB; ABX13168.
XX
PT New chimeric molecule from humanized antibody against carcinoembryonic
PT antigen and having signaling molecules of T cells and other effector
PT cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS Disclosure; Page 7-8; 20pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the
CC carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC which the cysteine residues have been mutated, with the IgTCR molecule
CC occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC NK (not defined) or other effector cells are useful in treating patients
CC with cancers expressing the CEA antigen, together with other or with
CC heterologous constructs to engage additional stimulatory and functional
CC properties of the effector cells to enhance the anti-tumour therapeutic
CC efficacy. The cancer disorder includes colorectal, breast and lung
CC cancers. The present sequence represents the chimaeric molecule of the
CC invention
XX
SQ Sequence 443 AA;

Query Match 100.0%; Score 51; DB 6; Length 443;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||||
Db 43 KASQDVGTSVA 53

RESULT 34
ABG74240
ID ABG74240 standard; protein; 443 AA.
XX
AC ABG74240;
XX
DT 23-OCT-2003 (revised)
DT 22-APR-2003 (first entry)
XX
DE Chimaeric hMN14/T-cell receptor.
XX
KW Retroviral vector; T-cell receptor; hMN14; antibody; IgTCR; receptor;
KW cytostatic; dermatological; neuroprotective; immunostimulant; GD3;
KW ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4; 3E11;
KW prostate-specific membrane antigen; zeta signalling chain; human; cancer;
KW melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer;
KW mouse; CD8alpha hinge.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
PN US2002132983-A1.
XX
PD 19-SEP-2002.
XX
PF 10-DEC-2001; 2001US-00006773.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250089P.
XX
PA (JUNG/) JUNGHANS R P.
XX
PI Junghans RP;
XX
DR WPI; 2003-208946/20.
DR N-PSDB; ABX16565.
XX
PT New chimeric molecule useful in treating patients with disorders, such as
PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer
PT comprises GD3 and/or PSMA binding domains of antibody.
XX
PS Disclosure; Page 7-8; 35pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the GD3
CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)
CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC sequences, the zeta signalling chain of the T cell receptor and an
CC intervening CD8alpha hinge in which cysteine residues have been mutated.
CC The chimaeric molecules expressed in T cells or NK cells or other
CC effector cells are useful in treating patients with cancers expressing

CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC and/or together with each other or with heterologous constructs to engage
CC additional stimulatory and functional properties of the effector cells to
CC enhance the antitumour therapeutic efficacy (claimed). They are
CC particularly useful in disorders including melanoma, neuroendocrine
CC tumours and prostate and small cell lung cancer. The present sequence is
CC a hMN14 antibody (specific to CEA antigen) in a fusion protein with the
CC modified CD8alpha hinge and the T-cell receptor zeta chain (IgTCR)
CC encoded by a retroviral vector. The hMN14 antibody coding region is
CC replaced with the MB3.6, 3D8, 4D4 or 3E11 genes of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 443 AA;

Query Match 100.0%; Score 51; DB 6; Length 443;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||||
Db 43 KASQDVGTSVA 53

RESULT 35
ADY97271
ID ADY97271 standard; protein; 669 AA.
XX
AC ADY97271;
XX
DT 16-JUN-2005 (first entry)
XX
DE Exemplary antibody fusion protein SEQ ID NO:3.
XX
KW antibody engineering; fusion protein; cytostatic; antimicrobial;
KW virucide; antibacterial; cancer; infection.
XX
OS Synthetic.
XX
PN US2005069552-A1.
XX
PD 31-MAR-2005.
XX
PF 28-JUL-2004; 2004US-00900928.
XX
PR 28-JUL-2003; 2003US-0490569P.
XX
PA (BLEC/) BLECK G T.
PA (YORK/) YORK D.
PA (COLL/) COLLINS I.
XX
PI Bleck GT, York D, Collins I;
XX
DR WPI; 2005-261600/27.
DR N-PSDB; ADY97269.
XX
PT Composition useful as cancer vaccine, comprises polypeptide having
PT antibody heavy chain fused to antibody light chain, or multivalent
PT antibody having two polypeptides with antibody heavy chain fused to
PT antibody light chain.
XX
PS Disclosure; SEQ ID NO 3; 101pp; English.
XX
CC The invention describes a composition (I) comprising: (a) a polypeptide
CC comprising at least one antibody heavy chain fused to at least one
CC antibody light chain; or (b) a multivalent antibody comprising at least
CC two polypeptides, where each of the polypeptides comprises at least one
CC antibody heavy chain fused to at least one antibody light chain. Also
CC described: (1) a composition (II) comprising a nucleic acid comprising at
CC least one antibody heavy chain gene and at least one antibody light chain
CC gene, where the nucleic acid encodes a polypeptide comprising at least
CC one antibody heavy chain fused to at least one antibody light chain; (2)
CC a method (M1) of binding an antigen, involves providing a polypeptide
CC comprising at least one antibody heavy chain fused to at least one
CC antibody light chain, and contacting the polypeptide with a sample having
CC an antigen under conditions such that the polypeptide binds to the
CC antigen; (3) a method (M2), which involves providing a vector comprising
CC a bicistronic expression construct comprising genes encoding an antibody
CC heavy chain gene and an antibody light chain gene, and altering the
CC nucleic acid sequence of a splice acceptor sequence or a splice donor
CC sequence in the antibody light chain gene or the antibody heavy chain
CC gene under conditions such that splicing is prevented at the splice
CC acceptor sequence or donor sequence; (4) a nucleic acid sequence produced
CC by (M2); (5) a vector (III) comprising a modified antibody heavy or light
CC gene, where modification eliminates a splice donor or acceptor sequence
CC in antibody heavy or light chain gene; and (6) a host cell comprising
CC (III). (I) is useful in in vitro binding assays for identifying antigens
CC in a mixture or determining the presence or absence of expression of a
CC particular protein. (I) is also useful as vaccine for treating cancer and
CC infections caused by pathogens e.g. virus or bacteria. The present
CC sequence represents an exemplary antibody fusion protein from the present
CC invention.
XX
SQ Sequence 669 AA;

Query Match 100.0%; Score 51; DB 9; Length 669;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||||
Db 480 KASQDVGTSVA 490

RESULT 36
AAU72806
ID AAU72806 standard; peptide; 11 AA.
XX
AC AAU72806;
XX
DT 26-FEB-2002 (first entry)
XX
DE TRA-8 light chain CDR 1.
XX
KW Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;
KW TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;
KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;
KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;
KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.
XX
OS Mus musculus.
XX
PN WO200183560-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014151.
XX
PR 02-MAY-2000; 2000US-0201344P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;
XX
DR WPI; 2002-049338/06.
XX
PT Novel antibody specific for tumor necrosis factor-related apoptosis-
PT inducing ligand, useful for inhibiting cell proliferation in cancer.
XX
PS Example 16; Page 201; 229pp; English.
XX
CC The invention describes a novel antibody which recognizes a tumour
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing

CC activity to a cell expressing DR5 in vivo. It is also useful for
CC preparing a therapeutic for selective apoptosis of abnormal or
CC dysregulated cells, and for inhibiting cell proliferation in a cell,
CC preferably a human breast, ovary, colon, haematopoietic, prostate,
CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
CC also be administered e.g. paclitaxel, taxol or cycloheximide. The
CC antibody is used to treat an autoimmune disease, systemic lupus
CC erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-
CC host disease, Sjogren's syndrome, Chron's disease, pernicious anaemia,
CC Addison disease, scleroderma, Goodpasture's syndrome, autoimmune
CC haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,
CC Basedow's disease, insulin-dependent diabetes mellitus, allergy, atopic
CC disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, rejection after organ transplantation,
CC and numerous malignancies of lung, prostate, liver, ovary, lymphatic or
CC breast tissue. Complementarity determining regions of the heavy and light
CC chains of TRA-8 are shown in AAU72803-AAU72808 and the heavy chain
CC variable region in AAU72809
XX
SQ Sequence 11 AA;

Query Match 94.1%; Score 48; DB 5; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.014;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||:||
Db 1 KASQDVGTAVA 11

RESULT 37
ABB07360
ID ABB07360 standard; peptide; 11 AA.
XX
AC ABB07360;
XX
DT 09-APR-2002 (first entry)
XX
DE 22A5 IgM light chain variable region CDR1 sequence.
XX
KW Immunoglobulin; Ig; reperfusion; ischaemic injury; pathogenic; CDR;
KW vasotropic; antibody; 22A5; IgM; complementarity determining region.
XX
OS Mus musculus.
XX
PN WO200193892-A1.
XX
PD 13-DEC-2001.
XX
PF 08-JUN-2001; 2001WO-US018510.
XX
PR 08-JUN-2000; 2000US-0210272P.
XX
PA (BLOO-) CENT BLOOD RES INC.
XX
PI Carroll MC, Moore FD, Hechtman HB;
XX
DR WPI; 2002-139643/18.
DR N-PSDB; ABA94517.
XX
PT Treating or preventing immunoglobulin-mediated reperfusion or ischemic
PT injury resulting from e.g. angioplasty or bypass surgery, by
PT administering an inhibitor of pathogenic immunoglobulin and ischemic
PT antigen interaction.
XX
PS Claim 52; Page 74; 77pp; English.
XX
CC The invention provides a method of treating or preventing immunoglobulin-
CC mediated reperfusion or ischemic injury in a subject. The method involves
CC administering an inhibitor of an interaction between a pathogenic
CC immunoglobulin, and an ischemic-specific antigen or a component of the
CC complement pathway. The method is useful for treating or preventing
CC immunoglobulin-mediated reperfusion or ischemic injury, in particular,
CC injury that results following a naturally occurring episode, a surgical
CC procedure (e.g. angioplasty, stenting procedure, atherectomy or bypass
CC surgery), or in an injury that occurs in a cardiovascular tissue. The
CC method is also useful for treating or preventing, in a subject, tissue
CC damage following reperfusion caused by a pathogenic immunoglobulin, e.g.
CC pathogenic IgMs. The present sequence represents the complementarity
CC determining region (CDR1) of a light chain variable region of 22A5 IgM, a
CC pathogenic immunoglobulin
XX
SQ Sequence 11 AA;

Query Match 94.1%; Score 48; DB 5; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.014;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||:||
Db 1 KASQDVGTAVA 11

RESULT 38
AAO29874
ID AAO29874 standard; peptide; 11 AA.
XX
AC AAO29874;
XX
DT 27-AUG-2003 (first entry)
XX
DE Mouse anti-human DR5 antibody (TRA-8) light chain CDR 1.
XX
KW Tumour necrosis factor; TNF-related apoptosis-inducing ligand; allergy;
KW inflammatory disease; TRAIL receptor; systemic lupus erythematosus; DR4;
KW Hashimoto's disease; rheumatoid arthritis; inflammatory disease; cancer;
KW multiple sclerosis; graft-versus-host disease; arteriosclerosis; asthma;
KW Goodpasture's syndrome; autoimmune disease; glomerular nephritis; DR5;
KW Crohn's disease; diabetes mellitus; complementarity determining region;
KW CDR; TRA-8 antibody; mouse.
XX
OS Mus sp.
XX
PN WO2003037913-A2.
XX
PD 08-MAY-2003.
XX
PF 01-NOV-2002; 2002WO-US035333.
XX
PR 01-NOV-2001; 2001US-0346402P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Zhou T, Kimberly RP, Koopman WJ, Lobuglio AF, Buchsbaum DJ;
XX
DR WPI; 2003-441350/41.
XX
PT New purified antibody that specifically binds a TNF-related apoptosis-
PT inducing ligand receptor DR4 or DR5, useful for treating cancer,
PT inflammatory disease or autoimmune disease in a subject, e.g. asthma or
PT rheumatoid arthritis.
XX
PS Example 16; Page 227; 251pp; English.
XX
CC The invention relates to an antibody that specifically binds a tumour
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR4 or DR5. Antibodies of the invention are useful for selectively
CC inducing apoptosis in target cells expressing DR4, for inhibiting
CC proliferation of target cells expressing DR4 or for treating cancer,
CC inflammatory disease or autoimmune disease in a subject e.g. systemic
CC lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-
CC versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple
CC sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or
CC glomerular nephritis. The present sequence is mouse anti-human DR5
CC antibody (TRA-8) light chain complementarity determining region (CDR)
XX

```
SQ   Sequence 11 AA;

  Query Match             94.1%;  Score 48;  DB 6;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 0.014;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||||:||
Db          1 KASQDVGTAVA 11


RESULT 39
ADJ79792
ID   ADJ79792 standard; protein; 11 AA.
XX
AC   ADJ79792;
XX
DT   06-MAY-2004  (first entry)
XX
DE   TRA-8 light chain CDR1.
XX
KW   nephrotropic; antiarteriosclerotic; cardiant; antiasthmatic;
KW   antiallergic; antiinflammatory; antidiabetic; haemostatic;
KW   neuroprotective; antiinfertility; immunosuppressive; dermatological;
KW   antianaemic; antirheumatic; antiarthritic; thyromimetic; apoptosis;
KW   proliferation;
KW   tumor necrosis factor-related apoptosis-inducing ligand receptor; TNF;
KW   TRAIL; synovial cell; lymphocyte; neutrophil;
KW   systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis;
KW   graft-versus-host disease; Sjogren's syndrome; pernicious anemia;
KW   Addison disease; scleroderma; Goodpasture's syndrome; Crohn's disease;
KW   autoimmune hemolytic anemia; sterility; myasthenia gravis;
KW   multiple sclerosis; Basedow's disease; thrombotic; thrombocytopenia;
KW   thrombopenia purpura; insulin dependent diabetes mellitus; allergy;
KW   asthma; atopic disease; arteriosclerosis; myocarditis; cardiomyopathy;
KW   glomerular nephritis; hypoplastic anemia.
XX
OS   Homo sapiens.
XX
PN   WO2003038043-A2.
XX
PD   08-MAY-2003.
XX
PF   25-OCT-2002; 2002WO-US034420.
XX
PR   01-NOV-2001; 2001US-0346402P.
PR   24-JUN-2002; 2002US-0391478P.
XX
PA   (UABR-) UAB RES FOUND.
XX
PI   Zhou T,  Ichikawa K,  Kimberly RP,  Koopman WJ,  Oshumi J;
PI   Lobuglio AF,  Buchsbaum DJ;
XX
DR   WPI; 2003-421518/39.
XX
PT   Inducing apoptosis and inhibiting proliferation of target cells
PT   expressing DR5, by contacting the target cell with an antibody that binds
PT   TNF-related apoptosis-inducing ligand receptor DR5 and with therapeutic
PT   agents.
XX
PS   Example 16; SEQ ID NO 28; 274pp; English.
XX
CC   The invention relates to a method of selectively inducing apoptosis in
CC   and inhibiting (M1) proliferation of target cells expressing DR5,
CC   comprising contacting the cell with an antibody that specifically binds
CC   tumor necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL)
CC   receptor DR5, where the antibody, in its soluble form, has in vivo and in
CC   vitro apoptosis-inducing activity in the cell expressing DR5, and
CC   contacting the cell with one or more therapeutic agents. M1 is useful for
CC   inducing apoptosis in target cell and inhibiting proliferation of target
CC   cell expressing DR5, where the target cell is an abnormally proliferating
CC   synovial cells (e.g. rheumatoid arthritis synovial cell), activated
CC   immune cell (e.g. activated lymphocyte), neutrophil, or virally infected
CC   cell. M2 is useful for treating a subject having inflammatory and
CC   autoimmune diseases. The inflammatory or autoimmune disease are selected
CC   from systemic lupus erythematosus, Hashimoto's disease, rheumatoid
CC   arthritis, graft-versus-host disease, Sjogren's syndrome, pernicious
CC   anemia, Addison disease, scleroderma, Goodpasture's syndrome, Crohn's
CC   disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC   multiple sclerosis, Basedow's disease, thrombotic, thrombocytopenia,
CC   thrombopenia purpura, insulin dependent diabetes mellitus, allergy,
CC   asthma, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,
CC   glomerular nephritis, and hypoplastic anemia. This sequence represents a
CC   protein used in the method of the invention.
XX
SQ   Sequence 11 AA;

  Query Match             94.1%;  Score 48;  DB 7;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 0.014;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||||:||
Db          1 KASQDVGTAVA 11


RESULT 40
ADZ45502
ID   ADZ45502 standard; peptide; 11 AA.
XX
AC   ADZ45502;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Murine factor IX directed antibody CDR1 SEQ ID NO 206.
XX
KW   bispecific antibody; blood coagulation factor VIII; bleeding;
KW   fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;
KW   factor VIII deficiency; von Willebrands disease; hemostatic;
KW   immunostimulator; antibody engineering.
XX
OS   Mus musculus.
XX
PN   WO2005035756-A1.
XX
PD   21-APR-2005.
XX
PF   08-OCT-2004; 2004WO-JP014911.
XX
PR   10-OCT-2003; 2003WO-JP013062.
PR   14-OCT-2003; 2003WO-JP013123.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Hattori K,  Kojima T,  Miyazaki T,  Soeda T;
XX
DR   WPI; 2005-315563/32.
XX
PT   Novel bispecific antibody substituting for function of cofactor that
PT   enhances enzyme reaction, and recognizing both enzyme and substrates of
PT   enzyme, useful for treating hemophilia A.
XX
PS   Disclosure; SEQ ID NO 206; 69pp; Japanese.
XX
CC   This invention describes a novel bispecific antibody which can act as a
CC   cofactor to enhance an enzyme reaction and can recognize the enzyme and
CC   the enzyme substrate. The antibody specifically binds to blood
CC   coagulation factor VIII. The invention also describes a composition
CC   comprising the antibody and a carrier, a kit useful in preventing and/or
CC   treating bleeding associated with a disorder or from a disease caused by
CC   bleeding. The composition includes blood coagulation factor VIII. The
CC   antibody of the invention can be a blood-coagulation fibrinolysis related
CC   factor including blood-coagulation factor VIII, blood coagulation factor
CC   X, or blood-coagulation factor IX. The antibody comprises a complementary
CC   determining region (CDR) of anti-blood-coagulation factor IX/IXa factor
CC   antibody. The novel antibody or composition is useful for preventing
```

CC and/or treating a disease accompanying bleeding, or the disease resulting
CC from bleeding, where the disease accompanying bleeding or the disease
CC resulting from bleeding develops and/or progresses by an active reduction
CC or deletion of the blood coagulation factor VIII. The disease the
CC develops and/or progresses by an active reduction or deletion of the
CC blood coagulation factor VIII and/or activation blood coagulation factor
CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is
CC an acquired hemophilia A. This sequence represents a fragment of the
CC antibody described in the method of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 11 AA;

Query Match 94.1%; Score 48; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.014;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||:||
Db 1 KASQDVGTAVA 11

RESULT 41
ADZ45548
ID ADZ45548 standard; peptide; 11 AA.
XX
AC ADZ45548;
XX
DT 30-JUN-2005 (first entry)
XX
DE Murine factor IX directed antibody CDR1 SEQ ID NO 252.
XX
KW bispecific antibody; blood coagulation factor VIII; bleeding;
KW fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;
KW factor VIII deficiency; von Willebrands disease; hemostatic;
KW immunostimulator; antibody engineering; ds; gene.
XX
OS Mus musculus.
XX
PN WO2005035756-A1.
XX
PD 21-APR-2005.
XX
PF 08-OCT-2004; 2004WO-JP014911.
XX
PR 10-OCT-2003; 2003WO-JP013062.
PR 14-OCT-2003; 2003WO-JP013123.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Hattori K, Kojima T, Miyazaki T, Soeda T;
XX
DR WPI; 2005-315563/32.
DR N-PSDB; ADZ45547.
XX
PT Novel bispecific antibody substituting for function of cofactor that
PT enhances enzyme reaction, and recognizing both enzyme and substrates of
PT enzyme, useful for treating hemophilia A.
XX
PS Disclosure; SEQ ID NO 252; 69pp; Japanese.
XX
CC This invention describes a novel bispecific antibody which can act as a
CC cofactor to enhance an enzyme reaction and can recognize the enzyme and
CC the enzyme substrate. The antibody specifically binds to blood
CC coagulation factor VIII. The invention also describes a composition
CC comprising the antibody and a carrier, a kit useful in preventing and/or
CC treating bleeding associated with a disorder or from a disease caused by
CC bleeding. The composition includes blood coagulation factor VIII. The
CC antibody of the invention can be a blood-coagulation fibrinolysis related
CC factor including blood-coagulation factor VIII, blood coagulation factor
CC X, or blood-coagulation factor IX. The antibody comprises a complementary
CC determining region (CDR) of anti-blood-coagulation factor IX/IXa factor
CC antibody. The novel antibody or composition is useful for preventing
CC and/or treating a disease accompanying bleeding, or the disease resulting
CC from bleeding, where the disease accompanying bleeding or the disease
CC resulting from bleeding develops and/or progresses by an active reduction
CC or deletion of the blood coagulation factor VIII. The disease the
CC develops and/or progresses by an active reduction or deletion of the
CC blood coagulation factor VIII and/or activation blood coagulation factor
CC VIII, is hemophilia A or von Willebrand disease, where the hemophilia is
CC an acquired hemophilia A. This sequence encodes a fragment of the
CC antibody described in the method of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 11 AA;

Query Match 94.1%; Score 48; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.014;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||:||
Db 1 KASQDVGTAVA 11

RESULT 42
ADT75007
ID ADT75007 standard; protein; 105 AA.
XX
AC ADT75007;
XX
DT 13-JAN-2005 (first entry)
XX
DE Light chain murine anti-hL-SIGN scFV antibody protein G3LC Seq 53.
XX
KW autoimmune disease; antibody; antigen presenting cell; APC;
KW diabetes mellitus; immune tolerance; antidiabetic; immunosuppressive;
KW vaccine; hL-SIGN.
XX
OS Mus sp.
XX
PN WO2004091543-A2.
XX
PD 28-OCT-2004.
XX
PF 04-MAR-2004; 2004WO-US006570.
XX
PR 04-MAR-2003; 2003US-0451816P.
PR 15-DEC-2003; 2003US-0529500P.
PR 28-FEB-2004; 2004US-0548385P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Kretz-Rommel A, Dakappagari N;
XX
DR WPI; 2004-758274/74.
XX
PT Treating an autoimmune disease comprises providing an
PT antibody/autoantigen construct containing an autoantigen linked to an
PT antibody to a receptor of an antigen presenting cell and administering
PT the construct to a subject.
XX
PS Example 9; Fig 8; 71pp; English.
XX
CC This invention relates to the novel treatment of an autoimmune disease
CC that utilises an antibody/ autoantigen construct. Specifically, it refers
CC to a peptide autoantigen that is linked to an antibody raised against an
CC antigen presenting cell (APC) receptor. The present invention describes a
CC method for treating diabetes mellitus by inducing an immune tolerance to
CC an autoantigen, which can be chosen from glutamic acid decarboxylase
CC (GAD), insulin or a heat shock protein (HSP), as well as epitopes derived
CC from each thereof or beta cell antigens that are linked to an APC

```
CC   receptor antibody. In particular, the antibody recognises a receptor
CC   chosen from DC-SIGNR, MHC, toll receptor or mannose receptor amongst
CC   others, which is expressed on the surface of the APC. The antibody/
CC   autoantigen construct then works to interfere with the interaction
CC   between the APC and immune cells such as autoreactive T cells, and hence
CC   inhibits T-cell proliferation. Accordingly, such compositions exhibit
CC   antidiabetic and immunosuppressive activities and can be used in the
CC   development of vaccines. Note that the single chain antibodies (scFVs)
CC   used in this specification contain both variable light and heavy chain
CC   regions connected by a linker, their short length makes these antibody
CC   fragments particularly suitable for antigen linkage, and the capacity for
CC   binding to the receptor is preserved. This polypeptide sequence is a
CC   light chain murine anti-human L-SIGN (hL-SIGN) antibody protein of the
CC   invention.
XX
SQ   Sequence 105 AA;

  Query Match             94.1%;  Score 48;  DB 8;  Length 105;
  Best Local Similarity   90.9%;  Pred. No. 0.15;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||:||
Db         24 KASQDVGTAVA 34


RESULT 43
ADZ45501
ID   ADZ45501 standard; protein; 107 AA.
XX
AC   ADZ45501;
XX
DT   30-JUN-2005  (first entry)
XX
DE   Murine factor IX directed antibody fragment SEQ ID NO 205.
XX
KW   bispecific antibody; blood coagulation factor VIII; bleeding;
KW   fibrinolysis; blood coagulation factor X; blood-coagulation factor IX;
KW   factor VIII deficiency; von Willebrands disease; hemostatic;
KW   immunostimulator; antibody engineering.
XX
OS   Mus musculus.
XX
PN   WO2005035756-A1.
XX
PD   21-APR-2005.
XX
PF   08-OCT-2004; 2004WO-JP014911.
XX
PR   10-OCT-2003; 2003WO-JP013062.
PR   14-OCT-2003; 2003WO-JP013123.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Hattori K,  Kojima T,  Miyazaki T,  Soeda T;
XX
DR   WPI; 2005-315563/32.
XX
PT   Novel bispecific antibody substituting for function of cofactor that
PT   enhances enzyme reaction, and recognizing both enzyme and substrates of
PT   enzyme, useful for treating hemophilia A.
XX
PS   Disclosure; SEQ ID NO 205; 69pp; Japanese.
XX
CC   This invention describes a novel bispecific antibody which can act as a
CC   cofactor to enhance an enzyme reaction and can recognize the enzyme and
CC   the enzyme substrate. The antibody specifically binds to blood
CC   coagulation factor VIII. The invention also describes a composition
CC   comprising the antibody and a carrier, a kit useful in preventing and/or
CC   treating bleeding associated with a disorder or from a disease caused by
CC   bleeding. The composition includes blood coagulation factor VIII. The
CC   antibody of the invention can be a blood-coagulation fibrinolysis related
CC   factor including blood-coagulation factor VIII, blood coagulation factor
CC   X, or blood-coagulation factor IX. The antibody comprises a complementary
CC   determining region (CDR) of anti-blood-coagulation factor IX/IXa factor
CC   antibody. The novel antibody or composition is useful for preventing
CC   and/or treating a disease accompanying bleeding, or the disease resulting
CC   from bleeding, where the disease accompanying bleeding or the disease
CC   resulting from bleeding develops and/or progresses by an active reduction
CC   or deletion of the blood coagulation factor VIII. The disease the
CC   develops and/or progresses by an active reduction or deletion of the
CC   blood coagulation factor VIII and/or activation blood coagulation factor
CC   VIII, is hemophilia A or von Willebrand disease, where the hemophilia is
CC   an acquired hemophilia A. This sequence represents a fragment of the
CC   antibody described in the method of the invention. Note: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 107 AA;

  Query Match             94.1%;  Score 48;  DB 9;  Length 107;
  Best Local Similarity   90.9%;  Pred. No. 0.15;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||:||
Db         24 KASQDVGTAVA 34


RESULT 44
AAY21817
ID   AAY21817 standard; protein; 108 AA.
XX
AC   AAY21817;
XX
DT   10-SEP-1999  (first entry)
XX
DE   Anti-STX1 light chain variable region.
XX
KW   Humanised; monoclonal antibody; MAb; Shiga toxin; immunoglobulin;
KW   Ig constant region; enterohemorrhagic Escherichia coli; EHEC; uremia;
KW   edema; bloody diarrhoea; hemorrhagic colitis; hemolytic uremic syndrome;
KW   thrombocytopenia; EHEC-mediated disease; anti-STX1.
XX
OS   Shigella dysenteriae.
XX
FH   Key             Location/Qualifiers
FT   Region          24. .34
FT                   /note= "complementarity determining region (CDR) 1;
FT                   specifically claimed for in claim 10"
FT   Region          50. .56
FT                   /note= "complementarity determining region (CDR) 2;
FT                   specifically claimed for in claim 10"
FT   Region          89. .97
FT                   /note= "complementarity determining region (CDR) 3;
FT                   specifically claimed for in claim 10"
XX
PN   WO9932645-A1.
XX
PD   01-JUL-1999.
XX
PF   22-DEC-1998;   98WO-US027267.
XX
PR   23-DEC-1997;   97US-0068635P.
PR   18-DEC-1998;   98US-00215163.
XX
PA   (STIN/) STINSON J L.
PA   (WONG/) WONG H.
PA   (OBRI/) O'BRIEN A D.
PA   (SCHM/) SCHMITT C K.
PA   (MELT/) MELTON-CELSA A.
XX
PI   Stinson JL,  Wong H,  O'brien AD,  Schmitt CK,  Melton-Celsa A;
XX
DR   WPI; 1999-418935/35.
```

DR N-PSDB; AAX82029.
XX
PT Humanized monoclonal antibodies against Shiga toxins, useful for
PT protection against enterohemorrhagic Escherichia coli or other Shiga
PT toxin producing bacteria.
XX
PS Claim 5; Fig 3; 75pp; English.
XX
CC The invention relates to humanised monoclonal antibodies (MAb) against
CC Shiga toxins. The humanised MAb that binds to Shiga toxin comprises a
CC constant and a variable region, where: (a) the constant region contains
CC at least part of a human immunoglobulin (Ig) constant region; and (b) the
CC variable region contains at least part of a non-human Ig variable region.
CC Host cells transformed with vectors encoding a humanised MAb against
CC Shiga toxin type 2 is useful for treating a patient with an infection
CC caused by enterohemorrhagic Escherichia coli (EHEC) or other Shiga toxin
CC producing bacteria. The humanised MAb can also be used to reduce illness
CC caused by EHEC or other Shiga toxin producing bacteria. EHEC are
CC associated with food-borne outbreaks of bloody diarrhoea (hemorrhagic
CC colitis) and the hemolytic uremic syndrome. In particular, the humanised
CC MAbs ameliorate edema, thrombocytopenia and uremia associated with EHEC-
CC mediated disease. The present sequence represents an anti-STX1 light
CC chain variable region
XX
SQ Sequence 108 AA;

Query Match 94.1%; Score 48; DB 2; Length 108;
Best Local Similarity 90.9%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||:||
Db 24 KASQDVGTAVA 34

RESULT 45
ADT75006
ID ADT75006 standard; protein; 108 AA.
XX
AC ADT75006;
XX
DT 13-JAN-2005 (first entry)
XX
DE Light chain murine anti-hL-SIGN scFV antibody protein G1LC Seq 52.
XX
KW autoimmune disease; antibody; antigen presenting cell; APC;
KW diabetes mellitus; immune tolerance; antidiabetic; immunosuppressive;
KW vaccine; hL-SIGN.
XX
OS Mus sp.
XX
PN WO2004091543-A2.
XX
PD 28-OCT-2004.
XX
PF 04-MAR-2004; 2004WO-US006570.
XX
PR 04-MAR-2003; 2003US-0451816P.
PR 15-DEC-2003; 2003US-0529500P.
PR 28-FEB-2004; 2004US-0548385P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Kretz-Rommel A, Dakappagari N;
XX
DR WPI; 2004-758274/74.
XX
PT Treating an autoimmune disease comprises providing an
PT antibody/autoantigen construct containing an autoantigen linked to an
PT antibody to a receptor of an antigen presenting cell and administering
PT the construct to a subject.
XX
PS Example 9; Fig 8; 71pp; English.
XX
CC This invention relates to the novel treatment of an autoimmune disease
CC that utilises an antibody/ autoantigen construct. Specifically, it refers
CC to a peptide autoantigen that is linked to an antibody raised against an
CC antigen presenting cell (APC) receptor. The present invention describes a
CC method for treating diabetes mellitus by inducing an immune tolerance to
CC an autoantigen, which can be chosen from glutamic acid decarboxylase
CC (GAD), insulin or a heat shock protein (HSP), as well as epitopes derived
CC from each thereof or beta cell antigens that are linked to an APC
CC receptor antibody. In particular, the antibody recognises a receptor
CC chosen from DC-SIGNR, MHC, toll receptor or mannose receptor amongst
CC others, which is expressed on the surface of the APC. The antibody/
CC autoantigen construct then works to interfere with the interaction
CC between the APC and immune cells such as autoreactive T cells, and hence
CC inhibits T-cell proliferation. Accordingly, such compositions exhibit
CC antidiabetic and immunosuppressive activities and can be used in the
CC development of vaccines. Note that the single chain antibodies (scFVs)
CC used in this specification contain both variable light and heavy chain
CC regions connected by a linker, their short length makes these antibody
CC fragments particularly suitable for antigen linkage, and the capacity for
CC binding to the receptor is preserved. This polypeptide sequence is a
CC light chain murine anti-human L-SIGN (hL-SIGN) antibody protein of the
CC invention.
XX
SQ Sequence 108 AA;

Query Match 94.1%; Score 48; DB 8; Length 108;
Best Local Similarity 90.9%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||:||
Db 24 KASQDVGTAVA 34

RESULT 46
ADT75004
ID ADT75004 standard; protein; 108 AA.
XX
AC ADT75004;
XX
DT 13-JAN-2005 (first entry)
XX
DE Light chain murine anti-hL-SIGN scFV antibody protein E3LC Seq 50.
XX
KW autoimmune disease; antibody; antigen presenting cell; APC;
KW diabetes mellitus; immune tolerance; antidiabetic; immunosuppressive;
KW vaccine; hL-SIGN.
XX
OS Mus sp.
XX
PN WO2004091543-A2.
XX
PD 28-OCT-2004.
XX
PF 04-MAR-2004; 2004WO-US006570.
XX
PR 04-MAR-2003; 2003US-0451816P.
PR 15-DEC-2003; 2003US-0529500P.
PR 28-FEB-2004; 2004US-0548385P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Kretz-Rommel A, Dakappagari N;
XX
DR WPI; 2004-758274/74.
XX
PT Treating an autoimmune disease comprises providing an
PT antibody/autoantigen construct containing an autoantigen linked to an
PT antibody to a receptor of an antigen presenting cell and administering
PT the construct to a subject.
XX
PS Example 9; Fig 8; 71pp; English.

```
XX
CC   This invention relates to the novel treatment of an autoimmune disease
CC   that utilises an antibody/ autoantigen construct. Specifically, it refers
CC   to a peptide autoantigen that is linked to an antibody raised against an
CC   antigen presenting cell (APC) receptor. The present invention describes a
CC   method for treating diabetes mellitus by inducing an immune tolerance to
CC   an autoantigen, which can be chosen from glutamic acid decarboxylase
CC   (GAD), insulin or a heat shock protein (HSP), as well as epitopes derived
CC   from each thereof or beta cell antigens that are linked to an APC
CC   receptor antibody. In particular, the antibody recognises a receptor
CC   chosen from DC-SIGNR, MHC, toll receptor or mannose receptor amongst
CC   others, which is expressed on the surface of the APC. The antibody/
CC   autoantigen construct then works to interfere with the interaction
CC   between the APC and immune cells such as autoreactive T cells, and hence
CC   inhibits T-cell proliferation. Accordingly, such compositions exhibit
CC   antidiabetic and immunosuppressive activities and can be used in the
CC   development of vaccines. Note that the single chain antibodies (scFVs)
CC   used in this specification contain both variable light and heavy chain
CC   regions connected by a linker, their short length makes these antibody
CC   fragments particularly suitable for antigen linkage, and the capacity for
CC   binding to the receptor is preserved. This polypeptide sequence is a
CC   light chain murine anti-human L-SIGN (hL-SIGN) antibody protein of the
CC   invention.
XX
SQ   Sequence 108 AA;

  Query Match             94.1%;  Score 48;  DB 8;  Length 108;
  Best Local Similarity   90.9%;  Pred. No. 0.16;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||:||
Db         23 KASQDVGTAVA 33


RESULT 47
ADT74999
ID   ADT74999 standard; protein; 108 AA.
XX
AC   ADT74999;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Light chain murine anti-hL-SIGN scFV antibody protein B4LC Seq 45.
XX
KW   autoimmune disease; antibody; antigen presenting cell; APC;
KW   diabetes mellitus; immune tolerance; antidiabetic; immunosuppressive;
KW   vaccine; hL-SIGN.
XX
OS   Mus sp.
XX
PN   WO2004091543-A2.
XX
PD   28-OCT-2004.
XX
PF   04-MAR-2004; 2004WO-US006570.
XX
PR   04-MAR-2003; 2003US-0451816P.
PR   15-DEC-2003; 2003US-0529500P.
PR   28-FEB-2004; 2004US-0548385P.
XX
PA   (ALEX-) ALEXION PHARM INC.
XX
PI   Bowdish KS,  Kretz-Rommel A,  Dakappagari N;
XX
DR   WPI; 2004-758274/74.
XX
PT   Treating an autoimmune disease comprises providing an
PT   antibody/autoantigen construct containing an autoantigen linked to an
PT   antibody to a receptor of an antigen presenting cell and administering
PT   the construct to a subject.
XX
PS   Example 9; Fig 8; 71pp; English.
```

```
XX
CC   This invention relates to the novel treatment of an autoimmune disease
CC   that utilises an antibody/ autoantigen construct. Specifically, it refers
CC   to a peptide autoantigen that is linked to an antibody raised against an
CC   antigen presenting cell (APC) receptor. The present invention describes a
CC   method for treating diabetes mellitus by inducing an immune tolerance to
CC   an autoantigen, which can be chosen from glutamic acid decarboxylase
CC   (GAD), insulin or a heat shock protein (HSP), as well as epitopes derived
CC   from each thereof or beta cell antigens that are linked to an APC
CC   receptor antibody. In particular, the antibody recognises a receptor
CC   chosen from DC-SIGNR, MHC, toll receptor or mannose receptor amongst
CC   others, which is expressed on the surface of the APC. The antibody/
CC   autoantigen construct then works to interfere with the interaction
CC   between the APC and immune cells such as autoreactive T cells, and hence
CC   inhibits T-cell proliferation. Accordingly, such compositions exhibit
CC   antidiabetic and immunosuppressive activities and can be used in the
CC   development of vaccines. Note that the single chain antibodies (scFVs)
CC   used in this specification contain both variable light and heavy chain
CC   regions connected by a linker, their short length makes these antibody
CC   fragments particularly suitable for antigen linkage, and the capacity for
CC   binding to the receptor is preserved. This polypeptide sequence is a
CC   light chain murine anti-human L-SIGN (hL-SIGN) antibody protein of the
CC   invention.
XX
SQ   Sequence 108 AA;

  Query Match             94.1%;  Score 48;  DB 8;  Length 108;
  Best Local Similarity   90.9%;  Pred. No. 0.16;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||:||
Db         23 KASQDVGTAVA 33


RESULT 48
ADT75067
ID   ADT75067 standard; protein; 109 AA.
XX
AC   ADT75067;
XX
DT   13-JAN-2005  (first entry)
XX
DE   Light chain murine anti-hDC-SIGNR IgG1k antibody protein G3 Seq 113.
XX
KW   autoimmune disease; antibody; antigen presenting cell; APC;
KW   diabetes mellitus; immune tolerance; antidiabetic; immunosuppressive;
KW   vaccine; hDC-SIGNR; IgG1k.
XX
OS   Mus sp.
XX
PN   WO2004091543-A2.
XX
PD   28-OCT-2004.
XX
PF   04-MAR-2004; 2004WO-US006570.
XX
PR   04-MAR-2003; 2003US-0451816P.
PR   15-DEC-2003; 2003US-0529500P.
PR   28-FEB-2004; 2004US-0548385P.
XX
PA   (ALEX-) ALEXION PHARM INC.
XX
PI   Bowdish KS,  Kretz-Rommel A,  Dakappagari N;
XX
DR   WPI; 2004-758274/74.
XX
PT   Treating an autoimmune disease comprises providing an
PT   antibody/autoantigen construct containing an autoantigen linked to an
PT   antibody to a receptor of an antigen presenting cell and administering
PT   the construct to a subject.
XX
PS   Example 10; Fig 11; 71pp; English.
```

XX
CC This invention relates to the novel treatment of an autoimmune disease
CC that utilises an antibody/ autoantigen construct. Specifically, it refers
CC to a peptide autoantigen that is linked to an antibody raised against an
CC antigen presenting cell (APC) receptor. The present invention describes a
CC method for treating diabetes mellitus by inducing an immune tolerance to
CC an autoantigen, which can be chosen from glutamic acid decarboxylase
CC (GAD), insulin or a heat shock protein (HSP), as well as epitopes derived
CC from each thereof or beta cell antigens that are linked to an APC
CC receptor antibody. In particular, the antibody recognises a receptor
CC chosen from DC-SIGNR, MHC, toll receptor or mannose receptor amongst
CC others, which is expressed on the surface of the APC. The antibody/
CC autoantigen construct then works to interfere with the interaction
CC between the APC and immune cells such as autoreactive T cells, and hence
CC inhibits T-cell proliferation. Accordingly, such compositions exhibit
CC antidiabetic and immunosuppressive activities and can be used in the
CC development of vaccines. Note that the single chain antibodies (scFVs)
CC used in this specification contain both variable light and heavy chain
CC regions connected by a linker, their short length makes these antibody
CC fragments particularly suitable for antigen linkage, and the capacity for
CC binding to the receptor is preserved. This polypeptide sequence is a
CC light chain murine anti-human DC-SIGNR (hDC-SIGNR) IgG1k antibody protein
CC of the invention.
XX
SQ Sequence 109 AA;

```
  Query Match             94.1%;  Score 48;  DB 8;  Length 109;
  Best Local Similarity   90.9%;  Pred. No. 0.16;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||:||
Db         24 KASQDVGTAVA 34
```

RESULT 49
ABB07359
ID ABB07359 standard; protein; 115 AA.
XX
AC ABB07359;
XX
DT 09-APR-2002 (first entry)
XX
DE 22A5 IgM light chain variable region.
XX
KW Immunoglobulin; Ig; reperfusion; ischaemic injury; pathogenic;
KW vasotropic; antibody; 22A5; IgM.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Misc-difference 109
FT /note= "encoded by TGA"
XX
PN WO200193892-A1.
XX
PD 13-DEC-2001.
XX
PF 08-JUN-2001; 2001WO-US018510.
XX
PR 08-JUN-2000; 2000US-0210272P.
XX
PA (BLOO-) CENT BLOOD RES INC.
XX
PI Carroll MC, Moore FD, Hechtman HB;
XX
DR WPI; 2002-139643/18.
DR N-PSDB; ABA94516.
XX
PT Treating or preventing immunoglobulin-mediated reperfusion or ischemic
PT injury resulting from e.g. angioplasty or bypass surgery, by
PT administering an inhibitor of pathogenic immunoglobulin and ischemic
PT antigen interaction.
XX
PS Claim 50; Page 73-74; 77pp; English.
XX
CC The invention provides a method of treating or preventing immunoglobulin-
CC mediated reperfusion or ischemic injury in a subject. The method involves
CC administering an inhibitor of an interaction between a pathogenic
CC immunoglobulin, and an ischemic-specific antigen or a component of the
CC complement pathway. The method is useful for treating or preventing
CC immunoglobulin-mediated reperfusion or ischemic injury, in particular,
CC injury that results following a naturally occurring episode, a surgical
CC procedure (e.g. angioplasty, stenting procedure, atherectomy or bypass
CC surgery), or in an injury that occurs in a cardiovascular tissue. The
CC method is also useful for treating or preventing, in a subject, tissue
CC damage following reperfusion caused by a pathogenic immunoglobulin, e.g.
CC pathogenic IgMs. The present sequence represents the light chain variable
CC region of 22A5 IgM, a pathogenic immunoglobulin
XX
SQ Sequence 115 AA;

```
  Query Match             94.1%;  Score 48;  DB 5;  Length 115;
  Best Local Similarity   90.9%;  Pred. No. 0.17;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||:||
Db         23 KASQDVGTAVA 33
```

RESULT 50
ADT74992
ID ADT74992 standard; protein; 115 AA.
XX
AC ADT74992;
XX
DT 13-JAN-2005 (first entry)
XX
DE Light chain murine anti-hL-SIGN scFV antibody protein A1LC Seq 38.
XX
KW autoimmune disease; antibody; antigen presenting cell; APC;
KW diabetes mellitus; immune tolerance; antidiabetic; immunosuppressive;
KW vaccine; hL-SIGN.
XX
OS Mus sp.
XX
PN WO2004091543-A2.
XX
PD 28-OCT-2004.
XX
PF 04-MAR-2004; 2004WO-US006570.
XX
PR 04-MAR-2003; 2003US-0451816P.
PR 15-DEC-2003; 2003US-0529500P.
PR 28-FEB-2004; 2004US-0548385P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Kretz-Rommel A, Dakappagari N;
XX
DR WPI; 2004-758274/74.
XX
PT Treating an autoimmune disease comprises providing an
PT antibody/autoantigen construct containing an autoantigen linked to an
PT antibody to a receptor of an antigen presenting cell and administering
PT the construct to a subject.
XX
PS Example 9; Fig 8; 71pp; English.
XX
CC This invention relates to the novel treatment of an autoimmune disease
CC that utilises an antibody/ autoantigen construct. Specifically, it refers
CC to a peptide autoantigen that is linked to an antibody raised against an
CC antigen presenting cell (APC) receptor. The present invention describes a
CC method for treating diabetes mellitus by inducing an immune tolerance to
CC an autoantigen, which can be chosen from glutamic acid decarboxylase

CC (GAD), insulin or a heat shock protein (HSP), as well as epitopes derived
CC from each thereof or beta cell antigens that are linked to an APC
CC receptor antibody. In particular, the antibody recognises a receptor
CC chosen from DC-SIGNR, MHC, toll receptor or mannose receptor amongst
CC others, which is expressed on the surface of the APC. The antibody/
CC autoantigen construct then works to interfere with the interaction
CC between the APC and immune cells such as autoreactive T cells, and hence
CC inhibits T-cell proliferation. Accordingly, such compositions exhibit
CC antidiabetic and immunosuppressive activities and can be used in the
CC development of vaccines. Note that the single chain antibodies (scFVs)
CC used in this specification contain both variable light and heavy chain
CC regions connected by a linker, their short length makes these antibody
CC fragments particularly suitable for antigen linkage, and the capacity for
CC binding to the receptor is preserved. This polypeptide sequence is a
CC light chain murine anti-human L-SIGN (hL-SIGN) antibody protein of the
CC invention.
XX
SQ Sequence 115 AA;

Query Match 94.1%; Score 48; DB 8; Length 115;
Best Local Similarity 90.9%; Pred. No. 0.17;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 KASQDVGTSVA 11
              ||||||||:||
Db         24 KASQDVGTAVA 34
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Search completed: March 23, 2006, 01:51:27
Job time : 117.685 secs

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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:54:26 ; Search time 15.2192 Seconds
(without alignments)
69.543 Million cell updates/sec

Title: US-10-755-382-20
Perfect score: 51
Sequence: 1 KASQDVGTSVA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	48	94.1	117	2	S42466	Ig kappa chain V r
2	43	84.3	82	2	S38560	Ig light chain V r
3	43	84.3	90	2	S38561	Ig light chain V r
4	42	82.4	93	2	S38559	Ig light chain V r
5	42	82.4	107	2	S09967	Ig kappa chain V-J
6	42	82.4	107	2	S32191	Ig kappa chain V r
7	42	82.4	107	2	S32192	Ig kappa chain V r
8	42	82.4	119	2	PQ0265	Ig kappa chain V r
9	42	82.4	149	1	KVMS11	Ig kappa chain pre
10	39	76.5	88	2	A37262	Ig kappa chain V r
11	38	74.5	86	2	C28195	Ig kappa chain V r
12	38	74.5	106	2	PL0088	Ig kappa chain V r
13	38	74.5	107	2	B28195	Ig kappa chain V r
14	38	74.5	107	2	A28195	Ig kappa chain V r
15	38	74.5	128	2	A47159	Ig lambda chain V
16	37	72.5	98	2	PH1073	Ig light chain V r
17	37	72.5	110	2	D72673	hypothetical prote
18	37	72.5	115	2	A25924	Ig kappa chain pre
19	37	72.5	127	2	S04577	Ig kappa chain pre
20	37	72.5	152	2	S30751	Ig kappa chain pre
21	37	72.5	254	2	E69853	conserved hypothet
22	37	72.5	520	2	T19661	hypothetical prote
23	36	70.6	87	2	PH1082	Ig light chain V r
24	36	70.6	88	2	PL0261	Ig kappa chain V r
25	36	70.6	106	2	PL0260	Ig kappa chain V r
26	36	70.6	115	1	KVMSL7	Ig kappa chain pre
27	36	70.6	124	2	T40071	cytochrome b5 - fi
28	36	70.6	128	2	PN0445	Ig kappa chain pre
29	36	70.6	130	1	KVMSM4	Ig kappa chain pre
30	36	70.6	317	2	T33277	hypothetical prote
31	36	70.6	572	1	HNNZB3	hemagglutinin-neur
32	36	70.6	737	2	A87626	catalase/peroxidas
33	35	68.6	94	2	F33730	Ig kappa chain V r
34	35	68.6	165	2	JC5737	membrane-bound pro
35	35	68.6	250	2	G81447	major antigenic pe
36	35	68.6	298	2	B75429	hypothetical prote
37	34	66.7	91	2	PH1071	Ig light chain V r
38	34	66.7	96	2	PH1070	Ig light chain V r
39	34	66.7	98	2	PH1072	Ig light chain V r
40	34	66.7	100	2	H38601	Ig kappa chain V r
41	34	66.7	106	2	PL0259	Ig kappa chain V r
42	34	66.7	107	2	PL0268	Ig kappa chain V r
43	34	66.7	108	2	PL0083	Ig kappa chain V r
44	34	66.7	108	2	C30502	Ig kappa chain V r
45	34	66.7	108	2	PL0204	anti-DNA autoantib
46	34	66.7	125	2	S34435	protein-tyrosine k
47	34	66.7	131	2	PL0207	anti-idiotypic ant
48	34	66.7	252	2	T38219	40s ribosomal prot
49	34	66.7	565	2	A83361	penicillin-binding
50	34	66.7	975	1	TVMSKT	protein-tyrosine k
51	34	66.7	1052	2	T04439	hypothetical prote
52	33	64.7	90	2	I38601	Ig kappa chain V r
53	33	64.7	108	2	B44371	Ig kappa chain V r
54	33	64.7	122	2	S40351	Ig kappa chain V-J
55	33	64.7	144	2	B30502	Ig heavy chain V r
56	33	64.7	220	2	T23704	hypothetical prote
57	33	64.7	377	2	H89930	hypothetical prote
58	33	64.7	429	1	A31950	leucine dehydrogen
59	33	64.7	472	2	S39507	glucuronosyl trans
60	33	64.7	561	2	E82395	methyl-accepting c
61	33	64.7	609	1	JT0903	vibriolysin (EC 3.
62	33	64.7	962	2	T01688	starch debranching
63	33	64.7	984	2	AE0290	insecticial toxin
64	32.5	63.7	162	2	H75289	hypothetical prote
65	32	62.7	108	2	S40330	Ig kappa chain V-J
66	32	62.7	124	1	VKLJSI	trans-regulatory s
67	32	62.7	124	2	AH0558	probable exported
68	32	62.7	129	2	B23986	Ig kappa chain pre
69	32	62.7	218	2	B71056	hypothetical prote
70	32	62.7	341	2	F71042	hypothetical prote
71	32	62.7	375	2	E89862	hypothetical prote
72	32	62.7	407	2	S63136	probable membrane
73	32	62.7	465	2	T30155	hypothetical prote
74	32	62.7	493	2	H64072	ribose transport p
75	32	62.7	532	2	AB3552	alcohol dehydrogen
76	32	62.7	535	2	AB3064	GMC type oxidoredu
77	32	62.7	535	2	F98222	probable gmc-type
78	32	62.7	567	2	E84504	hypothetical prote
79	32	62.7	575	2	D96585	hypothetical prote
80	32	62.7	793	2	AB1750	exoribonuclease RN
81	32	62.7	970	2	T28234	ORF MSV076 probabl
82	32	62.7	976	1	TVMSMD	macrophage colony-
83	32	62.7	978	2	S16385	macrophage colony-
84	32	62.7	1417	2	T00661	hypothetical prote
85	32	62.7	13055	2	T16580	hypothetical prote
86	31	60.8	72	2	H36025	Ig heavy chain V r
87	31	60.8	81	2	G36025	Ig light chain V r
88	31	60.8	85	2	F36025	Ig light chain V r
89	31	60.8	91	2	S37511	Ig kappa chain V r
90	31	60.8	94	2	E33730	Ig kappa chain V r
91	31	60.8	97	2	PH1064	Ig light chain V r
92	31	60.8	104	2	S26330	Ig kappa chain V r
93	31	60.8	104	2	S26329	Ig kappa chain V r
94	31	60.8	119	2	G86642	hypothetical prote
95	31	60.8	125	2	S09365	Ig kappa chain - m
96	31	60.8	145	2	S43224	insulin-related pr
97	31	60.8	190	2	B69708	signal peptidase I
98	31	60.8	246	2	D70724	hypothetical prote
99	31	60.8	266	2	I49050	Ly-49E-GE antigen
100	31	60.8	266	2	I49051	Ly-49F-GE antigen
101	31	60.8	270	2	D84308	hypothetical prote
102	31	60.8	333	2	A36925	transcription acti

103	31	60.8	346	2	H71473	probable leucine d
104	31	60.8	364	2	S11981	variable major pro
105	31	60.8	431	2	S25196	mitochondrial impo
106	31	60.8	435	2	H87516	D-alanyl-D-alanine
107	31	60.8	474	2	A83347	probable outer mem
108	31	60.8	489	2	S71955	MDM2-like p53-bind
109	31	60.8	507	2	JC7855	pyridoxine 4-oxida
110	31	60.8	508	2	T20757	hypothetical prote
111	31	60.8	732	2	A69086	cell division cont
112	31	60.8	735	2	T49622	hypothetical prote
113	31	60.8	1089	2	S53978	PSE1 protein - yea
114	31	60.8	1124	2	T30340	dsRNA adenosine de
115	31	60.8	1270	2	T30339	dsRNA adenosine de
116	31	60.8	1358	2	A29360	SIR4 protein - yea
117	31	60.8	1403	2	T49093	hypothetical prote
118	31	60.8	3869	2	A48205	All-1 protein +GTE
119	31	60.8	4385	2	T29042	hypothetical prote
120	30	58.8	45	2	B43859	ORF overlapping ca
121	30	58.8	101	2	B37262	Ig kappa chain V r
122	30	58.8	114	2	S00996	Ig kappa chain pre
123	30	58.8	115	2	B25924	Ig kappa chain pre
124	30	58.8	167	2	F83686	hypothetical prote
125	30	58.8	194	2	H69169	hypothetical prote
126	30	58.8	207	2	AF0199	probable lipoprote
127	30	58.8	225	2	S37484	Ig kappa chain - m
128	30	58.8	227	2	A82500	hypothetical prote
129	30	58.8	239	1	LNMSMA	mannose-binding le
130	30	58.8	243	2	F83838	oxidoreductase (sh
131	30	58.8	252	2	S62431	40s ribosomal prot
132	30	58.8	260	2	T02051	14-3-3 protein hom
133	30	58.8	266	2	F86245	hypothetical prote
134	30	58.8	278	2	G64393	hypothetical prote
135	30	58.8	279	2	F84902	hypothetical prote
136	30	58.8	300	2	A86076	aldose 1-epimerase
137	30	58.8	300	2	B91229	probable aldose-1-
138	30	58.8	308	2	S40823	hypothetical 34K p
139	30	58.8	312	2	B96512	hypothetical prote
140	30	58.8	350	2	AD3170	two component sens
141	30	58.8	413	2	G95965	conserved hypothet
142	30	58.8	429	2	D64499	glycine hydroxymet
143	30	58.8	437	2	C75632	probable hemolysin
144	30	58.8	458	2	A26940	nitrogenase molybd
145	30	58.8	466	2	PC4296	nicotinic acetylch
146	30	58.8	481	2	T05270	probable serine/th
147	30	58.8	506	1	S31229	probable RNA helic
148	30	58.8	513	2	E83069	catalase PA4613 [i
149	30	58.8	523	2	B75467	phosphoribosylamin
150	30	58.8	524	2	E81678	glucose-6-phosphat
151	30	58.8	585	2	T47364	hypothetical prote
152	30	58.8	589	2	A71277	arginine-tRNA liga
153	30	58.8	594	1	D55514	dihydrolipoamide d
154	30	58.8	604	2	JC7252	transcription acti
155	30	58.8	610	2	T16194	hypothetical prote
156	30	58.8	633	2	H84336	Htr3 transducer [i
157	30	58.8	633	2	E31265	ipaA protein - Shi
158	30	58.8	749	2	E71275	hypothetical integ
159	30	58.8	751	2	B87391	TonB-dependent rec
160	30	58.8	805	2	T48840	transducer protein
161	30	58.8	852	2	C98310	hasR protein (Y089
162	30	58.8	873	2	E83148	leucyl-tRNA synthe
163	30	58.8	873	2	H96503	protein F9C16.17 [
164	30	58.8	888	2	E65057	hypothetical prote
165	30	58.8	923	2	AH2972	heme receptor hasR
166	30	58.8	983	2	B45583	receptor tyrosine
167	30	58.8	983	2	A38224	protein-tyrosine k
168	30	58.8	983	2	A45583	receptor tyrosine
169	30	58.8	984	2	T44496	cellulose 1,4-beta
170	30	58.8	998	2	A96827	hypothetical prote
171	30	58.8	1009	2	S64734	retrovirus-related
172	30	58.8	1009	2	S26840	retrovirus-related
173	30	58.8	1021	2	T51497	hypothetical prote
174	30	58.8	1035	1	GNFFG1	HIV-1 retropepsin
175	30	58.8	1065	2	H95321	NolG efflux transp
176	30	58.8	1113	2	T14260	period protein Per
177	30	58.8	1115	2	T13955	period protein Per
178	30	58.8	1286	2	S28634	adhesin AIDA-I pre
179	30	58.8	1662	2	T18540	mofA protein precu
180	30	58.8	1896	2	T08851	Down syndrome cell
181	30	58.8	1975	2	B81192	hemagglutinin/hemo
182	30	58.8	1995	2	G81044	hemagglutinin/hemo
183	30	58.8	2113	2	G91286	probable RNA helic
184	30	58.8	2113	2	C86128	probable helicase
185	30	58.8	5175	2	T20992	hypothetical prote
186	30	58.8	5198	2	T43290	hemicentin precurs
187	30	58.8	6669	2	S55024	nebulin, skeletal
188	29	56.9	59	2	T38172	hypothetical prote
189	29	56.9	67	1	Q7BPE7	gene 17.5 protein
190	29	56.9	67	1	Q7BPT3	lysis protein - ph
191	29	56.9	72	2	AF2574	hypothetical prote
192	29	56.9	83	2	S05975	tetracenomycin C-p
193	29	56.9	92	2	S37523	Ig kappa chain V r
194	29	56.9	105	2	PH0087	Ig kappa chain V r
195	29	56.9	106	2	C33936	Ig kappa chain V r
196	29	56.9	107	2	I69017	anti-HIV1 envelope
197	29	56.9	129	2	S40317	Ig kappa chain - h
198	29	56.9	129	2	S29627	Ig kappa chain V r
199	29	56.9	146	2	A40575	bradykinin-like pe
200	29	56.9	161	2	C83907	hypothetical prote
201	29	56.9	171	2	A49851	2-vinyl bacterioch
202	29	56.9	175	2	S56188	probable membrane
203	29	56.9	182	2	A64834	fimbrial-like prot
204	29	56.9	182	2	E90756	probable fimbrial-
205	29	56.9	182	2	C85620	probable fimbrial-
206	29	56.9	210	2	F72490	hypothetical prote
207	29	56.9	215	2	JE0243	Ig kappa chain NIG
208	29	56.9	229	2	B31775	clathrin light cha
209	29	56.9	238	1	LRRTB2	clathrin light cha
210	29	56.9	240	1	A70031	conserved hypothet
211	29	56.9	240	2	S13498	repressor protein
212	29	56.9	240	2	C69793	conserved hypothet
213	29	56.9	247	2	S37342	chitinase (EC 3.2.
214	29	56.9	250	1	Q5ADB2	polypeptide VI pre
215	29	56.9	250	1	Q5ADB5	polypeptide VI pre
216	29	56.9	251	2	S42356	triose-phosphate i
217	29	56.9	260	2	G87400	conserved hypothet
218	29	56.9	261	2	T40796	hypothetical prote
219	29	56.9	266	2	B87498	hypothetical prote
220	29	56.9	267	2	C97690	exodeoxyribonuclea
221	29	56.9	267	2	AH2915	exodeoxyribonuclea
222	29	56.9	268	2	E70551	probable oxidoredu
223	29	56.9	303	2	S50749	movement protein,
224	29	56.9	315	2	H83276	probable lipase PA
225	29	56.9	317	2	A83304	hypothetical prote
226	29	56.9	319	2	T47852	hypothetical prote
227	29	56.9	332	2	B75286	hypothetical prote
228	29	56.9	334	2	F84374	replication factor
229	29	56.9	334	2	T34485	hypothetical prote
230	29	56.9	337	2	T23591	cysteine synthase
231	29	56.9	338	2	H82615	3-oxoacyl-[ACP] sy
232	29	56.9	341	2	T27654	hypothetical prote
233	29	56.9	349	2	B83973	hypothetical prote
234	29	56.9	351	2	A88103	protein W10G11.7 [
235	29	56.9	357	2	T06308	protein phosphatas
236	29	56.9	364	1	B69962	probable leucine d
237	29	56.9	364	2	E83995	leucine dehydrogen
238	29	56.9	366	2	S45607	leucine dehydrogen
239	29	56.9	371	2	E84709	hypothetical prote
240	29	56.9	382	2	AG0567	glycerate kinase [
241	29	56.9	387	2	G97295	periplasmic trypsi
242	29	56.9	393	2	T25063	hypothetical prote
243	29	56.9	397	1	DCNCOP	orotidine-5'-phosp
244	29	56.9	401	2	B82868	plasmid replicatio
245	29	56.9	401	2	AD2385	hypothetical prote
246	29	56.9	404	2	F87393	aminotransferase,
247	29	56.9	407	2	T49708	probable 3-methyl-
248	29	56.9	425	2	AH1041	Vi polysaccharide

249	29	56.9	425	2	B36892	Vi polysaccharide
250	29	56.9	425	2	T36067	seryl-tRNA synthas
251	29	56.9	429	2	G42365	flagellar hook-len
252	29	56.9	430	2	T36892	hypothetical prote
253	29	56.9	436	2	T39118	probable alpha-gal
254	29	56.9	452	2	F70552	probable lpqF prot
255	29	56.9	454	2	H70167	xylulokinase (xylB
256	29	56.9	460	2	T51560	probable flavonol
257	29	56.9	461	2	S65666	actin-binding prot
258	29	56.9	464	2	T45612	N-hydroxycinnamoyl
259	29	56.9	492	2	T16659	hypothetical prote
260	29	56.9	503	2	G75262	hypothetical prote
261	29	56.9	505	2	JC2291	protein disulfide-
262	29	56.9	517	2	T18226	cytochrome P450 -
263	29	56.9	521	2	S40933	probable replicati
264	29	56.9	538	2	S54015	C-22 sterol desatu
265	29	56.9	570	2	A97238	membrane associate
266	29	56.9	605	2	JC5673	receptor tyrosine
267	29	56.9	610	2	I48612	developmental kina
268	29	56.9	611	1	A47015	vibriolysin (EC 3.
269	29	56.9	613	2	T01586	probable phragmopl
270	29	56.9	620	2	T39074	yeast chs5 homolog
271	29	56.9	621	2	T47843	dynamin-like prote
272	29	56.9	626	2	I48614	developmental kina
273	29	56.9	627	2	A98344	hypothetical prote
274	29	56.9	627	2	AF2938	conserved hypothet
275	29	56.9	663	2	C71551	probable DNA ligas
276	29	56.9	665	2	T18979	hypothetical prote
277	29	56.9	675	2	D65083	murein-lipoprotein
278	29	56.9	680	2	T27078	hypothetical prote
279	29	56.9	683	2	A82704	1,4-beta-cellobios
280	29	56.9	685	2	AF0850	hypothetical prote
281	29	56.9	688	2	T09941	transcription fact
282	29	56.9	692	2	T00025	PSD-95 binding pro
283	29	56.9	709	2	S73497	cell division prot
284	29	56.9	720	2	JQ1676	ABI3 protein - Ara
285	29	56.9	762	2	T14815	hypothetical prote
286	29	56.9	790	2	T12203	transcription fact
287	29	56.9	805	2	I40029	nitrite reductase
288	29	56.9	810	2	H88565	protein ZK632.1 [i
289	29	56.9	820	2	B72575	hypothetical prote
290	29	56.9	849	2	I50617	protein-tyrosine k
291	29	56.9	853	1	A41220	transforming growt
292	29	56.9	854	2	T23155	hypothetical prote
293	29	56.9	877	2	I48967	brain-specific kin
294	29	56.9	893	2	S51603	receptor-like tyro
295	29	56.9	898	2	S47489	receptor tyrosine
296	29	56.9	925	2	S45391	probable membrane
297	29	56.9	963	2	AF2119	hypothetical prote
298	29	56.9	964	2	T15746	hypothetical prote
299	29	56.9	976	2	A36355	protein-tyrosine k
300	29	56.9	977	2	S49004	tyrosine kinase Mp
301	29	56.9	981	2	S51604	receptor-like tyro
302	29	56.9	985	2	I51549	receptor tyrosine
303	29	56.9	986	2	I78844	receptor protein-t
304	29	56.9	986	2	S78059	protein-tyrosine k
305	29	56.9	991	2	I78843	receptor protein-t
306	29	56.9	998	2	I58351	receptor protein-t
307	29	56.9	998	2	JC5672	receptor tyrosine
308	29	56.9	1005	2	S49015	receptor tyrosine
309	29	56.9	1013	2	I50615	receptor-type prot
310	29	56.9	1176	2	S51408	hypothetical prote
311	29	56.9	1329	2	AB2934	peptide synthetase
312	29	56.9	1344	2	E98348	hypothetical prote
313	29	56.9	1374	2	A84888	hypothetical prote
314	29	56.9	1474	2	F69009	probable membrane
315	29	56.9	1779	2	T23130	hypothetical prote
316	29	56.9	2013	2	AD1129	probable peptidogl
317	29	56.9	2013	2	AI1489	probable peptidogl
318	29	56.9	2110	2	B44110	mycocerosate synth
319	29	56.9	2111	2	A70668	mycocerosate synth
320	29	56.9	2193	2	S44251	polyprotein - echo
321	29	56.9	2193	2	S44194	polyprotein - echo
322	29	56.9	2396	2	T13714	kakapo gene protei
323	29	56.9	3375	2	T19821	hypothetical prote
324	28.5	55.9	769	2	F89870	serine proteinase
325	28	54.9	45	2	F56273	probable bacterioc
326	28	54.9	77	2	B95003	hypothetical prote
327	28	54.9	89	2	A22775	Ig kappa chain pre
328	28	54.9	101	2	S59640	Ig light chain V r
329	28	54.9	102	2	PH1077	Ig light chain V r
330	28	54.9	103	2	S59846	hypothetical prote
331	28	54.9	106	2	S20652	Ig kappa chain V r
332	28	54.9	108	1	KVMS54	Ig kappa chain V r
333	28	54.9	108	1	KVRB12	Ig kappa chain V r
334	28	54.9	111	2	B37266	Ig kappa chain V r
335	28	54.9	112	2	F97875	hypothetical prote
336	28	54.9	115	1	KVMSL6	Ig kappa chain pre
337	28	54.9	120	2	E75344	hypothetical prote
338	28	54.9	123	2	B64774	ybaV protein - Esc
339	28	54.9	128	1	KVMST1	Ig kappa chain pre
340	28	54.9	128	2	PL0101	Ig kappa chain pre
341	28	54.9	143	2	A96819	hypothetical prote
342	28	54.9	148	2	F86718	hypothetical prote
343	28	54.9	153	2	T09521	embryonic abundant
344	28	54.9	153	2	T09518	embryonic abundant
345	28	54.9	164	2	T09516	embryonic abundant
346	28	54.9	164	2	T09517	embryonic abundant
347	28	54.9	176	2	T47724	peptidylprolyl iso
348	28	54.9	176	2	F71958	hypothetical prote
349	28	54.9	176	2	F69179	hypothetical prote
350	28	54.9	180	1	IGRT2	insulin-like growt
351	28	54.9	180	2	A24913	insulin-like growt
352	28	54.9	183	2	G96018	probable methylate
353	28	54.9	196	2	AC3629	3-octaprenyl-4-hyd
354	28	54.9	211	2	S08522	probable sodium-de
355	28	54.9	213	2	D86170	hypothetical prote
356	28	54.9	217	2	AB3476	hypothetical prote
357	28	54.9	227	2	S77870	dnaK-type molecula
358	28	54.9	228	2	C26599	clathrin light cha
359	28	54.9	232	2	H75189	cobalamin (5'-phos
360	28	54.9	233	2	H82789	conserved hypothet
361	28	54.9	234	2	S14237	Ig kappa chain pre
362	28	54.9	247	2	A81388	3-oxoacyl-[acyl-ca
363	28	54.9	248	2	S61960	hypothetical prote
364	28	54.9	249	2	F75272	N-acetylglutamate
365	28	54.9	255	2	JS0054	hypothetical 26.6K
366	28	54.9	255	2	B97087	ABC-type transport
367	28	54.9	259	2	S39741	3-oxoacyl- acyl-ca
368	28	54.9	260	2	A34752	proliferating cell
369	28	54.9	262	2	S57276	14-3-3 protein hom
370	28	54.9	267	2	H85090	14-3-3-like protei
371	28	54.9	268	2	E86962	probable oxidoredu
372	28	54.9	275	2	H87538	hypothetical prote
373	28	54.9	280	2	D70803	hypothetical prote
374	28	54.9	281	2	S54137	probable movement
375	28	54.9	284	2	H64204	spermidine/putresc
376	28	54.9	286	2	S73423	spermidine/putresc
377	28	54.9	300	2	AH0605	ribosomal protein
378	28	54.9	302	2	AG0594	probable membrane
379	28	54.9	304	2	S12975	coat protein - pot
380	28	54.9	310	2	T43147	hypothetical prote
381	28	54.9	312	2	D95111	dihydroorotate deh
382	28	54.9	312	2	T02406	hypothetical prote
383	28	54.9	312	2	B97427	hypothetical prote
384	28	54.9	313	2	AD3208	dihydrodipicolinat
385	28	54.9	314	2	S30900	deacetoxycephalosp
386	28	54.9	316	2	B70620	hypothetical prote
387	28	54.9	322	2	S56633	plant fibrillin pr
388	28	54.9	325	2	T38308	hypothetical prote
389	28	54.9	326	2	C69119	sodium-dependent p
390	28	54.9	327	2	B97318	probable membrane
391	28	54.9	330	2	B97980	dihydroorotate oxi
392	28	54.9	337	2	C87366	hypothetical prote
393	28	54.9	338	2	F82419	UDP-glucose 4-epim
394	28	54.9	341	2	T51311	malate dehydrogena

395	28	54.9	341	2	S57958	malate dehydrogena
396	28	54.9	346	2	T35215	hypothetical prote
397	28	54.9	347	1	DEPUMW	malate dehydrogena
398	28	54.9	347	2	S44167	malate dehydrogena
399	28	54.9	351	2	T48218	hypothetical prote
400	28	54.9	351	2	AH2205	hypothetical prote
401	28	54.9	362	2	A69769	hypothetical prote
402	28	54.9	370	1	BVECRD	rod shape-determin
403	28	54.9	370	2	AB0581	rod shape-determin
404	28	54.9	370	2	D85563	rod shape-determin
405	28	54.9	370	2	H90712	rod shape-determin
406	28	54.9	370	2	AG0317	rod shape-determin
407	28	54.9	371	2	E71446	probable protein k
408	28	54.9	373	2	T08077	malate dehydrogena
409	28	54.9	374	2	T22149	hypothetical prote
410	28	54.9	379	2	T36831	probable two-compo
411	28	54.9	379	2	B86712	hypothetical prote
412	28	54.9	379	2	S49999	40K protein - frog
413	28	54.9	386	1	A64433	probable hydro-lya
414	28	54.9	388	2	T43907	DNA gyrase chain B
415	28	54.9	388	2	T43899	DNA gyrase chain B
416	28	54.9	388	2	T43900	DNA gyrase chain B
417	28	54.9	388	2	T43906	DNA gyrase chain B
418	28	54.9	388	2	T43897	DNA gyrase chain B
419	28	54.9	388	2	T43898	DNA gyrase chain B
420	28	54.9	388	2	T43904	DNA gyrase chain B
421	28	54.9	389	2	T43903	DNA gyrase chain B
422	28	54.9	389	2	T43905	DNA gyrase chain B
423	28	54.9	389	2	T43902	DNA gyrase chain B
424	28	54.9	389	2	D86424	43.3K hypothetical
425	28	54.9	390	2	D69757	multidrug-efflux t
426	28	54.9	395	2	T21679	hypothetical prote
427	28	54.9	398	2	T26274	hypothetical prote
428	28	54.9	404	2	S73372	hypothetical prote
429	28	54.9	422	2	C89998	thereonine dehydra
430	28	54.9	422	2	S73369	hypothetical prote
431	28	54.9	425	2	H97964	pyrimidine-nucleos
432	28	54.9	425	2	D95097	pyrimidine-nucleos
433	28	54.9	428	2	T05521	alpha-amylase (EC
434	28	54.9	432	2	AI2097	phosphate permease
435	28	54.9	448	1	WMBP89	gene 8 protein - p
436	28	54.9	448	1	WMBP8Z	gene 8 protein - p
437	28	54.9	451	2	E97234	ethanolamine ammon
438	28	54.9	451	2	E72398	hypothetical prote
439	28	54.9	453	2	S40943	hypothetical prote
440	28	54.9	455	1	GQHUT1	tumor necrosis fac
441	28	54.9	467	2	B86225	protein T12M4.6 [i
442	28	54.9	469	2	T36496	probable dihydroli
443	28	54.9	469	2	AE1220	ethanolamine utili
444	28	54.9	469	2	AH1573	ethanolamine utili
445	28	54.9	474	2	T20694	hypothetical prote
446	28	54.9	477	2	T47819	hypothetical prote
447	28	54.9	478	2	T35759	pyruvate kinase -
448	28	54.9	479	2	T47415	transporter-like p
449	28	54.9	485	2	C72801	gp14 protein - Myc
450	28	54.9	485	2	T27548	hypothetical prote
451	28	54.9	491	1	S24354	p53-binding protei
452	28	54.9	493	2	F84689	probable cytochrom
453	28	54.9	493	2	G84689	probable cytochrom
454	28	54.9	498	2	AC1086	ATP synthase alpha
455	28	54.9	498	2	AI1449	ATP synthase alpha
456	28	54.9	500	2	H91283	hypothetical prote
457	28	54.9	500	2	B86125	hypothetical prote
458	28	54.9	500	2	S56489	hypothetical 54.3K
459	28	54.9	516	2	S44191	carboxypeptidase D
460	28	54.9	517	2	T49310	hypothetical prote
461	28	54.9	527	2	E72016	lysine-tRNA ligase
462	28	54.9	527	2	A86607	lysyl tRNA synthet
463	28	54.9	527	2	H85230	hypothetical prote
464	28	54.9	527	2	A45611	probable hexose tr
465	28	54.9	529	1	VGNZSP	cell fusion glycop
466	28	54.9	530	2	A70589	probable efpA prot
467	28	54.9	533	2	T50401	hypothetical coile
468	28	54.9	540	2	G90068	choline transporte
469	28	54.9	543	2	B82215	methyl-accepting c
470	28	54.9	546	2	B47073	chaperonin GroEL -
471	28	54.9	546	2	B54539	heat shock protein
472	28	54.9	548	2	S27958	transcription fact
473	28	54.9	554	2	T48483	hypothetical prote
474	28	54.9	558	2	S63148	probable membrane
475	28	54.9	566	2	AC0559	probable solute-bi
476	28	54.9	571	2	A81797	hypothetical prote
477	28	54.9	573	2	B70942	hypothetical prote
478	28	54.9	583	2	S67571	hypothetical prote
479	28	54.9	589	2	D84530	probable Ta11-like
480	28	54.9	599	2	A48863	limonene cyclase -
481	28	54.9	602	2	E97551	single-strandeD-DN
482	28	54.9	602	2	AF2771	single-stranded-DN
483	28	54.9	607	2	D86305	hypothetical prote
484	28	54.9	609	2	JC5756	vibriolysin (EC 3.
485	28	54.9	611	2	T44560	hypothetical prote
486	28	54.9	616	2	A40595	methylmalonyl-CoA
487	28	54.9	640	2	AB2251	glucose inhibited
488	28	54.9	641	2	S69651	SAC2 protein - yea
489	28	54.9	658	2	S50831	endoglin precursor
490	28	54.9	663	2	S67259	MNE1 protein - yea
491	28	54.9	676	2	T33853	hypothetical prote
492	28	54.9	703	2	AG0242	probable membrane
493	28	54.9	709	2	H95104	transcription regu
494	28	54.9	710	2	S60042	phenylalanine ammo
495	28	54.9	715	2	H97972	hypothetical prote
496	28	54.9	739	2	T12964	subtilisin homolog
497	28	54.9	748	2	H84913	probable ATP-depen
498	28	54.9	780	2	AC3443	glycine-tRNA ligas
499	28	54.9	787	2	S72725	guanosine-3',5'bis
500	28	54.9	790	2	F70725	probable relA prot
501	28	54.9	803	2	T18246	DNA mismatch repai
502	28	54.9	806	1	A64078	DNA topoisomerase
503	28	54.9	806	1	S12608	DNA topoisomerase
504	28	54.9	806	2	H83644	DNA gyrase subunit
505	28	54.9	815	2	T36671	probable helicase
506	28	54.9	825	2	T46311	hypothetical prote
507	28	54.9	830	2	I50455	prolactin receptor
508	28	54.9	831	2	JC7880	glucosylceramidase
509	28	54.9	832	2	G85497	probable fimbrial
510	28	54.9	853	2	S49876	gamma-adaptin - sm
511	28	54.9	863	2	T49709	related to glucan
512	28	54.9	866	2	G90646	hypothetical prote
513	28	54.9	882	2	C83234	hypothetical prote
514	28	54.9	905	2	AH2892	hypothetical prote
515	28	54.9	905	2	C97668	ABC transporter re
516	28	54.9	948	2	S51605	receptor-like tyro
517	28	54.9	980	1	S45444	BEM1 protein-bindi
518	28	54.9	982	2	A53253	microtubule-associ
519	28	54.9	987	1	JQ0016	6-phosphofructokin
520	28	54.9	992	2	T27479	hypothetical prote
521	28	54.9	1029	2	H86179	hypothetical prote
522	28	54.9	1029	2	D83120	probable RND efflu
523	28	54.9	1045	2	A39199	endoglucanase B (E
524	28	54.9	1152	2	A33183	microtubule-associ
525	28	54.9	1175	2	S26874	DNA-directed RNA p
526	28	54.9	1185	2	T46428	hypothetical prote
527	28	54.9	1188	2	T20333	hypothetical prote
528	28	54.9	1223	2	S29717	adenylate cyclase
529	28	54.9	1254	2	E86160	hypothetical prote
530	28	54.9	1277	2	T30532	neural cell adhesi
531	28	54.9	1375	2	T42586	major capsid prote
532	28	54.9	1376	1	VCBED6	major capsid prote
533	28	54.9	1451	2	S65571	pattern formation
534	28	54.9	1475	2	F86399	protein F17L21.22
535	28	54.9	1517	2	T13329	hypothetical prote
536	28	54.9	1585	2	B69948	phage-related prot
537	28	54.9	1621	2	S62356	TRP-185 protein -
538	28	54.9	2035	2	A40718	host cell factor C
539	28	54.9	2285	2	T12796	probable transglyc
540	28	54.9	2322	2	T10542	hypothetical prote

541	28	54.9	2541	2	S11661	talin - mouse
542	28	54.9	3429	2	T13853	hypothetical prote
543	28	54.9	13288	2	T03099	mucin, submaxillar
544	27.5	53.9	184	2	D75305	conserved hypothet
545	27.5	53.9	185	2	A97118	probable sigma fac
546	27.5	53.9	2338	2	I73957	kinase-related pro
547	27	52.9	37	2	G01887	MEK kinase - human
548	27	52.9	43	2	PH0883	Ig kappa chain V r
549	27	52.9	54	2	B36943	chemoreceptor prot
550	27	52.9	83	2	E71267	hypothetical prote
551	27	52.9	93	2	S37501	Ig kappa chain V r
552	27	52.9	93	2	I47624	Ig heavy chain V-V
553	27	52.9	94	2	PH1063	Ig light chain V r
554	27	52.9	98	2	PH1065	Ig kappa chain V r
555	27	52.9	101	2	S13701	Ig kappa chain V r
556	27	52.9	102	2	H87678	hypothetical prote
557	27	52.9	103	2	S13703	Ig kappa chain V r
558	27	52.9	104	2	S13700	Ig kappa chain V r
559	27	52.9	107	2	S57444	Ig kappa chain V-J
560	27	52.9	107	2	S38713	Ig light chain V r
561	27	52.9	107	2	S33132	Ig kappa chain V r
562	27	52.9	114	2	S22559	Ig heavy chain V r
563	27	52.9	115	1	K3HU15	Ig kappa chain pre
564	27	52.9	117	2	S46376	Ig kappa chain V-J
565	27	52.9	119	2	S08077	Ig kappa chain pre
566	27	52.9	125	2	S40344	Ig kappa chain V-J
567	27	52.9	127	2	S52447	Ig kappa chain V r
568	27	52.9	128	2	T06985	probable phenylala
569	27	52.9	129	2	S40332	Ig kappa chain - h
570	27	52.9	129	2	S50381	probable membrane
571	27	52.9	131	2	H95339	hypothetical prote
572	27	52.9	135	2	S31604	Ig heavy chain V r
573	27	52.9	145	2	S43680	csmN protein - Chl
574	27	52.9	145	2	T00987	hypothetical prote
575	27	52.9	147	2	AD3081	hypothetical prote
576	27	52.9	147	2	D98205	hypothetical prote
577	27	52.9	148	2	B87366	MaoC family protei
578	27	52.9	148	2	B71137	hypothetical prote
579	27	52.9	151	2	E43584	15K cysteine-rich
580	27	52.9	152	2	F43584	15K cysteine-rich
581	27	52.9	154	2	G82980	conserved hypothet
582	27	52.9	161	1	S76604	hypothetical prote
583	27	52.9	165	2	D84200	hypothetical prote
584	27	52.9	171	2	AF0601	outer membrane pro
585	27	52.9	171	2	F85590	outer membrane pro
586	27	52.9	171	2	D90740	outer membrane pro
587	27	52.9	171	2	I55173	outer membrane pro
588	27	52.9	171	2	AD3400	N utilization subs
589	27	52.9	173	2	E41841	hypothetical prote
590	27	52.9	173	2	AF1872	bilin biosynthesis
591	27	52.9	176	2	T50767	peptidylprolyl iso
592	27	52.9	178	2	E88637	protein W09G12.6 [
593	27	52.9	180	2	AF2397	hypothetical prote
594	27	52.9	184	1	A24181	probable alcohol d
595	27	52.9	185	2	G96597	hypothetical prote
596	27	52.9	192	2	A95901	conserved hypothet
597	27	52.9	205	2	H87489	NADH dehydrogenase
598	27	52.9	208	2	T35820	probable integral
599	27	52.9	209	2	S69275	cGMP-gated cation
600	27	52.9	213	2	S17537	fibrinolytic prote
601	27	52.9	213	2	G75521	ABC transporter, A
602	27	52.9	219	2	D97793	cytidylate kinase
603	27	52.9	219	2	B71656	cytidylate kinase
604	27	52.9	221	1	F53402	cysteine-tRNA liga
605	27	52.9	221	2	F84960	membrane-bound lyt
606	27	52.9	221	2	JC7587	stromal cell-deriv
607	27	52.9	229	2	B83281	histidine transpor
608	27	52.9	229	2	G97138	hypothetical prote
609	27	52.9	237	1	A36056	tumor-associated a
610	27	52.9	241	2	A69885	hypothetical prote
611	27	52.9	241	2	AG0857	hypothetical prote
612	27	52.9	242	2	A43904	homeotic protein G
613	27	52.9	243	2	T13105	minor tail protein
614	27	52.9	245	2	F90597	protein phosphatas
615	27	52.9	245	2	F84270	ornithine carbamoy
616	27	52.9	246	2	B89896	3-oxoacyl-(acyl-ca
617	27	52.9	246	2	A69621	3-oxoacyl-[acyl-ca
618	27	52.9	256	2	F82304	sugar fermentation
619	27	52.9	256	2	E83949	hypothetical prote
620	27	52.9	256	2	AE1203	conserved hypothet
621	27	52.9	258	2	T11741	25K protein - fles
622	27	52.9	259	2	T36157	probable secreted
623	27	52.9	262	2	S42540	ribosomal protein
624	27	52.9	263	2	AB0812	probable oxidoredu
625	27	52.9	264	2	S52102	thioether S-methyl
626	27	52.9	265	2	AD0214	PTS system, mannos
627	27	52.9	268	2	F87487	ribosomal protein
628	27	52.9	269	2	H70179	spermidine/putresc
629	27	52.9	269	2	AH1175	spermidine/putresc
630	27	52.9	269	2	AF1532	spermidine/putresc
631	27	52.9	272	2	I51164	chip aquaporin - e
632	27	52.9	272	2	F75412	spermidine/putresc
633	27	52.9	272	2	S59762	L-aminoadipate-sem
634	27	52.9	273	2	T47822	hypothetical prote
635	27	52.9	276	2	D83786	glycerol uptake fa
636	27	52.9	276	2	T37562	probable n-acetylg
637	27	52.9	278	2	F70065	two-component sens
638	27	52.9	281	1	MMECUE	sn-Glycerol-3-phos
639	27	52.9	281	2	A86012	hypothetical prote
640	27	52.9	281	2	A91166	hypothetical prote
641	27	52.9	286	2	A82159	hypothetical prote
642	27	52.9	288	2	C70722	hypothetical prote
643	27	52.9	292	2	A64073	D-ribose-binding p
644	27	52.9	293	2	B87303	chemotaxis protein
645	27	52.9	294	2	A90542	hypothetical prote
646	27	52.9	296	2	C82640	hypothetical prote
647	27	52.9	298	2	H64901	probable oligopept
648	27	52.9	298	2	A90890	probable transport
649	27	52.9	298	2	H85727	probable transport
650	27	52.9	298	2	E95286	hypothetical prote
651	27	52.9	299	2	AH0602	probable formate a
652	27	52.9	302	2	B83748	transcription regu
653	27	52.9	304	2	C84387	L-malate dehydroge
654	27	52.9	305	2	F86456	unknown protein [i
655	27	52.9	305	2	AB2149	hypothetical prote
656	27	52.9	307	2	C70621	probable argF prot
657	27	52.9	307	2	S26215	ornithine carbamoy
658	27	52.9	310	1	S68977	tetrahydromethanop
659	27	52.9	310	1	A69021	tetrahydromethanop
660	27	52.9	310	2	F84098	HPr (Ser/Thr) prot
661	27	52.9	313	2	A34677	secretory pathway
662	27	52.9	314	2	D87576	oxidoreductase, al
663	27	52.9	318	2	AG0829	sigma-E factor reg
664	27	52.9	318	2	T02998	sigma-E factor reg
665	27	52.9	322	2	AE3617	dihydrodipicolinat
666	27	52.9	323	2	T45531	agaB protein [impo
667	27	52.9	323	2	G83291	probable transcrip
668	27	52.9	324	2	G69515	transcription regu
669	27	52.9	325	2	T02117	hypothetical prote
670	27	52.9	330	2	D97235	probable hydrolase
671	27	52.9	330	2	F69471	atrazine chlorohyd
672	27	52.9	331	2	F64047	D-2-hydroxy-acid d
673	27	52.9	333	2	T52594	squamosa promoter
674	27	52.9	337	2	A83939	transcription regu
675	27	52.9	339	2	T06546	phenylalanine ammo
676	27	52.9	340	2	B71258	probable histidine
677	27	52.9	343	2	F95915	probable sugar ABC
678	27	52.9	344	2	C82835	anthranilate phosp
679	27	52.9	345	2	H72429	muconate cycloisom
680	27	52.9	349	2	F84246	hypothetical prote
681	27	52.9	351	2	A82006	hypothetical prote
682	27	52.9	355	2	G95332	probable adenylate
683	27	52.9	357	2	AF1729	protein gp20 (Bact
684	27	52.9	357	2	AD3491	hypothetical membr
685	27	52.9	358	2	JC5176	valine dehydrogena
686	27	52.9	359	2	S52650	omega-3 fatty acid

687	27	52.9	359	2	AG2005	omega-3 fatty acid
688	27	52.9	359	2	S55032	dpy-20 protein - C
689	27	52.9	359	2	T25097	hypothetical prote
690	27	52.9	360	2	AB0160	probable FecCD-fam
691	27	52.9	361	2	T46704	hypothetical prote
692	27	52.9	362	1	S43454	3-isopropylmalate
693	27	52.9	362	2	AI2113	hypothetical prote
694	27	52.9	364	2	B40657	valine dehydrogena
695	27	52.9	364	2	A84099	hypothetical prote
696	27	52.9	369	2	AF3508	membrane-bound lyt
697	27	52.9	370	2	AB0090	probable flagellar
698	27	52.9	372	2	T02346	hypothetical prote
699	27	52.9	377	2	C97129	moxR-like ATPase [
700	27	52.9	384	2	T35407	conserved hypothet
701	27	52.9	387	2	H82176	carboxynorspermidi
702	27	52.9	389	2	T02158	hypothetical prote
703	27	52.9	391	2	S23341	paired box transcr
704	27	52.9	391	2	H70041	probable transcrip
705	27	52.9	394	2	E70135	flagellar protein
706	27	52.9	395	2	D83412	probable secretion
707	27	52.9	396	2	A45608	pyruvate dehydroge
708	27	52.9	396	2	H96675	hypothetical prote
709	27	52.9	397	2	S09813	hypothetical prote
710	27	52.9	400	2	C97200	uncharacterized co
711	27	52.9	402	2	AC1945	chromate transport
712	27	52.9	403	2	JS0066	S-antigen - mouse
713	27	52.9	403	2	S03960	S-antigen - rat
714	27	52.9	404	2	A28404	S-antigen - bovine
715	27	52.9	408	2	G83406	conserved hypothet
716	27	52.9	414	2	F70778	hypothetical prote
717	27	52.9	418	2	F82638	hypothetical prote
718	27	52.9	422	2	H64600	UDP-N-acetylglucos
719	27	52.9	424	2	E96902	seryl-tRNA synthet
720	27	52.9	425	2	A83478	probable two-compo
721	27	52.9	425	2	H82183	conserved hypothet
722	27	52.9	429	1	VHVUHV	nucleocapsid prote
723	27	52.9	430	2	H86842	hypothetical prote
724	27	52.9	430	2	S52580	3-phosphoshikimate
725	27	52.9	434	2	B72328	conserved hypothet
726	27	52.9	435	2	S27453	meiotic recombinat
727	27	52.9	442	2	H86276	F14L17.4 protein -
728	27	52.9	444	2	AB1986	nitrogenase olybde
729	27	52.9	446	2	F64172	hypothetical prote
730	27	52.9	447	2	G85614	probable polynucle
731	27	52.9	447	2	AH0611	conserevd hypothet
732	27	52.9	447	2	C64828	probable polynucle
733	27	52.9	447	2	A99751	probable polynucle
734	27	52.9	447	2	AD0168	probable ATPase pr
735	27	52.9	448	2	I50730	yes-associated pro
736	27	52.9	449	2	G82241	conserved hypothet
737	27	52.9	449	2	T22777	hypothetical prote
738	27	52.9	450	2	G83536	hypothetical prote
739	27	52.9	450	2	T17234	hypothetical prote
740	27	52.9	454	2	D71895	probable type I re
741	27	52.9	454	2	A56954	yes-associated pro
742	27	52.9	454	2	F87149	probale secreted p
743	27	52.9	455	2	AI1352	fumarate hydratase
744	27	52.9	455	2	AD1723	fumarate hydratase
745	27	52.9	455	2	S71344	purinergic recepto
746	27	52.9	455	2	T32189	zinc finger protei
747	27	52.9	455	2	B64860	ymfN protein - Esc
748	27	52.9	456	2	T36912	probable periplasm
749	27	52.9	461	2	JC4302	tumor necrosis fac
750	27	52.9	461	2	A53370	arginine catabolis
751	27	52.9	464	2	E82865	conjugal transfer
752	27	52.9	467	1	HLMSP3	poliovirus recepto
753	27	52.9	472	2	B56954	yes-associated pro
754	27	52.9	472	2	AF2803	transcription regu
755	27	52.9	472	2	F97582	probable transcrip
756	27	52.9	474	2	AB2990	polysaccharide bio
757	27	52.9	474	2	G98293	polysaccharide bio
758	27	52.9	475	2	B37761	ntrA protein - Thi
759	27	52.9	478	2	A72721	probable Glycerol
760	27	52.9	482	2	S76127	hypothetical prote
761	27	52.9	482	2	AC0426	serine-type D-Ala-
762	27	52.9	487	2	T35308	probable regulator
763	27	52.9	487	2	S65811	finger protein (cl
764	27	52.9	489	2	S15349	mdm2 protein - mou
765	27	52.9	491	2	S73110	hypothetical prote
766	27	52.9	491	2	T20061	hypothetical prote
767	27	52.9	492	2	T28025	hypothetical prote
768	27	52.9	495	2	C83598	hypothetical prote
769	27	52.9	502	2	D84119	ATP synthase alpha
770	27	52.9	502	2	I40366	H+-transporting tw
771	27	52.9	504	2	S17724	H+-transporting tw
772	27	52.9	507	2	S33192	phase-1 flagellin
773	27	52.9	508	2	A53465	phase 1 flagellin
774	27	52.9	510	2	T49308	hypothetical prote
775	27	52.9	512	2	AB2047	hypothetical prote
776	27	52.9	514	2	F64899	nitrate reductase
777	27	52.9	519	2	S23796	modifier-3 protein
778	27	52.9	521	2	D96668	protein F1N19.1 [i
779	27	52.9	522	2	AE0137	cytochrome D ubiqu
780	27	52.9	522	2	T40520	hypothetical prote
781	27	52.9	524	1	T40127	IMP dehydrogenase
782	27	52.9	524	1	S36175	glycerol kinase (E
783	27	52.9	524	2	JN0606	ATP-stimulated glu
784	27	52.9	524	2	S71961	translation initia
785	27	52.9	544	2	A55146	guanine nucleotide
786	27	52.9	544	2	T29325	hypothetical prote
787	27	52.9	545	2	E97728	DNA repair protein
788	27	52.9	547	2	S75904	hypothetical prote
789	27	52.9	551	2	JC2562	chaperonin groELx
790	27	52.9	567	2	C82183	catalase VC1585 [i
791	27	52.9	567	2	A70603	hypothetical prote
792	27	52.9	569	2	S59398	probable membrane
793	27	52.9	572	2	A47127	tetracenomycin syn
794	27	52.9	582	2	A70841	probable oxalyl-Co
795	27	52.9	585	2	A83020	probable carbamoyl
796	27	52.9	586	2	T36252	probable arginyl-t
797	27	52.9	588	2	A43740	DG42 protein - Afr
798	27	52.9	591	2	A30098	developmental prot
799	27	52.9	596	2	F82174	methyl-accepting c
800	27	52.9	610	2	S59558	dynamin-like prote
801	27	52.9	610	2	S63667	phragmoplastin 12
802	27	52.9	610	2	S63668	phragmoplastin 5 -
803	27	52.9	611	2	C81388	succinate dehydrog
804	27	52.9	617	2	S48160	metalloproteinase
805	27	52.9	620	2	AF0273	probable iron-sulf
806	27	52.9	623	2	AH1209	B. subtilis minor
807	27	52.9	626	2	AD2053	ATP-binding protei
808	27	52.9	627	2	T47968	dynamin-like prote
809	27	52.9	629	2	E64046	mismatch repair pr
810	27	52.9	631	2	T29926	hypothetical prote
811	27	52.9	632	2	E69407	NADH oxidase (noxB
812	27	52.9	632	2	G69306	NADH oxidase (noxB
813	27	52.9	633	2	F83028	DNA mismatch repai
814	27	52.9	636	2	AI0057	chaperone protein
815	27	52.9	636	2	T37843	probable beta-gluc
816	27	52.9	637	2	S35221	globulin Beg1 prec
817	27	52.9	638	1	IQECDK	dnaK-type molecula
818	27	52.9	638	2	AE0503	DnaK protein (heat
819	27	52.9	638	2	F90630	heat shock protein
820	27	52.9	638	2	F85481	dnaK-type molecula
821	27	52.9	640	2	T45924	protein kinase-lik
822	27	52.9	643	2	H64119	threonine-tRNA lig
823	27	52.9	661	2	A55877	tumor necrosis fac
824	27	52.9	663	2	D97047	DNA ligase (NAD de
825	27	52.9	664	2	F70483	glycine-tRNA ligas
826	27	52.9	669	2	A97229	NAD-dependent DNA
827	27	52.9	669	2	S53948	hypothetical prote
828	27	52.9	672	2	F36891	transfer complex p
829	27	52.9	673	2	T00328	hypothetical prote
830	27	52.9	676	2	G96593	probable protein k
831	27	52.9	681	1	H82059	2',3'-cyclic-nucle
832	27	52.9	687	2	A46212	MEK kinase - mouse

833	27	52.9	694	2	F82511	vgrG protein VCA00
834	27	52.9	695	2	G84137	methyl-accepting c
835	27	52.9	708	2	T19474	hypothetical prote
836	27	52.9	709	2	S33907	glycerol kinase (E
837	27	52.9	709	2	A35364	carcinoembryonic a
838	27	52.9	710	1	XJHQFK	formaldehyde trans
839	27	52.9	722	2	S52205	mesI protein - Leu
840	27	52.9	730	2	T46074	hypothetical prote
841	27	52.9	731	2	T15664	hypothetical prote
842	27	52.9	732	2	A90987	hypothetical prote
843	27	52.9	732	2	D85832	hypothetical prote
844	27	52.9	732	2	C64972	probable ATPase -
845	27	52.9	735	2	JC5869	beta-glucosidase (
846	27	52.9	748	2	T08612	ankyrin-like prote
847	27	52.9	755	2	T00066	hypothetical prote
848	27	52.9	763	2	JC4376	beta-glucosidase (
849	27	52.9	765	2	T04186	subtilisin-like pr
850	27	52.9	772	2	AG2367	DNA helicase II [i
851	27	52.9	774	2	A86454	hypothetical prote
852	27	52.9	775	1	JQ1638	outer layer protei
853	27	52.9	775	1	JQ1639	outer layer protei
854	27	52.9	775	2	T04189	subtilisin-like pr
855	27	52.9	785	2	H85036	hypothetical prote
856	27	52.9	786	2	S44837	K02D10.1 protein -
857	27	52.9	790	2	T30081	hypothetical prote
858	27	52.9	803	2	T04190	subtilisin-like pr
859	27	52.9	804	1	YFBSB	phenylalanine-tRNA
860	27	52.9	805	2	C86525	DNA gyrase subunit
861	27	52.9	805	2	H72098	DNA gyrase, chain
862	27	52.9	808	2	F84038	phenylalanyl-tRNA
863	27	52.9	815	2	AH0206	probable outer mem
864	27	52.9	816	2	AE2578	DNA gyrase subunit
865	27	52.9	816	2	D97360	hypothetical prote
866	27	52.9	822	2	S70012	methionine-S-oxide
867	27	52.9	826	2	D95330	cu2+-exporting ATP
868	27	52.9	836	2	S61570	regulatory protein
869	27	52.9	846	2	C82135	chitinase VC1952 [
870	27	52.9	859	1	VCLJST	env polyprotein pr
871	27	52.9	883	2	A36511	mannosyl-glycoprot
872	27	52.9	891	2	T30812	ubiquitin-protein
873	27	52.9	907	2	A27754	avirulence protein
874	27	52.9	910	2	A86782	cation-transportin
875	27	52.9	938	2	A56731	chromatin assembly
876	27	52.9	946	2	JC2130	protein kinase (EC
877	27	52.9	952	2	T18837	hypothetical prote
878	27	52.9	976	2	T01553	hypothetical prote
879	27	52.9	998	2	G83022	probable two-compo
880	27	52.9	1000	2	T21970	hypothetical prote
881	27	52.9	1039	2	A34269	integrin alpha-2b
882	27	52.9	1051	2	C95367	conserved hypothet
883	27	52.9	1071	2	T30881	dynein heavy chain
884	27	52.9	1081	2	T18223	histidine kinase -
885	27	52.9	1081	2	T18258	histidine kinase -
886	27	52.9	1081	2	T14003	histidine kinase h
887	27	52.9	1081	2	T14173	histidine kinase h
888	27	52.9	1095	2	G96746	hypothetical prote
889	27	52.9	1097	1	RNBYL3	DNA-directed DNA p
890	27	52.9	1106	2	T40931	nad-specific gluta
891	27	52.9	1141	2	A44093	cGMP-inhibited cAM
892	27	52.9	1165	2	I40644	botulinum neurotox
893	27	52.9	1174	2	AH0663	probable pyruvate-
894	27	52.9	1174	2	B85740	probable oxidoredu
895	27	52.9	1174	2	E64888	probable pyruvate
896	27	52.9	1174	2	H90878	probable oxidoredu
897	27	52.9	1177	2	AG0284	probable pyruvate-
898	27	52.9	1215	2	S60904	hypothetical prote
899	27	52.9	1275	2	T38397	probable GTPase ac
900	27	52.9	1321	2	T30537	adenylate cyclase
901	27	52.9	1329	2	T29074	hypothetical prote
902	27	52.9	1333	2	S30356	CDC25 protein homo
903	27	52.9	1398	2	T28159	pyrolysin (EC 3.4.
904	27	52.9	1444	1	A30588	140K adhesin precu
905	27	52.9	1493	2	T10757	MAP kinase kinase
906	27	52.9	1528	2	A60338	surface antigen A
907	27	52.9	1546	2	G90603	lipoprotein [impor
908	27	52.9	1557	2	T02859	probable serine/th
909	27	52.9	1687	2	T39072	DNA2-NAM7 helicase
910	27	52.9	1751	1	MMHUMH	laminin alpha-2 ch
911	27	52.9	1773	2	T05128	hypothetical prote
912	27	52.9	1788	2	T29043	hypothetical prote
913	27	52.9	1805	2	A34736	nestin - rat
914	27	52.9	1972	2	S68176	TOG protein - huma
915	27	52.9	2265	2	T26183	hypothetical prote
916	27	52.9	2271	2	F90073	hypothetical prote
917	27	52.9	2329	2	T28125	hypothetical prote
918	27	52.9	2409	1	A60979	versican precursor
919	27	52.9	2508	2	S61441	surface-associated
920	27	52.9	2617	2	AE2136	peptide synthetase
921	27	52.9	3034	2	T14119	seven-pass transme
922	27	52.9	3255	2	G81702	adherence factor T
923	27	52.9	3473	1	A46112	genome polyprotein
924	27	52.9	3473	2	S27927	polyprotein - rice
925	27	52.9	7962	2	I38346	elastic titin - hu
926	26.5	52.0	153	1	MYLEM	myoglobin - weasel
927	26.5	52.0	153	1	MYOY	myoglobin - aardva
928	26.5	52.0	153	1	MYRTNG	myoglobin - northe
929	26.5	52.0	246	2	T16371	hypothetical prote
930	26.5	52.0	510	2	AI2012	hypothetical prote
931	26	51.0	34	2	S55440	betaA2 crystallin
932	26	51.0	50	2	C34643	cathepsin E (EC 3.
933	26	51.0	59	2	D42799	photosystem I chai
934	26	51.0	66	2	S16201	photosystem I chai
935	26	51.0	70	2	AH2345	photosystem I prot
936	26	51.0	70	2	S51096	UMP kinase - Therm
937	26	51.0	72	2	A95351	Protein [imported
938	26	51.0	75	2	S60857	M protein precurso
939	26	51.0	80	1	G71267	conserved hypothet
940	26	51.0	80	2	T45103	H+-transporting tw
941	26	51.0	82	2	E87579	hypothetical prote
942	26	51.0	83	2	S78489	Ig kappa chain V r
943	26	51.0	84	2	S34099	Ig kappa chain V r
944	26	51.0	86	2	S16834	Ig kappa chain V r
945	26	51.0	86	2	S16824	Ig kappa chain V r
946	26	51.0	86	2	S16836	Ig kappa chain V r
947	26	51.0	86	2	S16839	Ig kappa chain V r
948	26	51.0	86	2	S16828	Ig kappa chain V r
949	26	51.0	86	2	S16829	Ig kappa chain V r
950	26	51.0	86	2	S16835	Ig kappa chain V r
951	26	51.0	87	2	S34098	Ig kappa chain V r
952	26	51.0	91	2	S37525	Ig kappa chain V r
953	26	51.0	91	2	S37527	Ig kappa chain V r
954	26	51.0	91	2	C30305	submandibular glan
955	26	51.0	91	2	AH0760	probable propanedi
956	26	51.0	91	2	AG1219	carboxysome struct
957	26	51.0	91	2	AB1573	carboxysome struct
958	26	51.0	91	2	A90350	conserved hypothet
959	26	51.0	94	2	AI0759	probable propanedi
960	26	51.0	94	2	AD1222	probable carboxyso
961	26	51.0	94	2	AG1575	probable carboxyso
962	26	51.0	95	2	PH0868	Ig kappa chain V r
963	26	51.0	96	1	XKPGC	cathelin - pig
964	26	51.0	99	1	S40865	C4-dicarboxylate t
965	26	51.0	99	2	G86081	hypothetical prote
966	26	51.0	99	2	G91234	hypothetical prote
967	26	51.0	100	2	B28487	apolipoprotein C-I
968	26	51.0	100	2	T50611	hypothetical prote
969	26	51.0	102	2	AH2151	hypothetical prote
970	26	51.0	102	2	B83934	hypothetical prote
971	26	51.0	106	2	PL0262	Ig kappa chain V r
972	26	51.0	106	2	S07520	host specificity p
973	26	51.0	107	2	S34005	Ig kappa chain V r
974	26	51.0	108	1	K1HUBI	Ig kappa chain V-I
975	26	51.0	108	2	S40377	Ig kappa chain - h
976	26	51.0	108	2	E87651	hypothetical prote
977	26	51.0	110	1	KVRB54	Ig kappa chain V r
978	26	51.0	110	2	S40326	Ig kappa chain V-J

979	26	51.0	111	2	G91043	detox protein [imp
980	26	51.0	111	2	H65020	cchA protein - Esc
981	26	51.0	111	2	B85888	detox protein [imp
982	26	51.0	113	2	G70754	hypothetical prote
983	26	51.0	115	1	VKLJND	trans-regulatory s
984	26	51.0	115	2	B46518	Ig L1 chain V regi
985	26	51.0	117	2	S40362	Ig kappa chain - h
986	26	51.0	120	2	B84364	H+-transporting AT
987	26	51.0	120	2	D82656	hypothetical prote
988	26	51.0	122	2	C87405	ribosomal protein
989	26	51.0	125	2	S04936	Ig kappa chain pre
990	26	51.0	125	2	C83760	hypothetical prote
991	26	51.0	126	2	F82072	holo-(acyl-carrier
992	26	51.0	128	1	K3HU41	Ig kappa chain pre
993	26	51.0	128	2	I57671	insulin-like growt
994	26	51.0	128	2	S40343	Ig kappa chain V-J
995	26	51.0	130	2	PL0113	Ig kappa chain pre
996	26	51.0	130	2	S08079	Ig kappa chain pre
997	26	51.0	130	2	C69061	hypothetical prote
998	26	51.0	132	1	MTON2K	melanin-concentrat
999	26	51.0	133	2	B71050	hypothetical prote
1000	26	51.0	135	1	B64116	translation initia

ALIGNMENTS

RESULT 1
S42466
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42466
R;Shiyanov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
submitted to the EMBL Data Library, March 1994
A;Reference number: S42466
A;Accession: S42466
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <SHI>
A;Cross-references: UNIPARC:UPI00001161DC; EMBL:X78108; NID:g460824; PIDN:CAA54998.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;26-100/Domain: immunoglobulin homology <IMM>

Query Match 94.1%; Score 48; DB 2; Length 117;
Best Local Similarity 90.9%; Pred. No. 0.018;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||:||
Db 34 KASQDVGTAVA 44

RESULT 2
S38560
Ig light chain V region (ASWB1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38560
R;Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
submitted to the EMBL Data Library, September 1993
A;Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s M
A;Reference number: S38559
A;Accession: S38560
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-82 <MON>
A;Cross-references: UNIPARC:UPI00001158E2; EMBL:X75102; NID:g414147; PIDN:CAA52993.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin

Query Match 84.3%; Score 43; DB 2; Length 82;
Best Local Similarity 81.8%; Pred. No. 0.13;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||:|||:||
Db 24 KASQNVGTAVA 34

RESULT 3
S38561
Ig light chain V region (ASWP1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38561
R;Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
submitted to the EMBL Data Library, September 1993
A;Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s M
A;Reference number: S38559
A;Accession: S38561
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-90 <MON>
A;Cross-references: UNIPARC:UPI00001161C8; EMBL:X75103; NID:g414155; PIDN:CAA52994.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 43; DB 2; Length 90;
Best Local Similarity 81.8%; Pred. No. 0.15;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||:|||:||
Db 24 KASQNVGTAVA 34

RESULT 4
S38559
Ig light chain V region (ASWA1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38559
R;Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.
submitted to the EMBL Data Library, September 1993
A;Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s M
A;Reference number: S38559
A;Accession: S38559
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-93 <MON>
A;Cross-references: UNIPARC:UPI00001161C7; EMBL:X75101; NID:g414145; PIDN:CAA52992.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 82.4%; Score 42; DB 2; Length 93;
Best Local Similarity 81.8%; Pred. No. 0.25;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
|||||| |:||
Db 24 KASQDVSTAVA 34

RESULT 5
S09967
Ig kappa chain V-J region (31-9D) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Aug-1996
C;Accession: S09967
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodies

```
A;Reference number: S09955; MUID:90269328; PMID:2347362
A;Accession: S09967
A;Molecule type: mRNA
A;Residues: 1-107 <REI>
A;Cross-references: UNIPARC:UPI00001769EE; EMBL:X51855
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             82.4%;  Score 42;  DB 2;  Length 107;
  Best Local Similarity   81.8%;  Pred. No. 0.28;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||| |:||
Db         24 KASQDVNTAVA 34


RESULT 6
S32191
Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S32191
R;Izui, S.
submitted to the EMBL Data Library, February 1993
A;Reference number: S32185
A;Accession: S32191
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <IZU>
A;Cross-references: UNIPARC:UPI0000116105; EMBL:X70095; NID:g288260; PIDN:CAA49700.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             82.4%;  Score 42;  DB 2;  Length 107;
  Best Local Similarity   81.8%;  Pred. No. 0.28;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||| |:||
Db         24 KASQDVSTAVA 34


RESULT 7
S32192
Ig kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S32192
R;Izui, S.
submitted to the EMBL Data Library, February 1993
A;Reference number: S32185
A;Accession: S32192
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <IZU>
A;Cross-references: UNIPARC:UPI0000116106; EMBL:X70097; NID:g288262; PIDN:CAA49701.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             82.4%;  Score 42;  DB 2;  Length 107;
  Best Local Similarity   81.8%;  Pred. No. 0.28;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||| |:||
Db         24 KASQDVSTAVA 34


RESULT 8
PQ0265
Ig kappa chain V region (MC1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PQ0265
R;Lohman, K.L.; Carrillo, M.A.; Kennedy, R.C.
Gene 105, 283-284, 1991
A;Title: Sequence analysis of the variable region of a mouse gene encoding a monoclonal a
A;Reference number: PQ0265; MUID:92039046; PMID:1937027
A;Accession: PQ0265
A;Molecule type: mRNA
A;Residues: 1-119 <LOH>
A;Cross-references: UNIPARC:UPI000017678E; GB:M59985
C;Comment: This protein recognizes a restricted idiotype associated with antibodies speci
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;28-102/Domain: immunoglobulin homology <IMM>
F;36-46/Region: complementarity-determining 1
F;62-68/Region: complementarity-determining 2
F;101-109/Region: complementarity-determining 3

  Query Match             82.4%;  Score 42;  DB 2;  Length 119;
  Best Local Similarity   81.8%;  Pred. No. 0.32;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||| |:||
Db         36 KASQDVSTTVA 46


RESULT 9
KVMS11
Ig kappa chain precursor V region (MPC11) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 09-Jul-2004
C;Accession: A90823; A90753; A90298; A01916
R;Kelley, D.E.; Coleclough, C.; Perry, R.P.
Cell 29, 681-689, 1982
A;Title: Functional significance and evolutionary development of the 5'-terminal regions
A;Reference number: A90823; MUID:83001944; PMID:6288267
A;Accession: A90823
A;Molecule type: DNA
A;Residues: 1-71 <KEL>
A;Cross-references: UNIPROT:P01633; UNIPARC:UPI0000173712
A;Note: the sequence was determined from the differentiated gene
R;Rabbitts, T.H.; Hamlyn, P.H.; Matthyssens, G.; Roe, B.A.
Can. J. Biochem. 58, 176-187, 1980
A;Title: The variability, arrangement, and rearrangement of immunoglobulin genes.
A;Reference number: A90753; MUID:80176554; PMID:6245773
A;Accession: A90753
A;Molecule type: mRNA
A;Residues: 41-149 <RAB>
A;Cross-references: UNIPARC:UPI0000173713
R;Smith, G.P.
Biochem. J. 171, 337-347, 1978
A;Title: Sequence of the full-length immunoglobulin kappa-chain of mouse myeloma MPC 11.
A;Reference number: A90298; MUID:78186617; PMID:418775
A;Contents: myeloma protein MPC11
A;Accession: A90298
A;Molecule type: protein
A;Residues: 30-149 <SMI>
A;Cross-references: UNIPARC:UPI0000173714
A;Note: the amidation states of residues 58, 69, 101, 111, 120, 122, and 123 were not det
C;Comment: The mature chain has 12 additional residues at its amino end, due to a tandem
 42 corresponds to the amino-terminal residue of typical kappa chains.
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: duplication; heterotetramer; immunoglobulin
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-149/Product: Ig kappa chain V region (MPC11) #status experimental <MAT>
F;57-131/Domain: immunoglobulin homology <IMM>
F;64-129/Disulfide bonds: #status predicted
```

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  Query Match             82.4%;  Score 42;  DB 1;  Length 149;
  Best Local Similarity   81.8%;  Pred. No. 0.4;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||| |:||
Db         65 KASQDVSTTVA 75


RESULT 10
A37262
Ig kappa chain V region (6H2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 03-Apr-1992 #text_change 31-Dec-2004
C;Accession: A37262
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same antigen
A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: A37262
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-88 <GOS>
A;Cross-references: UNIPROT:Q8VIJ0; UNIPARC:UPI0000176D7C; GB:M57987
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             76.5%;  Score 39;  DB 2;  Length 88;
  Best Local Similarity   72.7%;  Pred. No. 0.96;
  Matches    8;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:||::||
Db          4 KASQNVGSNVA 14


RESULT 11
C28195
Ig kappa chain V region (anti-haloperidol antibody C) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-May-1997
C;Accession: C28195
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid s
A;Reference number: A28195; MUID:88153717; PMID:3267217
A;Accession: C28195
A;Molecule type: mRNA
A;Residues: 1-86 <SHE>
A;Cross-references: UNIPARC:UPI0000176D7D; GB:M19768
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             74.5%;  Score 38;  DB 2;  Length 86;
  Best Local Similarity   72.7%;  Pred. No. 1.5;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|| :||
Db          3 KASQNVGNNVA 13


RESULT 12
PL0088
Ig kappa chain V regions (12S18-1, 12S28-16) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C;Accession: PL0088
R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
J. Exp. Med. 169, 519-533, 1989
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are
A;Reference number: PL0080; MUID:89094248; PMID:2492056
A;Accession: PL0088
A;Molecule type: mRNA
A;Residues: 1-106 <MEE>
A;Cross-references: UNIPARC:UPI0000115F1C; GB:X58581; GB:Y00794; NID:g51592; PIDN:CAA414
A;Note: the sequence shown here is from the V kappa regions an antiidiotypic monoclonal a
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>

  Query Match             74.5%;  Score 38;  DB 2;  Length 106;
  Best Local Similarity   72.7%;  Pred. No. 1.9;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||| ::||
Db         24 KASQDVNSAVA 34


RESULT 13
B28195
Ig kappa chain V region (anti-haloperidol antibody B) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jan-2000
C;Accession: B28195
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid se
A;Reference number: A28195; MUID:88153717; PMID:3267217
A;Accession: B28195
A;Molecule type: mRNA
A;Residues: 1-107 <SHE>
A;Cross-references: UNIPARC:UPI0000114D6A; EMBL:M19767; NID:g197041; PIDN:AAA38892.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             74.5%;  Score 38;  DB 2;  Length 107;
  Best Local Similarity   72.7%;  Pred. No. 1.9;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|| :||
Db         24 KASQNVGNNVA 34


RESULT 14
A28195
Ig kappa chain V region (anti-haloperidol antibody A) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jan-2000
C;Accession: A28195
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.
J. Biol. Chem. 263, 4059-4063, 1988
A;Title: Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid se
A;Reference number: A28195; MUID:88153717; PMID:3267217
A;Accession: A28195
A;Molecule type: mRNA
A;Residues: 1-107 <SHE>
A;Cross-references: UNIPARC:UPI0000114D69; GB:M19766; NID:g197039; PIDN:AAA38891.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             74.5%;  Score 38;  DB 2;  Length 107;
  Best Local Similarity   72.7%;  Pred. No. 1.9;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|| :||
Db         24 KASQNVGNNVA 34


RESULT 15
A47159
```

Ig lambda chain V region (CEA-specific maId T84.66) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: A47159
R;Gaida, F.J.; Pieper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumaier, M.
J. Biol. Chem. 268, 14138-14145, 1993
A;Title: Molecular characterization of a cloned idiotypic cascade containing a network a
A;Reference number: A47159; MUID:93300804; PMID:7686150
A;Accession: A47159
A;Status: preliminary
A;Molecule type: DNA; protein
A;Residues: 1-128 <GAI>
A;Cross-references: UNIPARC:UPI00001767A5
A;Experimental source: hybridoma 6G6.C4
A;Note: sequence extracted from NCBI backbone (NCBIN:134419, NCBIP:134420)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

 Query Match 74.5%; Score 38; DB 2; Length 128;
 Best Local Similarity 72.7%; Pred. No. 2.3;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||:|| :||
Db 44 KASQNVGNNVA 54

RESULT 16
PH1073
Ig light chain V region (clone 17s.130) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1073
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1073
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-98 <TIL>
A;Cross-references: UNIPARC:UPI0000176ABD
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

 Query Match 72.5%; Score 37; DB 2; Length 98;
 Best Local Similarity 72.7%; Pred. No. 2.8;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
|||||| :||
Db 24 KASQDVNAAVA 34

RESULT 17
D72673
hypothetical protein APE0810 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: D72673
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: D72673
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 <KAW>
A;Cross-references: UNIPROT:Q9YDV9; UNIPARC:UPI000005DCC9; DDBJ:AP000060; NID:g5104188;
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0810
C;Superfamily: Aeropyrum pernix hypothetical protein APE0810

 Query Match 72.5%; Score 37; DB 2; Length 110;
 Best Local Similarity 72.7%; Pred. No. 3.1;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
| |||:| |||
Db 65 KLSQDLGQSVA 75

RESULT 18
A25924
Ig kappa chain precursor V region (Ser-a) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
C;Accession: A25924
R;Boyd, R.T.; Goldrick, M.M.; Gottlieb, P.D.
Proc. Natl. Acad. Sci. U.S.A. 83, 9134-9138, 1986
A;Title: Structural differences in a single gene encoding the V-kappa-Ser group of light
A;Reference number: A94141; MUID:87067464; PMID:3097643
A;Accession: A25924
A;Molecule type: DNA
A;Residues: 1-115 <BOY>
A;Cross-references: UNIPARC:UPI0000114C30; GB:M14361; NID:g197466; PIDN:AAA39035.1; PID:g
A;Experimental source: strain C.C58
C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Product: Ig kappa chain V region Ser-a #status predicted <MAT>
F;36-110/Domain: immunoglobulin homology <IMM>

 Query Match 72.5%; Score 37; DB 2; Length 115;
 Best Local Similarity 72.7%; Pred. No. 3.3;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
|||| || :||
Db 44 KASQSVGNNVA 54

RESULT 19
S04577
Ig kappa chain precursor V region (MRL-RF28L) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S04577
R;Kofler, R.; Duchosal, M.A.; Dixon, F.J.
submitted to the EMBL Data Library, March 1989
A;Description: Complexity, polymorphism and connectivity of murine V(kappa) gene familie
A;Reference number: S04577
A;Accession: S04577
A;Molecule type: mRNA
A;Residues: 1-127 <KOF>
A;Cross-references: UNIPARC:UPI000011678F; EMBL:X14622; NID:g52400; PIDN:CAA32775.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-127/Product: Ig kappa chain V region (fragment) #status predicted <MAT>
F;36-110/Domain: immunoglobulin homology <IMM>

 Query Match 72.5%; Score 37; DB 2; Length 127;
 Best Local Similarity 72.7%; Pred. No. 3.6;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
|||| || :||
Db 44 KASQSVGNNVA 54

```
RESULT 20
S30751
Ig kappa chain precursor V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
C;Accession: S30751
R;Grant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.
Nucleic Acids Res. 15, 5496, 1987
A;Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.
A;Reference number: S30751; MUID:87260030; PMID:3601683
A;Accession: S30751
A;Molecule type: mRNA
A;Residues: 1-152 <GRA>
A;Cross-references: UNIPARC:UPI0000115D91; EMBL:X05877; NID:g52195; PIDN:CAA29301.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;45-119/Domain: immunoglobulin homology <IMM>
F;138-152/Domain: C region (C-kappa) (fragment) #status predicted <CRE>

  Query Match             72.5%;  Score 37;  DB 2;  Length 152;
  Best Local Similarity   72.7%;  Pred. No. 4.3;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||| |:|:
Db         53 KASQDVTTAVS 63


RESULT 21
E69853
conserved hypothetical protein yjnA - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: E69853
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: E69853
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-254 <KUN>
A;Cross-references: UNIPROT:O34578; UNIPARC:UPI0000060268; GB:Z99110; GB:AL009126; NID:g
A;Experimental source: strain 168
C;Genetics:
A;Gene: yjnA
C;Superfamily: hypothetical protein HI0902

  Query Match             72.5%;  Score 37;  DB 2;  Length 254;
  Best Local Similarity   72.7%;  Pred. No. 7.4;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||| ||| :|
Db        178 KASQIVGTDIA 188


RESULT 22
T19661
hypothetical protein C33A12.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19661
R;Wilkinson, J.
submitted to the EMBL Data Library, January 1996
A;Reference number: Z19159
A;Accession: T19661
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-520 <WIL>
A;Cross-references: UNIPROT:Q18361; UNIPARC:UPI0000060F25; EMBL:Z68493; PIDN:CAA92791.1;
A;Experimental source: clone C33A12
C;Genetics:
A;Gene: CESP:C33A12.6
A;Map position: 4
A;Introns: 51/3; 110/3; 155/1; 214/3; 228/3; 379/3; 457/2
C;Superfamily: glucuronosyltransferase

  Query Match             72.5%;  Score 37;  DB 2;  Length 520;
  Best Local Similarity   63.6%;  Pred. No. 16;
  Matches    7;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||:||:||: |
Db        110 KAAQDMGTAFA 120


RESULT 23
PH1082
Ig light chain V region (clone 165.54) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1082
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B ce
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1082
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-87 <TIL>
A;Cross-references: UNIPARC:UPI00001767EB
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;6-80/Domain: immunoglobulin homology <IMM>

  Query Match             70.6%;  Score 36;  DB 2;  Length 87;
  Best Local Similarity   60.0%;  Pred. No. 3.9;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              :||| :|||:
Db         14 RASQSIGTSI 23


RESULT 24
PL0261
Ig kappa chain V region (anti-DNA, DP15VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-May-1997
C;Accession: PL0261
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic m
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0261
A;Molecule type: mRNA
A;Residues: 1-88 <SHL>
A;Cross-references: UNIPARC:UPI0000176D7B
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
```

```
F;1-5/Region: framework 1
F;6-16/Region: complementarity-determining 1
F;17-31/Region: framework 2
F;32-38/Region: complementarity-determining 2
F;39-70/Region: framework 3
F;71-79/Region: complementarity-determining 3
F;80-88/Region: framework 4

  Query Match             70.6%;  Score 36;  DB 2;  Length 88;
  Best Local Similarity   60.0%;  Pred. No. 4;
  Matches    6;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              :||||:|:|:
Db          6 RASQDIGSSL 15


RESULT 25
PL0260
Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0260
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0260
A;Molecule type: mRNA
A;Residues: 1-106 <SHL>
A;Cross-references: UNIPARC:UPI0000176B06
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-106/Region: framework 4

  Query Match             70.6%;  Score 36;  DB 2;  Length 106;
  Best Local Similarity   60.0%;  Pred. No. 4.8;
  Matches    6;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              :||||:|:|:
Db         24 RASQDIGSSL 33


RESULT 26
KVMSL7
Ig kappa chain precursor V region (L7) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 09-Jul-2004
C;Accession: A01925
R;Pech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.
Nature 291, 668-670, 1981
A;Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding sequ
A;Reference number: A93259; MUID:81220975; PMID:6264318
A;Accession: A01925
A;Molecule type: DNA
A;Residues: 1-115 <PEC>
A;Cross-references: UNIPROT:P01642; UNIPARC:UPI0000023365; GB:V01564; GB:J00574; NID:g51
A;Note: the sequence was determined from the germline gene
A;Note: there appear to be two possible splice junctions at the 3' end of the intron; th
C;Genetics:
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Product: Ig kappa chain V region (L7) #status predicted <MAT>
F;36-110/Domain: immunoglobulin homology <IMM>
F;43-108/Disulfide bonds: #status predicted

  Query Match             70.6%;  Score 36;  DB 1;  Length 115;
  Best Local Similarity   60.0%;  Pred. No. 5.2;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              :||| :|||:
Db         44 RASQSIGTSI 53


RESULT 27
T40071
cytochrome b5 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40071
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lelaure, V.; Galibert, F.
submitted to the EMBL Data Library, December 1998
A;Reference number: Z21903
A;Accession: T40071
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-124 <LYN>
A;Cross-references: UNIPROT:O94391; UNIPARC:UPI0000128869; EMBL:AL034463; PIDN:CAA22444.1
A;Experimental source: strain 972h-; cosmid c29A10
C;Genetics:
A;Gene: SPDB:SPBC29A10.16c
A;Map position: 2
A;Introns: 50/1; 101/2
C;Superfamily: cytochrome b5; cytochrome b5 core homology
C;Keywords: heme; iron; metalloprotein
F;38,62/Binding site: heme iron (His) (axial ligands) #status predicted

  Query Match             70.6%;  Score 36;  DB 2;  Length 124;
  Best Local Similarity   63.6%;  Pred. No. 5.6;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              || ||:| |:|
Db         55 KAYQDIGHSIA 65


RESULT 28
PN0445
Ig kappa chain precursor V-I region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PN0445
R;Kaluza, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A;Title: A general method for chimerization of monoclonal antibodies by inverse polymeras
A;Reference number: PN0444; MUID:93138402; PMID:1339379
A;Accession: PN0445
A;Molecule type: mRNA
A;Residues: 1-128 <KAL>
A;Cross-references: UNIPARC:UPI0000176795; GB:L02347
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-10/Domain: signal sequence #status predicted <SIG>
F;11-128/Product: Ig light chain kappa-1 V region #status predicted <MAT>
F;26-100/Domain: immunoglobulin homology <IMM>

  Query Match             70.6%;  Score 36;  DB 2;  Length 128;
  Best Local Similarity   60.0%;  Pred. No. 5.8;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              :||| :|||:
Db         34 RASQSIGTSI 43
```

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RESULT 29
KVMSM4
Ig kappa chain precursor V region (MOPC 41) - mouse
N;Contains: Ig kappa chain precursor V region VK41
C;Species: Mus musculus (house mouse)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A93211; B93211; A93815; A94239; A01922; A01923
R;Seidman, J.G.; Max, E.E.; Leder, P.
Nature 280, 370-375, 1979
A;Title: A kappa-immunoglobulin gene is formed by site-specific recombination without fu
A;Reference number: A93211; MUID:79221900; PMID:111146
A;Accession: A93211
A;Molecule type: DNA
A;Residues: 1-130 <PC41>
A;Cross-references: UNIPROT:P01639; UNIPARC:UPI000002A0B6
A;Accession: B93211
A;Molecule type: DNA
A;Residues: 1-117 <VK41>
A;Cross-references: UNIPARC:UPI0000115CB8; GB:V00804; GB:J00566; NID:g52127; PIDN:CAA241
A;Note: the sequences were determined from the differentiated gene MOPC 41 and the germl
R;Burstein, Y.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
A;Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursors
A;Reference number: A93815; MUID:77148916; PMID:403522
A;Accession: A93815
A;Molecule type: protein
A;Residues: 1-33 <BUR>
A;Cross-references: UNIPARC:UPI0000173715
A;Note: Met-3 is apparently used as an alternative initiator in 25% of the chains
R;Gray, W.R.; Dreyer, W.J.; Hood, L.
Science 155, 465-467, 1967
A;Title: Mechanism of antibody synthesis: size differences between mouse kappa chains.
A;Reference number: A94239; MUID:67056897; PMID:4162931
A;Accession: A94239
A;Molecule type: protein
A;Residues: 23-49,'B',51-53,'LSB',57-58,'ZZ',61-62,'BZ',65-76,'B',78-108,110-130 <GRA>
A;Cross-references: UNIPARC:UPI0000173716
A;Experimental source: Bence Jones protein MOPC 41
C;Genetics:
A;Introns: 19/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: alternative initiators; heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status experimental <SIG1>
F;3-22/Domain: signal sequence #status experimental <SIG2>
F;23-130/Product: Ig kappa chain V region (MOPC 41) #status experimental <M41>
F;38-112/Domain: immunoglobulin homology <IMM>
F;45-110/Disulfide bonds: #status predicted

  Query Match             70.6%;  Score 36;  DB 1;  Length 130;
  Best Local Similarity   60.0%;  Pred. No. 5.9;
  Matches    6;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              :||||:|:|:
Db         46 RASQDIGSSL 55


RESULT 30
T33277
hypothetical protein R09A1.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33277
R;Bentley, D.; Kemp, K.; Harper, M.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid R09A1.
A;Reference number: Z21312
A;Accession: T33277
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-317 <BEN>
A;Cross-references: UNIPROT:O61933; UNIPARC:UPI000008157B; EMBL:AF068711; PIDN:AAC17777.1
A;Experimental source: strain Bristol N2; clone R09A1
C;Genetics:
A;Gene: CESP:R09A1.3
A;Map position: 5
A;Introns: 22/3; 52/2; 131/1; 186/3; 284/3
C;Superfamily: Caenorhabditis elegans hypothetical protein R09A1.3

  Query Match             70.6%;  Score 36;  DB 2;  Length 317;
  Best Local Similarity   63.6%;  Pred. No. 15;
  Matches    7;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              | | |:||| |
Db         37 KRSMDIGTSTA 47


RESULT 31
HNNZB3
hemagglutinin-neuraminidase (EC 3.2.1.-) - parainfluenza virus type 3
C;Species: parainfluenza virus type 3
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 18-Jun-1999
C;Accession: B27218
R;Suzu, S.; Sakai, Y.; Shioda, T.; Shibuta, H.
Nucleic Acids Res. 15, 2945-2958, 1987
A;Title: Nucleotide sequence of the bovine parainfluenza 3 virus genome: the genes of the
A;Reference number: A93659; MUID:87174819; PMID:3031615
A;Accession: B27218
A;Molecule type: genomic RNA
A;Residues: 1-572 <SUZ>
A;Cross-references: UNIPARC:UPI0000046C1E; EMBL:Y00114; NID:g60891; PIDN:CAA68298.1; PID
C;Genetics:
A;Gene: HN
C;Superfamily: paramyxovirus hemagglutinin-neuraminidase
C;Keywords: glycoprotein; glycosidase; hemagglutinin; hydrolase; transmembrane protein
F;40-56/Domain: transmembrane #status predicted <TMN>
F;8,163,485,570/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             70.6%;  Score 36;  DB 1;  Length 572;
  Best Local Similarity   60.0%;  Pred. No. 28;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              | | |:|||:
Db         82 KTSDDIGTSI 91


RESULT 32
A87626
catalase/peroxidase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
C;Accession: A87626
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.E
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolona
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87626
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-737 <STO>
A;Cross-references: UNIPROT:O31066; UNIPARC:UPI0000127056; GB:AE005673; NID:g13424687; PI
C;Genetics:
A;Gene: CC3043
C;Superfamily: Catalase HPI

  Query Match             70.6%;  Score 36;  DB 2;  Length 737;
  Best Local Similarity   70.0%;  Pred. No. 36;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;
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```
Qy          1 KASQDVGTSV 10
              ||::| ||||
Db        550 KAAKDAGTSV 559


RESULT 33
F33730
Ig kappa chain V region (19.34) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
C;Accession: F33730
R;Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A;Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A;Reference number: A33730; MUID:89367325; PMID:2505260
A;Accession: F33730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-94 <LAW>
A;Cross-references: UNIPARC:UPI0000114E5A; GB:M26002; NID:g197123; PIDN:AAA38918.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             68.6%;  Score 35;  DB 2;  Length 94;
  Best Local Similarity   72.7%;  Pred. No. 6.8;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:| |:||
Db         24 KASQNVRTAVA 34


RESULT 34
JC5737
membrane-bound proton-translocating ATPase (EC 3.6.1.-) b chain - Streptococcus mutans
C;Species: Streptococcus mutans
C;Date: 09-Dec-1997 #sequence_revision 23-Jan-1998 #text_change 31-Dec-2004
C;Accession: JC5737
R;Smith, A.J.; Quivey Jr., R.G.; Faustoferri, R.C.
Gene 183, 87-96, 1996
A;Title: Cloning and nucleotide sequence analysis of the Streptococcus mutans membrane-b
A;Reference number: JC5735; MUID:97149283; PMID:8996091
A;Accession: JC5737
A;Molecule type: DNA
A;Residues: 1-165 <SMI>
A;Cross-references: UNIPROT:P95785; UNIPARC:UPI000017017B; GB:U31170; NID:g4239651; PIDN
A;Note: only a part of the nucleotide and amino acid sequence are given in this paper
C;Comment: This enzyme regulates cytoplasmic pH values for the purpose of maintaining de
C;Genetics:
A;Gene: uncF
C;Superfamily: H(+)-transporting ATP synthase chain I
C;Keywords: hydrolase

  Query Match             68.6%;  Score 35;  DB 2;  Length 165;
  Best Local Similarity   63.6%;  Pred. No. 12;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||:||: || |
Db        110 KANQDIATSKA 120


RESULT 35
G81447
major antigenic peptide PEB3 Cj0289c [imported] - Campylobacter jejuni (strain NCTC 1116
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C;Accession: G81447
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: G81447
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-250 <PAR>
A;Cross-references: UNIPROT:Q9PIK7; UNIPARC:UPI00000C20BB; GB:AL139074; GB:AL111168; NID
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: peb3; Cj0289c
C;Superfamily: Molybdate-binding periplasmic protein ModA

  Query Match             68.6%;  Score 35;  DB 2;  Length 250;
  Best Local Similarity   54.5%;  Pred. No. 19;
  Matches    6;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |:: |:||:||
Db        194 KSNPDIGTAVA 204


RESULT 36
B75429
hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: B75429
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mak
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: B75429
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-298 <WHI>
A;Cross-references: UNIPROT:Q9RV58; UNIPARC:UPI00000C18B4; GB:AE001966; GB:AE000513; NID
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1172
A;Map position: 1

  Query Match             68.6%;  Score 35;  DB 2;  Length 298;
  Best Local Similarity   77.8%;  Pred. No. 22;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 ASQDVGTSV 10
              |:||||:||
Db         49 AAQDVGSSV 57


RESULT 37
PH1071
Ig light chain V region (clone 165.3m) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1071
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B ce
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1071
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-91 <TIL>
A;Cross-references: UNIPARC:UPI0000176ABB
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;10-83/Domain: immunoglobulin homology <IMM>

  Query Match             66.7%;  Score 34;  DB 2;  Length 91;
```

```
  Best Local Similarity   63.6%;  Pred. No. 11;
  Matches    7;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||::|||  |:
Db         18 KASENVGTYVS 28


RESULT 38
PH1070
Ig light chain V region (clone 17s.5) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: PH1070
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1070
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-96 <TIL>
A;Cross-references: UNIPARC:UPI0000176ABA
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             66.7%;  Score 34;  DB 2;  Length 96;
  Best Local Similarity   63.6%;  Pred. No. 11;
  Matches    7;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||::|||  |:
Db         24 KASENVGTYVS 34


RESULT 39
PH1072
Ig light chain V region (clone 83-c1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
C;Accession: PH1072
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B c
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1072
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-98 <TIL>
A;Cross-references: UNIPROT:Q8VIJ0; UNIPARC:UPI0000176ABC
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin homology
C;Keywords: immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             66.7%;  Score 34;  DB 2;  Length 98;
  Best Local Similarity   63.6%;  Pred. No. 11;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||: | :||
Db         24 KASQNAGNNVA 34


RESULT 40
H38601
Ig kappa chain V region (3A3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C;Accession: H38601
R;Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, 2134-2142, 1991
A;Title: Common structural features among monoclonal antibodies binding the same antigen
A;Reference number: A38601; MUID:91115823; PMID:1703527
A;Accession: H38601
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-100 <GOS>
A;Cross-references: UNIPARC:UPI000011517C; GB:M57985; NID:g196416; PIDN:AAA63366.1; PID:g
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;8-82/Domain: immunoglobulin homology <IMM>

  Query Match             66.7%;  Score 34;  DB 2;  Length 100;
  Best Local Similarity   72.7%;  Pred. No. 12;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||| | |:||
Db         16 KASQTVDTAVA 26


RESULT 41
PL0259
Ig kappa chain V region (anti-DNA, DP11VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0259
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic m
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0259
A;Molecule type: mRNA
A;Residues: 1-106 <SHL>
A;Cross-references: UNIPARC:UPI0000176B08
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-106/Region: framework 4

  Query Match             66.7%;  Score 34;  DB 2;  Length 106;
  Best Local Similarity   60.0%;  Pred. No. 12;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              :||||:| |:
Db         24 RASQDIGRSL 33


RESULT 42
PL0268
Ig kappa chain V region (anti-DNA, DP9VK and DP17VK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C;Accession: PL0268
R;Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic m
A;Reference number: PL0231; MUID:90111618; PMID:2104919
A;Accession: PL0268
A;Molecule type: mRNA
A;Residues: 1-107 <SHL>
A;Cross-references: UNIPARC:UPI0000176B03
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
```

```
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

  Query Match             66.7%;  Score 34;  DB 2;  Length 107;
  Best Local Similarity   63.6%;  Pred. No. 12;
  Matches    7;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||::||| |:
Db         24 KASENVGTYVS 34


RESULT 43
PL0083
Ig kappa chain V region (E3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
C;Accession: PL0083
R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Ca
J. Exp. Med. 169, 519-533, 1989
A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s are
A;Reference number: PL0080; MUID:89094248; PMID:2492056
A;Accession: PL0083
A;Molecule type: mRNA
A;Residues: 1-108 <MEE>
A;Cross-references: UNIPARC:UPI0000176CC1
A;Experimental source: strain BALB/c
A;Note: the sequence shown here is from the V kappa region of an antiidiotypic monoclona
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology <IMM>

  Query Match             66.7%;  Score 34;  DB 2;  Length 108;
  Best Local Similarity   72.7%;  Pred. No. 13;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||| | |:||
Db         24 KASQAVSTAVA 34


RESULT 44
C30502
Ig kappa chain V region (D444) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 21-Jan-2000
C;Accession: C30502
R;Eilat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A;Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 mic
A;Reference number: A30502; MUID:88315787; PMID:2457627
A;Accession: C30502
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <EIL>
A;Cross-references: UNIPARC:UPI0000114DCF; GB:M21907; NID:g197071; PIDN:AAA38907.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             66.7%;  Score 34;  DB 2;  Length 108;
  Best Local Similarity   60.0%;  Pred. No. 13;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              :||| :|||:
Db         24 RASQSIGTSL 33


RESULT 45
PL0204
anti-DNA autoantibody BV17-45, kappa chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: PL0204
R;Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from NZ
A;Reference number: PL0198; MUID:90309768; PMID:2114528
A;Accession: PL0204
A;Molecule type: mRNA
A;Residues: 1-108 <SMI>
A;Cross-references: UNIPARC:UPI0000113787; GB:X53644; NID:g50198; PIDN:CAA37695.1; PID:g5
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;50-56/Region: complementarity-determining 2
F;89-97/Region: complementarity-determining 3
F;96-108/Region: JH region

  Query Match             66.7%;  Score 34;  DB 2;  Length 108;
  Best Local Similarity   72.7%;  Pred. No. 13;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:| | ||
Db         24 KASQNVNTYVA 34


RESULT 46
S34435
protein-tyrosine kinase (EC 2.7.1.112) kit - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 07-Feb-1997 #text_change 05-Oct-2004
C;Accession: S34435; S34436
R;Hayashi, S.I.; Kunisada, T.; Ogawa, M.; Yamaguchi, K.; Nishikawa, S.I.
Nucleic Acids Res. 19, 1267-1271, 1991
A;Title: Exon skipping by mutation of an authentic splice site of c-kit gene in W/W mouse
A;Reference number: S34435; MUID:91232907; PMID:1709486
A;Accession: S34435
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-125 <HAY>
A;Cross-references: UNIPROT:Q8C8K9; UNIPARC:UPI0000175610; EMBL:X58686
A;Experimental source: strain DBA/2
A;Accession: S34436
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-125 <HA2>
A;Cross-references: UNIPARC:UPI0000175610; EMBL:X58688
A;Experimental source: strain WB/Re-W/W
C;Genetics:
A;Introns: 29/1; 64/3; 107/1
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homology
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase

  Query Match             66.7%;  Score 34;  DB 2;  Length 125;
  Best Local Similarity   72.7%;  Pred. No. 15;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||| ||| | |
Db          7 KASNDVGKSSA 17


RESULT 47
PL0207
anti-idiotypic antibody E225, kappa chain V region precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: PL0207
R;Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.
```

Mol. Immunol. 27, 429-433, 1990
A;Title: Nucleotide sequence of the VH, VL regions of an anti-idiotopic antibody reactin
A;Reference number: PL0207; MUID:90309764; PMID:1973259
A;Accession: PL0207
A;Molecule type: mRNA
A;Residues: 1-131 <SOU>
A;Cross-references: UNIPARC:UPI000017678F
A;Note: This sequence corresponds to subgroup V mouse immunoglobulin light chain
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-20/Domain: signal sequence #status predicted <SIG>
F;36-110/Domain: immunoglobulin homology <IMM>
F;44-54/Region: complementarity-determining 1
F;70-76/Region: complementarity-determining 2
F;109-117/Region: complementarity-determining 3
F;116-127/Region: J region

 Query Match 66.7%; Score 34; DB 2; Length 131;
 Best Local Similarity 72.7%; Pred. No. 15;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
 |||||| :||
Db 44 KASQDVRIAVA 54

RESULT 48
T38219
40s ribosomal protein S1B - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38219; T51287
R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, December 1998
A;Reference number: Z21779
A;Accession: T38219
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-252 <BAD>
A;Cross-references: UNIPROT:O94438; UNIPARC:UPI000016202C; EMBL:AL034565; PIDN:CAA22556.
A;Experimental source: strain 972h-; cosmid c22H12
R;Shpakovski, G.V.; Lebedenko, E.N.
submitted to the EMBL Data Library, February 1999
A;Reference number: Z25352
A;Accession: T51287
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-252 <SHP>
A;Cross-references: UNIPARC:UPI000016202C; EMBL:AF127914; PIDN:AAD33346.1
A;Experimental source: strain 972h(-)
C;Genetics:
A;Gene: SPDB:SPAC22H12.04c; rps1-2
A;Map position: 1
C;Superfamily: rat ribosomal protein S3a

 Query Match 66.7%; Score 34; DB 2; Length 252;
 Best Local Similarity 87.5%; Pred. No. 30;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SQDVGTSV 10
 |||||| |
Db 235 SQDVGTKV 242

RESULT 49
A83361
penicillin-binding protein 3A PA2272 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: A83361
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathoc
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83361
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-565 <STO>
A;Cross-references: UNIPROT:Q9I1K1; UNIPARC:UPI00000C563C; GB:AE004653; GB:AE004091; NID
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: pbpC; PA2272
C;Superfamily: penicillin-binding protein 3

 Query Match 66.7%; Score 34; DB 2; Length 565;
 Best Local Similarity 70.0%; Pred. No. 70;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KASQDVGTSV 10
 |||||| |:
Db 209 KASQDVALSI 218

RESULT 50
TVMSKT
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - mouse
N;Alternate names: tyrosine kinase receptor c-kit
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 05-Oct-2004
C;Accession: S00474; B44876; I49596
R;Qiu, F.; Ray, P.; Brown, K.; Barker, P.E.; Jhanwar, S.; Ruddle, F.H.; Besmer, P.
EMBO J. 7, 1003-1011, 1988
A;Title: Primary structure of c-kit: relationship with the CSF-1/PDGF receptor kinase fan
A;Reference number: S00474; MUID:88296403; PMID:2456920
A;Accession: S00474
A;Molecule type: mRNA
A;Residues: 1-975 <QIU>
A;Cross-references: UNIPROT:P05532; UNIPARC:UPI000002852E; GB:Y00864; NID:g50423; PIDN:CA
R;Rossi, P.; Marziali, G.; Albanesi, C.; Charlesworth, A.; Geremia, R.; Sorrentino, V.
Dev. Biol. 152, 203-207, 1992
A;Title: A novel c-kit transcript, potentially encoding a truncated receptor, originates
A;Reference number: A44876; MUID:92331813; PMID:1378413
A;Accession: B44876
A;Molecule type: DNA
A;Residues: 771-814 <ROS>
A;Cross-references: UNIPARC:UPI00001725B4
A;Note: sequence extracted from NCBI backbone (NCBIN:108837, NCBIP:108840)
R;Yasuda, H.; Galli, S.J.; Geissler, E.N.
Biochem. Biophys. Res. Commun. 191, 893-901, 1993
A;Title: Cloning and functional analysis of the mouse c-kit promoter.
A;Reference number: I49596; MUID:93221533; PMID:7682073
A;Accession: I49596
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-22 <RES>
A;Cross-references: UNIPARC:UPI00000003B6; GB:L11358; NID:g293325; PIDN:AAA37420.1; PID:g
C;Genetics:
A;Gene: kit; c-kit
A;Map position: 5
C;Superfamily: Tyrosine-protein kinase, CSF-1/PDGF receptor type; immunoglobulin homolog
C;Keywords: ATP; autophosphorylation; glycoprotein; kinase-related transforming protein;
fic protein kinase
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-975/Product: protein-tyrosine kinase kit #status predicted <KTC>
F;23-519/Domain: extracellular #status predicted <EXT>
F;51-100/Domain: immunoglobulin homology <IMM1>
F;130-189/Domain: immunoglobulin homology <IMM2>
F;227-295/Domain: immunoglobulin homology <IMM3>
F;331-397/Domain: immunoglobulin homology <IMM4>
F;426-496/Domain: immunoglobulin homology <IMM5>
F;520-542/Domain: transmembrane #status predicted <TMM>
F;543-975/Domain: intracellular #status predicted <INT>
F;586-929/Domain: protein kinase homology <KIN>
F;594-602/Region: protein kinase ATP-binding motif
F;58-98,137-187,234-293,431-494/Disulfide bonds: #status predicted

F;146,296,303,323,355,370,466,489/Binding site: carbohydrate (Asn) (covalent) #status pr
F;622,639,790/Active site: Lys, Glu, Asp #status predicted
F;795,808/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 66.7%; Score 34; DB 1; Length 975;
Best Local Similarity 72.7%; Pred. No. 1.2e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 KASQDVGTSVA 11
              ||| ||| | |
Db        495 KASNDVGKSSA 505
```

Search completed: March 23, 2006, 02:03:57
Job time : 46.2192 secs

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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:40:40 ; Search time 94.6301 Seconds
(without alignments)
82.012 Million cell updates/sec

Title: US-10-755-382-20
Perfect score: 51
Sequence: 1 KASQDVGTSVA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	84.3	108	2	Q8VIJ0_MOUSE	Q8vij0 mus musculu
2	42	82.4	149	1	KV5A_MOUSE	P01633 mus musculu
3	40	78.4	238	2	Q58EU4_MOUSE	Q58eu4 mus musculu
4	37	72.5	110	2	Q9YDV9_AERPE	Q9ydv9 aeropyrum p
5	37	72.5	254	2	O34578_BACSU	O34578 bacillus su
6	37	72.5	409	2	Q8BK10_MOUSE	Q8bk10 mus musculu
7	37	72.5	409	2	Q8JZV7_MOUSE	Q8jzv7 mus musculu
8	37	72.5	520	2	Q18361_CAEEL	Q18361 caenorhabdi
9	36	70.6	115	1	KV5I_MOUSE	P01642 mus musculu
10	36	70.6	124	1	CYB5I_SCHPO	O94391 schizosacch
11	36	70.6	130	1	KV5G_MOUSE	P01639 mus musculu
12	36	70.6	317	2	O61933_CAEEL	O61933 caenorhabdi
13	36	70.6	373	2	Q4LRF1_9BURK	Q4lrf1 burkholderi
14	36	70.6	501	2	Q4XXF0_PLACH	Q4xxf0 plasmodium
15	36	70.6	572	1	HEMA_PI3B	P06167 bovine para
16	36	70.6	572	2	Q65689_PI3B	Q65689 bovine para
17	36	70.6	737	1	CATA_CAUCR	O31066 caulobacter
18	36	70.6	978	2	Q5AAV6_CANAL	Q5aav6 candida alb
19	36	70.6	1579	2	Q5B2F2_EMENI	Q5b2f2 aspergillus
20	36	70.6	2491	2	Q4YNQ6_PLABE	Q4ynq6 plasmodium
21	36	70.6	2598	2	Q7RNQ6_PLAYO	Q7rnq6 plasmodium
22	35	68.6	83	2	Q6Z997_ORYSA	Q6z997 oryza sativ
23	35	68.6	165	1	ATPF_STRMU	P95785 streptococc
24	35	68.6	250	2	Q5HWH8_CAMJR	Q5hwh8 campylobact
25	35	68.6	250	2	Q9PIK7_CAMJE	Q9pik7 campylobact
26	35	68.6	298	1	UB72_DEIRA	Q9rv58 deinococcus
27	35	68.6	311	2	Q9TNJ1_9MARC	Q9tnj1 haplomitriu
28	35	68.6	314	2	Q60ZB5_CAEBR	Q60zb5 caenorhabdi
29	35	68.6	374	2	Q5HP41_STAEQ	Q5hp41 staphylococ
30	35	68.6	374	2	Q8CP46_STAEP	Q8cp46 staphylococ
31	35	68.6	407	2	Q566R3_RAT	Q566r3 rattus norv
32	35	68.6	416	2	Q5B779_EMENI	Q5b779 aspergillus
33	35	68.6	494	2	Q4QIV2_LEIMA	Q4qiv2 leishmania
34	35	68.6	501	2	Q5UWB5_HALMA	Q5uwb5 haloarcula
35	35	68.6	661	2	Q8R0V4_MOUSE	Q8r0v4 mus musculu
36	35	68.6	801	2	Q5HLJ7_STAEQ	Q5hlj7 staphylococ
37	35	68.6	801	2	Q8CN69_STAEP	Q8cn69 staphylococ
38	35	68.6	930	2	Q9DBM1_MOUSE	Q9dbm1 mus musculu
39	35	68.6	1158	2	Q74ZC6_ASHGO	Q74zc6 ashbya goss
40	35	68.6	2245	2	Q55J08_CRYNE	Q55j08 cryptococcu
41	35	68.6	2245	2	Q5KCP4_CRYNE	Q5kcp4 cryptococcu
42	34	66.7	83	2	Q8CEY4_MOUSE	Q8cey4 mus musculu
43	34	66.7	120	2	Q5TTA0_ANOGA	Q5tta0 anopheles g
44	34	66.7	158	1	GREA_PSESM	Q87wp5 pseudomonas
45	34	66.7	158	2	Q4ZNQ2_PSESY	Q4znq2 pseudomonas
46	34	66.7	158	2	Q4KIG6_PSEF5	Q4kig6 pseudomonas
47	34	66.7	181	2	Q7QCN2_ANOGA	Q7qcn2 anopheles g
48	34	66.7	182	2	Q8TU86_METAC	Q8tu86 methanosarc
49	34	66.7	212	2	Q82CD8_STRAW	Q82cd8 streptomyce
50	34	66.7	213	2	Q5VNG3_ORYSA	Q5vng3 oryza sativ
51	34	66.7	218	2	Q7WLF0_BORBR	Q7wlf0 bordetella
52	34	66.7	220	2	Q7VX51_BORPE	Q7vx51 bordetella
53	34	66.7	220	2	Q7W806_BORPA	Q7w806 bordetella
54	34	66.7	251	1	RS3B_SCHPO	O94438 schizosacch
55	34	66.7	289	2	Q5BJY6_RAT	Q5bjy6 rattus norv
56	34	66.7	295	2	Q98D96_RHILO	Q98d96 rhizobium l
57	34	66.7	296	2	Q4SCV6_TETNG	Q4scv6 tetraodon n
58	34	66.7	319	2	Q741L9_MYCPA	Q741l9 mycobacteri
59	34	66.7	326	2	Q9LTW7_ARATH	Q9ltw7 arabidopsis
60	34	66.7	328	2	Q9C7B5_ARATH	Q9c7b5 arabidopsis
61	34	66.7	330	2	Q6RWQ8_9ZZZZ	Q6rwq8 uncultured
62	34	66.7	336	2	Q8NCQ7_HUMAN	Q8ncq7 homo sapien
63	34	66.7	395	2	Q8EQN5_OCEIH	Q8eqn5 oceanobacil
64	34	66.7	442	2	Q6MWC2_ORYSA	Q6mwc2 oryza sativ
65	34	66.7	463	2	Q7EZC9_ORYSA	Q7ezc9 oryza sativ
66	34	66.7	524	2	Q941Q3_ARATH	Q941q3 arabidopsis
67	34	66.7	565	2	Q51505_PSEAE	Q51505 pseudomonas
68	34	66.7	565	2	Q9I1K1_PSEAE	Q9i1k1 pseudomonas
69	34	66.7	707	2	Q9L1H5_STRCO	Q9l1h5 streptomyce
70	34	66.7	861	2	Q8TND8_METAC	Q8tnd8 methanosarc
71	34	66.7	911	2	Q8DXK6_STRA5	Q8dxk6 streptococc
72	34	66.7	948	2	Q9TTD7_TRIVU	Q9ttd7 trichosurus
73	34	66.7	975	1	KIT_MOUSE	P05532 mus musculu
74	34	66.7	975	2	Q6QJB7_MOUSE	Q6qjb7 mus musculu
75	34	66.7	975	2	Q6QJB8_MOUSE	Q6qjb8 mus musculu
76	34	66.7	975	2	Q7TS86_MOUSE	Q7ts86 mus musculu
77	34	66.7	979	2	Q8C8K9_MOUSE	Q8c8k9 mus musculu
78	34	66.7	1052	2	O49676_ARATH	O49676 arabidopsis
79	34	66.7	1193	2	Q7QD42_ANOGA	Q7qd42 anopheles g
80	34	66.7	1229	2	Q8I954_ANOGA	Q8i954 anopheles g
81	34	66.7	1350	2	Q4PAI1_USTMA	Q4pai1 ustilago ma
82	34	66.7	2486	2	Q9VXM5_DROME	Q9vxm5 drosophila
83	34	66.7	3433	2	Q6UAW1_9CAUD	Q6uaw1 bacteriopha
84	33	64.7	111	2	Q6IIB8_DROME	Q6iib8 drosophila
85	33	64.7	116	2	Q83EE0_COXBU	Q83ee0 coxiella bu
86	33	64.7	139	2	Q7P799_FUSNV	Q7p799 fusobacteri
87	33	64.7	140	2	Q7UCY3_SHIFL	Q7ucy3 shigella fl
88	33	64.7	150	2	Q4LTV8_9BURK	Q4ltv8 burkholderi
89	33	64.7	167	2	Q83LJ4_SHIFL	Q83lj4 shigella fl
90	33	64.7	186	2	Q4TQV0_9SPHN	Q4tqv0 erythrobact
91	33	64.7	196	2	Q73EF2_BACC1	Q73ef2 bacillus ce
92	33	64.7	220	2	P91906_CAEEL	P91906 caenorhabdi
93	33	64.7	222	2	Q6FPA6_CANGA	Q6fpa6 candida gla
94	33	64.7	229	2	Q4LRZ5_9BURK	Q4lrz5 burkholderi
95	33	64.7	237	2	Q87XN9_PSESM	Q87xn9 pseudomonas
96	33	64.7	242	2	Q4ZPL7_PSESY	Q4zpl7 pseudomonas
97	33	64.7	256	2	Q5JH93_PYRKO	Q5jh93 pyrococcus
98	33	64.7	261	2	Q6GMI7_BRARE	Q6gmi7 brachydanio
99	33	64.7	265	2	Q6KGH3_9CAUD	Q6kgh3 bacteriopha
100	33	64.7	266	2	Q65PX5_MANSM	Q65px5 mannheimia
101	33	64.7	276	2	Q5DYT1_VIBF1	Q5dyt1 vibrio fisc
102	33	64.7	284	2	Q7S615_NEUCR	Q7s615 neurospora
103	33	64.7	351	2	Q9F358_STRCO	Q9f358 streptomyce
104	33	64.7	365	2	Q65SW6_MANSM	Q65sw6 mannheimia

105	33	64.7	366	2	Q76GM9_9BACI	Q76gm9	geobacillus
106	33	64.7	367	1	DHLE_BACST	P13154	bacillus st
107	33	64.7	367	2	Q76GN4_MOOTH	Q76gn4	moorella th
108	33	64.7	367	2	Q75TF3_BACST	Q75tf3	bacillus st
109	33	64.7	367	2	Q75TA6_GEOKA	Q75ta6	geobacillus
110	33	64.7	373	2	Q7XQ57_ORYSA	Q7xq57	oryza sativ
111	33	64.7	375	2	Q6UU64_ORYSA	Q6uu64	oryza sativ
112	33	64.7	377	2	Q6G953_STAAS	Q6g953	staphylococ
113	33	64.7	377	2	Q6GGI6_STAAR	Q6ggi6	staphylococ
114	33	64.7	377	2	Q5HFR1_STAAC	Q5hfr1	staphylococ
115	33	64.7	377	2	Q7A5G2_STAAN	Q7a5g2	staphylococ
116	33	64.7	377	2	Q8NWE1_STAAW	Q8nwe1	staphylococ
117	33	64.7	377	2	Q99TY1_STAAM	Q99ty1	staphylococ
118	33	64.7	389	2	Q67V21_ORYSA	Q67v21	oryza sativ
119	33	64.7	395	2	Q7G6J7_ORYSA	Q7g6j7	oryza sativ
120	33	64.7	395	2	Q8RUK9_ORYSA	Q8ruk9	oryza sativ
121	33	64.7	402	2	Q5JPX7_ORYSA	Q5jpx7	oryza sativ
122	33	64.7	404	2	Q9Y303_HUMAN	Q9y303	homo sapien
123	33	64.7	406	2	Q5NV38_9BURK	Q5nv38	ralstonia m
124	33	64.7	410	2	Q7XX18_ORYSA	Q7xx18	oryza sativ
125	33	64.7	417	2	Q7XFY1_ORYSA	Q7xfy1	oryza sativ
126	33	64.7	417	2	Q8S6T6_ORYSA	Q8s6t6	oryza sativ
127	33	64.7	417	2	Q8S834_ORYSA	Q8s834	oryza sativ
128	33	64.7	423	2	Q6YVP5_ORYSA	Q6yvp5	oryza sativ
129	33	64.7	423	2	Q60D65_ORYSA	Q60d65	oryza sativ
130	33	64.7	423	2	Q69K34_ORYSA	Q69k34	oryza sativ
131	33	64.7	425	2	Q8H8E7_ORYSA	Q8h8e7	oryza sativ
132	33	64.7	425	2	Q60DH7_ORYSA	Q60dh7	oryza sativ
133	33	64.7	439	2	Q8WV54_HUMAN	Q8wv54	homo sapien
134	33	64.7	448	2	Q5ZDW3_ORYSA	Q5zdw3	oryza sativ
135	33	64.7	449	2	Q65WV1_ORYSA	Q65wv1	oryza sativ
136	33	64.7	467	2	Q7XDS7_ORYSA	Q7xds7	oryza sativ
137	33	64.7	467	2	Q5VMV6_ORYSA	Q5vmv6	oryza sativ
138	33	64.7	472	2	Q5VMS5_ORYSA	Q5vms5	oryza sativ
139	33	64.7	477	2	Q7XHR7_ORYSA	Q7xhr7	oryza sativ
140	33	64.7	477	2	Q7XMV0_ORYSA	Q7xmv0	oryza sativ
141	33	64.7	477	2	Q7XQL4_ORYSA	Q7xql4	oryza sativ
142	33	64.7	477	2	Q7XS20_ORYSA	Q7xs20	oryza sativ
143	33	64.7	477	2	Q5VMH3_ORYSA	Q5vmh3	oryza sativ
144	33	64.7	477	2	Q5VMV2_ORYSA	Q5vmv2	oryza sativ
145	33	64.7	477	2	Q6AUU2_ORYSA	Q6auu2	oryza sativ
146	33	64.7	481	2	Q6FQ36_CANGA	Q6fq36	candida gla
147	33	64.7	492	2	Q62YK9_BACLD	Q62yk9	bacillus li
148	33	64.7	493	2	Q65N60_BACLD	Q65n60	bacillus li
149	33	64.7	495	2	Q5VMU0_ORYSA	Q5vmu0	oryza sativ
150	33	64.7	498	2	Q5NHB4_FRATT	Q5nhb4	francisella
151	33	64.7	508	2	Q7XUY2_ORYSA	Q7xuy2	oryza sativ
152	33	64.7	528	2	Q5VMS4_ORYSA	Q5vms4	oryza sativ
153	33	64.7	543	2	Q7XFP6_ORYSA	Q7xfp6	oryza sativ
154	33	64.7	543	2	Q8LLY2_ORYSA	Q8lly2	oryza sativ
155	33	64.7	544	2	Q7FAA1_ORYSA	Q7faa1	oryza sativ
156	33	64.7	549	2	Q758K3_ASHGO	Q758k3	ashbya goss
157	33	64.7	549	2	Q8LMB8_ORYSA	Q8lmb8	oryza sativ
158	33	64.7	561	2	Q5JPY6_ORYSA	Q5jpy6	oryza sativ
159	33	64.7	561	2	Q9KKX6_VIBCH	Q9kkx6	vibrio chol
160	33	64.7	569	2	Q92KG9_RHIME	Q92kg9	rhizobium m
161	33	64.7	572	2	Q9J7D1_PI3B	Q9j7d1	bovine para
162	33	64.7	572	2	Q9J7D7_PI3B	Q9j7d7	bovine para
163	33	64.7	574	2	Q5VMU6_ORYSA	Q5vmu6	oryza sativ
164	33	64.7	575	2	Q6BN37_DEBHA	Q6bn37	debaryomyce
165	33	64.7	583	2	Q7XJZ6_ORYSA	Q7xjz6	oryza sativ
166	33	64.7	587	2	Q8S3Q8_ORYSA	Q8s3q8	oryza sativ
167	33	64.7	609	1	NPRV_VIBPR	Q00971	vibrio prot
168	33	64.7	616	2	Q6YV37_ORYSA	Q6yv37	oryza sativ
169	33	64.7	665	2	Q7XFW7_ORYSA	Q7xfw7	oryza sativ
170	33	64.7	665	2	Q8S851_ORYSA	Q8s851	oryza sativ
171	33	64.7	732	2	Q5VMZ5_ORYSA	Q5vmz5	oryza sativ
172	33	64.7	736	2	Q6NCP1_RHOPA	Q6ncp1	rhodopseudo
173	33	64.7	753	2	Q6XN87_RHOER	Q6xn87	rhodococcus
174	33	64.7	803	2	Q6AUT9_ORYSA	Q6aut9	oryza sativ
175	33	64.7	804	2	Q8H8P7_ORYSA	Q8h8p7	oryza sativ
176	33	64.7	863	2	Q7Y0F3_ORYSA	Q7y0f3	oryza sativ
177	33	64.7	883	2	Q7FB33_ORYSA	Q7fb33	oryza sativ
178	33	64.7	962	2	O81638_MAIZE	O81638	zea mays (m
179	33	64.7	982	2	Q66A38_YERPS	Q66a38	yersinia ps
180	33	64.7	984	2	Q8ZE10_YERPE	Q8ze10	yersinia pe
181	33	64.7	1077	2	Q4INK4_GIBZE	Q4ink4	gibberella
182	33	64.7	1130	2	Q4RTK0_TETNG	Q4rtk0	tetraodon n
183	33	64.7	1417	2	Q871Y7_NEUCR	Q871y7	neurospora
184	33	64.7	1525	2	Q4NEJ1_9MICC	Q4nej1	arthrobacte
185	33	64.7	1565	2	Q5W6Z3_ORYSA	Q5w6z3	oryza sativ
186	33	64.7	2408	2	Q60DH6_ORYSA	Q60dh6	oryza sativ
187	32.5	63.7	162	2	Q9RS25_DEIRA	Q9rs25	deinococcus
188	32	62.7	59	2	Q4RS93_TETNG	Q4rs93	tetraodon n
189	32	62.7	86	2	Q50750_METTF	Q50750	methanobact
190	32	62.7	118	2	Q4QDM4_LEIMA	Q4qdm4	leishmania
191	32	62.7	124	1	REV_SIVCZ	P17280	chimpanzee
192	32	62.7	124	2	Q57SB0_SALCH	Q57sb0	salmonella
193	32	62.7	124	2	Q5PFN9_SALPA	Q5pfn9	salmonella
194	32	62.7	124	2	Q7CR24_SALTY	Q7cr24	salmonella
195	32	62.7	124	2	Q8XGV0_SALTI	Q8xgv0	salmonella
196	32	62.7	137	2	Q8L4V8_ORYSA	Q8l4v8	oryza sativ
197	32	62.7	140	2	Q65G23_BACLD	Q65g23	bacillus li
198	32	62.7	150	1	MBF1_CRYNE	Q5kar7	cryptococcu
199	32	62.7	154	2	Q63XH6_BURPS	Q63xh6	burkholderi
200	32	62.7	163	2	Q6ITX8_9EURY	Q6itx8	uncultured
201	32	62.7	203	2	Q5V352_HALMA	Q5v352	haloarcula
202	32	62.7	212	2	Q8NB65_HUMAN	Q8nb65	homo sapien
203	32	62.7	213	2	Q5T0Y2_HUMAN	Q5t0y2	homo sapien
204	32	62.7	217	2	Q6ADB6_LEIXX	Q6adb6	leifsonia x
205	32	62.7	218	2	O58890_PYRHO	O58890	pyrococcus
206	32	62.7	233	2	Q5BCH7_EMENI	Q5bch7	aspergillus
207	32	62.7	234	2	Q4IK73_GIBZE	Q4ik73	gibberella
208	32	62.7	250	2	Q4P537_USTMA	Q4p537	ustilago ma
209	32	62.7	255	2	Q6GVQ5_MYCAV	Q6gvq5	mycobacteri
210	32	62.7	255	2	Q741M8_MYCPA	Q741m8	mycobacteri
211	32	62.7	262	2	Q82GA8_STRAW	Q82ga8	streptomyce
212	32	62.7	262	2	Q82H10_STRAW	Q82h10	streptomyce
213	32	62.7	269	2	Q83VR9_9PROT	Q83vr9	methylobaci
214	32	62.7	277	2	Q88J82_PSEPK	Q88j82	pseudomonas
215	32	62.7	283	2	Q5M8U0_XENTR	Q5m8u0	xenopus tro
216	32	62.7	283	2	Q6GR11_XENLA	Q6gr11	xenopus lae
217	32	62.7	289	2	Q4RUM4_TETNG	Q4rum4	tetraodon n
218	32	62.7	292	2	Q6AF83_LEIXX	Q6af83	leifsonia x
219	32	62.7	314	2	Q64AC2_9ARCH	Q64ac2	uncultured
220	32	62.7	341	2	O59296_PYRHO	O59296	pyrococcus
221	32	62.7	352	2	Q63WZ1_BURPS	Q63wz1	burkholderi
222	32	62.7	356	2	Q7PH43_ANOGA	Q7ph43	anopheles g
223	32	62.7	370	2	Q54WF6_DICDI	Q54wf6	dictyosteli
224	32	62.7	375	2	Q4L6L1_STAHJ	Q41611	staphylococ
225	32	62.7	375	2	Q6GAX0_STAAS	Q6gax0	staphylococ
226	32	62.7	375	2	Q7A6H9_STAAN	Q7a6h9	staphylococ
227	32	62.7	375	2	Q8NXF4_STAAW	Q8nxf4	staphylococ
228	32	62.7	375	2	Q99VD2_STAAM	Q99vd2	staphylococ
229	32	62.7	375	2	Q5HHC9_STAAC	Q5hhc9	staphylococ
230	32	62.7	376	2	Q6MLI1_BDEBA	Q6mli1	bdellovibri
231	32	62.7	383	2	Q6P5U6_HUMAN	Q6p5u6	homo sapien
232	32	62.7	388	2	Q4KDL9_PSEP5	Q4kdl9	pseudomonas
233	32	62.7	407	1	YNS1_YEAST	P53878	saccharomyc
234	32	62.7	417	2	Q8NCX0_HUMAN	Q8ncx0	homo sapien
235	32	62.7	422	2	Q4IHM6_GIBZE	Q4ihm6	gibberella
236	32	62.7	428	2	Q88K89_PSEPK	Q88k89	pseudomonas
237	32	62.7	429	2	Q6B7Z3_9VIRU	Q6b7z3	suchong vir
238	32	62.7	436	1	ATG18_ASPFU	Q4wvd0	aspergillus
239	32	62.7	439	2	Q941M0_BRAOL	Q941m0	brassica ol
240	32	62.7	439	2	Q8XZR8_RALSO	Q8xzr8	ralstonia s
241	32	62.7	446	2	Q9D7A0_MOUSE	Q9d7a0	mus musculu
242	32	62.7	471	1	TNR1A_BOVIN	O19131	bos taurus
243	32	62.7	479	2	Q4W9N0_ASPFU	Q4w9n0	aspergillus
244	32	62.7	480	2	Q5LPT6_SILPO	Q5lpt6	silicibacte
245	32	62.7	489	2	Q8FC58_ECOL6	Q8fc58	escherichia
246	32	62.7	490	1	MDM4_HUMAN	O15151	homo sapien
247	32	62.7	490	2	Q6GS18_HUMAN	Q6gs18	homo sapien
248	32	62.7	493	1	RBSA_HAEIN	P44735	haemophilus
249	32	62.7	493	2	Q4QN44_HAEI8	Q4qn44	haemophilus
250	32	62.7	501	2	Q5W1K7_9HEMI	Q5w1k7	nilaparvata

251	32	62.7	509	2	Q58NS5_9TRYP	Q58ns5 trypanosoma
252	32	62.7	532	2	Q579H5_BRUAB	Q579h5 brucella ab
253	32	62.7	532	2	Q8FV88_BRUSU	Q8fv88 brucella su
254	32	62.7	532	2	Q8YD38_BRUME	Q8yd38 brucella me
255	32	62.7	535	2	Q8U8G4_AGRT5	Q8u8g4 agrobacteri
256	32	62.7	537	2	Q5FHP2_EHRRG	Q5fhp2 ehrlichia r
257	32	62.7	537	2	Q5HBG8_EHRRW	Q5hbg8 ehrlichia r
258	32	62.7	539	2	Q6N3G4_RHOPA	Q6n3g4 rhodopseudo
259	32	62.7	539	2	Q89QV4_BRAJA	Q89qv4 bradyrhizob
260	32	62.7	567	2	Q9SKG0_ARATH	Q9skg0 arabidopsis
261	32	62.7	575	2	Q9SLJ7_ARATH	Q9slj7 arabidopsis
262	32	62.7	588	2	Q93L02_BURPS	Q93l02 burkholderi
263	32	62.7	588	2	Q63KH0_BURPS	Q63kh0 burkholderi
264	32	62.7	589	2	Q95JZ9_MACFA	Q95jz9 macaca fasc
265	32	62.7	592	2	Q8FTV9_COREF	Q8ftv9 corynebacte
266	32	62.7	614	2	Q7PXI6_ANOGA	Q7pxi6 anopheles g
267	32	62.7	651	2	Q4WTK2_ASPFU	Q4wtk2 aspergillus
268	32	62.7	665	2	Q7XE59_ORYSA	Q7xe59 oryza sativ
269	32	62.7	674	2	Q4IEY7_GIBZE	Q4iey7 gibberella
270	32	62.7	681	2	Q82JG1_STRAW	Q82jg1 streptomyce
271	32	62.7	697	2	Q89UE7_BRAJA	Q89ue7 bradyrhizob
272	32	62.7	771	2	Q4P3Q5_USTMA	Q4p3q5 ustilago ma
273	32	62.7	788	2	O01500_CAEEL	O01500 caenorhabdi
274	32	62.7	793	2	Q928I9_LISIN	Q928i9 listeria in
275	32	62.7	806	2	Q8I7I1_CAEEL	Q8i7i1 caenorhabdi
276	32	62.7	861	2	Q7S1W6_NEUCR	Q7s1w6 neurospora
277	32	62.7	861	2	Q8IN52_DROME	Q8in52 drosophila
278	32	62.7	897	2	Q5U165_DROME	Q5u165 drosophila
279	32	62.7	927	2	Q96UE1_NEUCR	Q96ue1 neurospora
280	32	62.7	936	1	MRTFA_XENLA	Q8ayc2 xenopus lae
281	32	62.7	970	2	Q9YW19_MSEPV	Q9yw19 melanoplus
282	32	62.7	977	1	CSF1R_MOUSE	P09581 mus musculu
283	32	62.7	977	2	Q6NXV8_MOUSE	Q6nxv8 mus musculu
284	32	62.7	978	1	CSF1R_RAT	Q00495 rattus norv
285	32	62.7	991	2	Q6GP66_XENLA	Q6gp66 xenopus lae
286	32	62.7	1002	2	Q4HTG9_CAMUP	Q4htg9 campylobact
287	32	62.7	1005	2	Q6CMB8_KLULA	Q6cmb8 kluyveromyc
288	32	62.7	1025	2	Q8MRH2_DROME	Q8mrh2 drosophila
289	32	62.7	1081	2	Q6Z8U1_ORYSA	Q6z8u1 oryza sativ
290	32	62.7	1084	2	Q4FXD4_LEIMA	Q4fxd4 leishmania
291	32	62.7	1111	2	Q7R3S0_GIALA	Q7r3s0 giardia lam
292	32	62.7	1117	2	Q52EW7_MAGGR	Q52ew7 magnaporthe
293	32	62.7	1124	1	PHYA1_TOBAC	P33530 nicotiana t
294	32	62.7	1202	2	Q4PFG1_USTMA	Q4pfg1 ustilago ma
295	32	62.7	1324	2	Q4PBU5_USTMA	Q4pbu5 ustilago ma
296	32	62.7	1332	2	Q8NJX4_USTMA	Q8njx4 ustilago ma
297	32	62.7	1417	2	O48697_ARATH	O48697 arabidopsis
298	32	62.7	1459	2	Q7R2K7_GIALA	Q7r2k7 giardia lam
299	32	62.7	1491	2	Q4QJI2_LEIMA	Q4qji2 leishmania
300	32	62.7	1494	2	Q23980_DROME	Q23980 drosophila
301	32	62.7	1896	2	Q6C9G0_YARLI	Q6c9g0 yarrowia li
302	32	62.7	2397	2	Q5GHS0_ASPNG	Q5ghs0 aspergillus
303	32	62.7	2538	2	Q5U7N6_BRARE	Q5u7n6 brachydanio
304	32	62.7	2691	2	Q618T4_CAEBR	Q618t4 caenorhabdi
305	32	62.7	2971	2	Q5CCS2_ACHTE	Q5ccs2 achaearanea
306	32	62.7	4097	2	Q9VZQ3_DROME	Q9vzq3 drosophila
307	32	62.7	4118	2	Q7KV69_DROME	Q7kv69 drosophila
308	32	62.7	4207	2	Q7KV70_DROME	Q7kv70 drosophila
309	32	62.7	12268	2	Q8MQ08_CAEEL	Q8mq08 caenorhabdi
310	32	62.7	13100	2	Q09165_CAEEL	Q09165 caenorhabdi
311	31	60.8	92	2	Q8A7K4_BACTN	Q8a7k4 bacteroides
312	31	60.8	105	2	Q6AC92_LEIXX	Q6ac92 leifsonia x
313	31	60.8	113	2	Q59QB3_CANAL	Q59qb3 candida alb
314	31	60.8	127	2	Q925S9_MOUSE	Q925s9 mus musculu
315	31	60.8	129	2	Q4UQT1_XANCP	Q4uqt1 xanthomonas
316	31	60.8	129	2	Q8PCN9_XANCP	Q8pcn9 xanthomonas
317	31	60.8	140	2	Q4XRZ4_PLACH	Q4xrz4 plasmodium
318	31	60.8	143	1	RUVX_LACLA	Q9cj63 lactococcus
319	31	60.8	145	1	LIRP_LOCMI	P15131 locusta mig
320	31	60.8	148	2	Q98HT5_RHILO	Q98ht5 rhizobium l
321	31	60.8	152	2	Q8ETR6_OCEIH	Q8etr6 oceanobacil
322	31	60.8	153	2	Q89C20_BRAJA	Q89c20 bradyrhizob
323	31	60.8	158	2	Q63I71_BURPS	Q63i71 burkholderi
324	31	60.8	172	2	Q6PTQ9_9ANNE	Q6ptq9 chaetopteru
325	31	60.8	178	2	Q505T1_9RHAB	Q505t1 rabies viru
326	31	60.8	179	2	Q505S5_9RHAB	Q505s5 rabies viru
327	31	60.8	179	2	Q505S8_9RHAB	Q505s8 rabies viru
328	31	60.8	189	2	Q99FP1_9ENTO	Q99fp1 human echov
329	31	60.8	190	1	LEPW_BACSU	P54506 bacillus su
330	31	60.8	194	2	Q5L9J2_BACFN	Q5l9j2 bacteroides
331	31	60.8	194	2	Q64PT0_BACFR	Q64pt0 bacteroides
332	31	60.8	194	2	Q505V6_9RHAB	Q505v6 rabies viru
333	31	60.8	194	2	Q505W6_9RHAB	Q505w6 rabies viru
334	31	60.8	195	2	Q505U2_9RHAB	Q505u2 rabies viru
335	31	60.8	195	2	Q505X4_9RHAB	Q505x4 rabies viru
336	31	60.8	200	2	Q505V0_9RHAB	Q505v0 rabies viru
337	31	60.8	200	2	Q505V7_9RHAB	Q505v7 rabies viru
338	31	60.8	204	2	Q94I88_ATRBE	Q94i88 atropa bell
339	31	60.8	215	2	Q9VIL4_DROME	Q9vil4 drosophila
340	31	60.8	241	2	Q921A6_MOUSE	Q921a6 mus musculu
341	31	60.8	246	2	Q7TYA5_MYCBO	Q7tya5 mycobacteri
342	31	60.8	246	2	Q73NM6_TREDE	Q73nm6 treponema d
343	31	60.8	248	2	O02399_9BILA	O02399 teladorsagi
344	31	60.8	250	2	Q527X6_MAGGR	Q527x6 magnaporthe
345	31	60.8	259	2	Q505T0_9RHAB	Q505t0 rabies viru
346	31	60.8	259	2	Q505T2_9RHAB	Q505t2 rabies viru
347	31	60.8	261	2	Q8GTE3_CICAR	Q8gte3 cicer ariet
348	31	60.8	266	1	KLRA5_MOUSE	Q60652 mus musculu
349	31	60.8	266	1	KLRA6_MOUSE	Q60653 mus musculu
350	31	60.8	266	2	Q6IVG1_MOUSE	Q6ivg1 mus musculu
351	31	60.8	266	2	Q9JHV3_MOUSE	Q9jhv3 mus musculu
352	31	60.8	266	2	Q548A2_MOUSE	Q548a2 mus musculu
353	31	60.8	270	2	Q9HPN5_HALSA	Q9hpn5 halobacteri
354	31	60.8	271	2	Q71TB3_BPP1	Q71tb3 bacteriopha
355	31	60.8	281	2	Q9QP49_9ENTO	Q9qp49 human echov
356	31	60.8	281	2	Q9YLK8_9ENTO	Q9ylk8 human echov
357	31	60.8	286	2	Q5M1W0_STRT1	Q5m1w0 streptococc
358	31	60.8	286	2	Q5M6F0_STRT2	Q5m6f0 streptococc
359	31	60.8	290	2	Q4NGG9_9MICC	Q4ngg9 arthrobacte
360	31	60.8	295	1	PANE_MYCTU	Q50648 mycobacteri
361	31	60.8	295	2	Q4TEN3_TETNG	Q4ten3 tetraodon n
362	31	60.8	296	2	Q9HGJ2_9ASCO	Q9hgj2 cerataphis
363	31	60.8	297	2	Q91RF0_9RHAB	Q91rf0 rabies viru
364	31	60.8	297	2	Q91RF1_9RHAB	Q91rf1 rabies viru
365	31	60.8	297	2	Q91RF3_9RHAB	Q91rf3 rabies viru
366	31	60.8	300	2	Q7WIS1_BORBR	Q7wis1 bordetella
367	31	60.8	310	2	Q4NND7_9DELT	Q4nnd7 anaeromyxob
368	31	60.8	313	2	Q7VZZ1_BORPE	Q7vzz1 bordetella
369	31	60.8	313	2	Q7WG06_BORBR	Q7wg06 bordetella
370	31	60.8	323	2	Q6LRT6_PHOPR	Q6lrt6 photobacter
371	31	60.8	324	2	Q4TEC8_TETNG	Q4tec8 tetraodon n
372	31	60.8	326	2	Q52AI1_MAGGR	Q52ai1 magnaporthe
373	31	60.8	331	2	Q98EL5_RHILO	Q98el5 rhizobium l
374	31	60.8	333	1	CBBR_XANFL	P25545 xanthobacte
375	31	60.8	336	2	Q4THB9_TETNG	Q4thb9 tetraodon n
376	31	60.8	338	2	Q5WMM4_ORYSA	Q5wmm4 oryza sativ
377	31	60.8	345	2	Q8L046_9BACT	Q8l046 uncultured
378	31	60.8	346	2	O84778_CHLTR	O84778 chlamydia t
379	31	60.8	352	2	Q9WWH7_PSESY	Q9wwh7 pseudomonas
380	31	60.8	352	2	Q4THA0_TETNG	Q4tha0 tetraodon n
381	31	60.8	357	2	Q7QG91_ANOGA	Q7qg91 anopheles g
382	31	60.8	361	2	Q7QA25_ANOGA	Q7qa25 anopheles g
383	31	60.8	363	2	Q7KT87_DROME	Q7kt87 drosophila
384	31	60.8	364	1	VMP21_BORHE	P21875 borrelia he
385	31	60.8	365	2	Q56VN2_PINSY	Q56vn2 pinus sylve
386	31	60.8	366	2	Q5H1N4_XANOR	Q5h1n4 xanthomonas
387	31	60.8	366	2	Q4USI4_XANCP	Q4usi4 xanthomonas
388	31	60.8	366	2	Q8PB27_XANCP	Q8pb27 xanthomonas
389	31	60.8	366	2	Q8PMS6_XANAC	Q8pms6 xanthomonas
390	31	60.8	369	1	VP6_AHSV3	Q64909 african hor
391	31	60.8	372	2	Q63QH7_BURPS	Q63qh7 burkholderi
392	31	60.8	372	2	Q62DC2_BURMA	Q62dc2 burkholderi
393	31	60.8	392	2	Q7ZW38_BRARE	Q7zw38 brachydanio
394	31	60.8	392	2	Q4RJR9_TETNG	Q4rjr9 tetraodon n
395	31	60.8	393	2	Q568R0_BRARE	Q568r0 brachydanio
396	31	60.8	398	2	Q4IKD8_GIBZE	Q4ikd8 gibberella

397	31	60.8	406	2	Q6H4X7_ORYSA	Q6h4x7	oryza sativ
398	31	60.8	420	2	Q5LEX2_BACFN	Q5lex2	bacteroides
399	31	60.8	420	2	Q64VW4_BACFR	Q64vw4	bacteroides
400	31	60.8	424	2	Q49553_MYCHO	Q49553	mycoplasma
401	31	60.8	431	1	TIM44_YEAST	Q01852	saccharomyc
402	31	60.8	434	2	Q6CP50_KLULA	Q6cp50	kluyveromyc
403	31	60.8	435	2	Q9A6D3_CAUCR	Q9a6d3	caulobacter
404	31	60.8	449	2	Q5FM39_LACAC	Q5fm39	lactobacill
405	31	60.8	454	2	Q5CNL2_CRYHO	Q5cnl2	cryptospori
406	31	60.8	454	2	Q6MR54_BDEBA	Q6mr54	bdellovibri
407	31	60.8	455	2	Q5CSW1_CRYPV	Q5csw1	cryptospori
408	31	60.8	456	2	Q5PBE1_ANAMM	Q5pbe1	anaplasma m
409	31	60.8	458	2	Q67TL3_ORYSA	Q67tl3	oryza sativ
410	31	60.8	472	2	Q5DIQ3_PSEAE	Q5diq3	pseudomonas
411	31	60.8	472	2	Q5DIS0_PSEAE	Q5dis0	pseudomonas
412	31	60.8	472	2	Q5DIU9_PSEAE	Q5diu9	pseudomonas
413	31	60.8	474	2	Q9VJQ7_DROME	Q9vjq7	drosophila
414	31	60.8	474	2	Q5RAA4_PONPY	Q5raa4	pongo pygma
415	31	60.8	474	2	Q9I189_PSEAE	Q9i189	pseudomonas
416	31	60.8	480	1	SEPC_PSEPU	Q849r1	pseudomonas
417	31	60.8	480	1	TTGF_PSEPU	Q9kwv3	pseudomonas
418	31	60.8	489	1	MDM4_MOUSE	O35618	mus musculu
419	31	60.8	489	2	Q9CYG1_MOUSE	Q9cyg1	m mus muscu
420	31	60.8	490	2	Q5XIN1_RAT	Q5xin1	rattus norv
421	31	60.8	490	2	Q99L86_MOUSE	Q99l86	mus musculu
422	31	60.8	491	2	Q89F44_BRAJA	Q89f44	bradyrhizob
423	31	60.8	497	2	Q7S5A5_NEUCR	Q7s5a5	neurospora
424	31	60.8	502	2	Q6MFD5_NEUCR	Q6mfd5	neurospora
425	31	60.8	507	2	Q9AJD6_9MICO	Q9ajd6	microbacter
426	31	60.8	508	2	O45345_CAEEL	O45345	caenorhabdi
427	31	60.8	508	2	Q5F3E7_CHICK	Q5f3e7	gallus gall
428	31	60.8	510	2	Q4ZR37_PSESY	Q4zr37	pseudomonas
429	31	60.8	515	2	Q4Q2I1_LEIMA	Q4q2i1	leishmania
430	31	60.8	519	2	Q55QC8_CRYNE	Q55qc8	cryptococcu
431	31	60.8	519	2	Q5KFT8_CRYNE	Q5kft8	cryptococcu
432	31	60.8	522	2	Q8XS12_RALSO	Q8xs12	ralstonia s
433	31	60.8	528	2	Q4QGG9_LEIMA	Q4qgg9	leishmania
434	31	60.8	545	1	CH601_METCA	Q60ay0	methylococc
435	31	60.8	546	2	Q6BK47_DEBHA	Q6bk47	debaryomyce
436	31	60.8	547	2	Q4RGV1_TETNG	Q4rgv1	tetraodon n
437	31	60.8	587	2	Q9Y8J0_METMP	Q9y8j0	methanococc
438	31	60.8	587	2	Q6LZH8_METMP	Q6lzh8	methanococc
439	31	60.8	590	2	Q73P28_TREDE	Q73p28	treponema d
440	31	60.8	594	2	Q4KAL6_PSEF5	Q4kal6	pseudomonas
441	31	60.8	598	2	Q8IPF9_DROME	Q8ipf9	drosophila
442	31	60.8	604	2	Q8MSA8_DROME	Q8msa8	drosophila
443	31	60.8	607	2	Q6FUB6_CANGA	Q6fub6	candida gla
444	31	60.8	610	2	Q8RR31_VIBFL	Q8rr31	vibrio fluv
445	31	60.8	619	2	Q59R29_CANAL	Q59r29	candida alb
446	31	60.8	623	2	Q4NQR4_9DELT	Q4nqr4	anaeromyxob
447	31	60.8	627	1	SYT_GLOVI	Q7ncu0	gloeobacter
448	31	60.8	643	2	Q9VLP4_DROME	Q9vlp4	drosophila
449	31	60.8	645	2	Q4WI09_ASPFU	Q4wi09	aspergillus
450	31	60.8	654	2	Q96U15_NEUCR	Q96u15	neurospora
451	31	60.8	655	2	Q4XS55_PLACH	Q4xs55	plasmodium
452	31	60.8	658	2	Q6CKM5_KLULA	Q6ckm5	kluyveromyc
453	31	60.8	658	2	Q4IAK2_GIBZE	Q4iak2	gibberella
454	31	60.8	665	2	Q23823_CALVI	Q23823	calliphora
455	31	60.8	666	2	Q5WWF9_LEGPL	Q5wwf9	legionella
456	31	60.8	666	2	Q5X531_LEGPA	Q5x531	legionella
457	31	60.8	666	2	Q5ZVA8_LEGPH	Q5zva8	legionella
458	31	60.8	674	2	Q6TGQ6_ENTMU	Q6tgq6	enterococcu
459	31	60.8	674	2	Q8RR64_ENTMU	Q8rr64	enterococcu
460	31	60.8	686	2	Q60Q69_CAEBR	Q60q69	caenorhabdi
461	31	60.8	710	2	Q61SN5_CAEBR	Q61sn5	caenorhabdi
462	31	60.8	715	2	Q6DCW5_XENLA	Q6dcw5	xenopus lae
463	31	60.8	732	2	O27676_METTH	O27676	methanobact
464	31	60.8	732	2	Q46767_ECOLI	Q46767	escherichia
465	31	60.8	738	2	Q5HWU0_CAMJR	Q5hwu0	campylobact
466	31	60.8	752	2	Q60WH5_CAEBR	Q60wh5	caenorhabdi
467	31	60.8	758	2	Q7S483_NEUCR	Q7s483	neurospora
468	31	60.8	778	2	Q4IQM2_GIBZE	Q4iqm2	gibberella
469	31	60.8	788	2	Q741P2_MYCPA	Q741p2	mycobacteri
470	31	60.8	789	2	Q67TK9_ORYSA	Q67tk9	oryza sativ
471	31	60.8	812	2	Q9RBA5_9MICC	Q9rba5	arthrobacte
472	31	60.8	812	2	Q4NTV2_9DELT	Q4ntv2	anaeromyxob
473	31	60.8	816	2	Q9N4F1_CAEEL	Q9n4f1	caenorhabdi
474	31	60.8	892	2	Q67RX2_SYMTH	Q67rx2	symbiobacte
475	31	60.8	904	2	Q4Q832_LEIMA	Q4q832	leishmania
476	31	60.8	938	2	Q8LRN5_TOBAC	Q8lrn5	nicotiana t
477	31	60.8	939	2	Q84KK7_NICBE	Q84kk7	nicotiana b
478	31	60.8	939	2	Q8RVJ9_TOBAC	Q8rvj9	nicotiana t
479	31	60.8	1017	1	PEX6_CANGA	Q6fw67	candida gla
480	31	60.8	1020	2	Q4KHX4_PSEF5	Q4khx4	pseudomonas
481	31	60.8	1020	2	Q6F779_ACIAD	Q6f779	acinetobact
482	31	60.8	1041	2	Q7S0H2_NEUCR	Q7s0h2	neurospora
483	31	60.8	1041	2	Q7NE52_GLOVI	Q7ne52	gloeobacter
484	31	60.8	1048	2	Q59SE0_CANAL	Q59se0	candida alb
485	31	60.8	1048	2	Q59SH1_CANAL	Q59sh1	candida alb
486	31	60.8	1049	2	Q6AWN7_DROME	Q6awn7	drosophila
487	31	60.8	1049	2	Q9VP79_DROME	Q9vp79	drosophila
488	31	60.8	1053	2	Q7SHC2_NEUCR	Q7shc2	neurospora
489	31	60.8	1085	2	Q800D4_CHICK	Q800d4	gallus gall
490	31	60.8	1089	1	IMB3_YEAST	P32337	saccharomyc
491	31	60.8	1124	2	O12983_XENLA	O12983	xenopus lae
492	31	60.8	1132	2	Q60CL9_METCA	Q60cl9	methylococc
493	31	60.8	1146	2	Q4Q9S0_LEIMA	Q4q9s0	leishmania
494	31	60.8	1211	2	Q88L35_PSEPK	Q88l35	pseudomonas
495	31	60.8	1270	2	O12982_XENLA	O12982	xenopus lae
496	31	60.8	1289	2	Q5KTC1_HUMAN	Q5ktc1	homo sapien
497	31	60.8	1318	2	Q5MZ21_SYNP6	Q5mz21	synechococc
498	31	60.8	1358	1	SIR4_YEAST	P11978	saccharomyc
499	31	60.8	1372	2	Q5PB95_ANAMM	Q5pb95	anaplasma m
500	31	60.8	1373	1	RPOC2_CHAGL	Q8ma10	chaetosphae
501	31	60.8	1403	2	Q9SUZ1_ARATH	Q9suz1	arabidopsis
502	31	60.8	1503	1	TRPM2_HUMAN	O94759	h transient
503	31	60.8	1503	2	Q5KTC2_HUMAN	Q5ktc2	homo sapien
504	31	60.8	1556	2	Q4Q626_LEIMA	Q4q626	leishmania
505	31	60.8	1579	2	Q9GRT7_LEIME	Q9grt7	leishmania
506	31	60.8	1790	2	Q4N6B8_THEPA	Q4n6b8	theileria p
507	31	60.8	2065	2	Q93DC7_YEREN	Q93dc7	yersinia en
508	31	60.8	2183	2	Q6W9F8_9ENTO	Q6w9f8	human echov
509	31	60.8	2239	2	Q4HXM5_GIBZE	Q4hxm5	gibberella
510	31	60.8	2522	2	Q8EKA6_SHEON	Q8eka6	shewanella
511	31	60.8	2906	2	Q4T143_TETNG	Q4t143	tetraodon n
512	31	60.8	3492	2	Q5PAK4_ANAMM	Q5pak4	anaplasma m
513	31	60.8	3866	1	HRX_MOUSE	P55200	mus musculu
514	31	60.8	4226	2	Q8TKD6_METAC	Q8tkd6	methanosarc
515	31	60.8	4326	2	Q5FJA7_LACAC	Q5fja7	lactobacill
516	31	60.8	5435	2	Q9L4X2_9ACTO	Q9l4x2	streptomyce
517	31	60.8	5644	2	Q93NX8_9ACTO	Q93nx8	streptomyce
518	31	60.8	7548	2	Q5WRU1_CAEEL	Q5wru1	caenorhabdi
519	31	60.8	8601	2	Q6VT95_9BACT	Q6vt95	symbiont ba
520	30.5	59.8	589	2	Q6A716_PROAC	Q6a716	propionibac
521	30	58.8	44	2	Q4XIS1_PLACH	Q4xis1	plasmodium
522	30	58.8	47	2	Q4RAU2_TETNG	Q4rau2	tetraodon n
523	30	58.8	61	2	Q6MB89_PARUW	Q6mb89	parachlamyd
524	30	58.8	99	2	Q9JL74_MOUSE	Q9jl74	mus musculu
525	30	58.8	103	1	CHLB_SELMO	P37856	selaginella
526	30	58.8	107	2	Q5YV31_NOCFA	Q5yv31	nocardia fa
527	30	58.8	116	2	Q8ZVI2_PYRAE	Q8zvi2	pyrobaculum
528	30	58.8	127	2	Q65RS9_MANSM	Q65rs9	mannheimia
529	30	58.8	130	2	Q5NWZ0_AZOSE	Q5nwz0	azoarcus sp
530	30	58.8	132	2	Q51590_BURCE	Q51590	burkholderi
531	30	58.8	134	2	Q4X5U1_PLACH	Q4x5u1	plasmodium
532	30	58.8	138	2	Q82NL6_STRAW	Q82nl6	streptomyce
533	30	58.8	141	2	Q7XR38_ORYSA	Q7xr38	oryza sativ
534	30	58.8	141	2	Q5FLV5_LACAC	Q5flv5	lactobacill
535	30	58.8	143	2	Q555C8_DICDI	Q555c8	dictyosteli
536	30	58.8	143	2	Q74KT9_LACJO	Q74kt9	lactobacill
537	30	58.8	144	2	Q5FTX3_GLUOX	Q5ftx3	gluconobact
538	30	58.8	147	2	Q55LE4_CRYNE	Q55le4	cryptococcu
539	30	58.8	147	2	Q5KA45_CRYNE	Q5ka45	cryptococcu
540	30	58.8	149	2	Q4RDG5_TETNG	Q4rdg5	tetraodon n
541	30	58.8	151	2	Q6ZCG2_ORYSA	Q6zcg2	oryza sativ
542	30	58.8	152	2	Q95LK1_MACFA	Q95lk1	macaca fasc

543	30	58.8	156	2	Q6JIA5_9EURY	Q6jia5	uncultured
544	30	58.8	156	2	Q6SEJ4_9EURY	Q6sej4	uncultured
545	30	58.8	167	2	Q9KG21_BACHD	Q9kg21	bacillus ha
546	30	58.8	168	2	Q6ZTF1_HUMAN	Q6ztf1	homo sapien
547	30	58.8	177	2	Q5H3Z9_XANOR	Q5h3z9	xanthomonas
548	30	58.8	178	2	Q4URN9_XANCP	Q4urn9	xanthomonas
549	30	58.8	178	2	Q8PBW2_XANCP	Q8pbw2	xanthomonas
550	30	58.8	179	2	Q8PWU8_METMA	Q8pwu8	methanosarc
551	30	58.8	179	2	Q69MK3_ORYSA	Q69mk3	oryza sativ
552	30	58.8	179	2	Q6B380_9PROT	Q6b380	uncultured
553	30	58.8	181	2	Q9GSB6_BOMMO	Q9gsb6	bombyx mori
554	30	58.8	183	2	Q5MGL1_9NEOP	Q5mgl1	lonomia obl
555	30	58.8	186	2	Q9GN07_BOMMO	Q9gn07	bombyx mori
556	30	58.8	186	2	Q8KV92_9BACT	Q8kv92	uncultured
557	30	58.8	187	2	Q5AGZ0_CANAL	Q5agz0	candida alb
558	30	58.8	188	2	Q5MGN8_9NEOP	Q5mgn8	lonomia obl
559	30	58.8	188	2	Q5H782_STRAT	Q5h782	streptomyce
560	30	58.8	188	2	Q4UYK7_XANCP	Q4uyk7	xanthomonas
561	30	58.8	188	2	Q8P5G8_XANCP	Q8p5g8	xanthomonas
562	30	58.8	194	2	O26159_METTH	O26159	methanobact
563	30	58.8	194	2	Q9RQQ6_BACAM	Q9rqq6	bacillus am
564	30	58.8	198	2	Q6IV08_DRORT	Q6iv08	drosera rot
565	30	58.8	201	2	Q8BRH8_MOUSE	Q8brh8	mus musculu
566	30	58.8	202	2	Q5V0F0_HALMA	Q5v0f0	haloarcula
567	30	58.8	204	2	Q948K2_TOBAC	Q948k2	nicotiana t
568	30	58.8	205	2	Q4XPV9_PLACH	Q4xpv9	plasmodium
569	30	58.8	205	2	Q7XSA7_ORYSA	Q7xsa7	oryza sativ
570	30	58.8	207	2	Q8ZFQ8_YERPE	Q8zfq8	yersinia pe
571	30	58.8	207	2	Q669Q1_YERPS	Q669q1	yersinia ps
572	30	58.8	213	2	Q72F76_DESVH	Q72f76	desulfovibr
573	30	58.8	215	2	Q9F2P8_STRCO	Q9f2p8	streptomyce
574	30	58.8	216	2	Q9L201_STRCO	Q9l201	streptomyce
575	30	58.8	223	2	Q4YZU2_PLABE	Q4yzu2	plasmodium
576	30	58.8	227	2	Q4QSL3_9LECA	Q4qsl3	pertusaria
577	30	58.8	227	2	Q9KN47_VIBCH	Q9kn47	vibrio chol
578	30	58.8	229	2	Q4LT41_9BURK	Q4lt41	burkholderi
579	30	58.8	229	2	Q4M055_9BURK	Q4m055	burkholderi
580	30	58.8	229	2	Q63LN2_BURPS	Q63ln2	burkholderi
581	30	58.8	229	2	Q63SD0_BURPS	Q63sd0	burkholderi
582	30	58.8	229	2	Q63W58_BURPS	Q63w58	burkholderi
583	30	58.8	229	2	Q4V2H9_BURMA	Q4v2h9	burkholderi
584	30	58.8	231	2	Q7RFI1_PLAYO	Q7rfi1	plasmodium
585	30	58.8	234	2	Q5JMS0_ORYSA	Q5jms0	oryza sativ
586	30	58.8	239	1	MBL1_MOUSE	P39039	mus musculu
587	30	58.8	239	2	Q4RQ82_TETNG	Q4rq82	tetraodon n
588	30	58.8	240	2	Q9Y864_ASPPA	Q9y864	aspergillus
589	30	58.8	242	2	Q4KH88_PSEF5	Q4kh88	pseudomonas
590	30	58.8	243	2	Q4TM37_9SPHN	Q4tm37	erythrobact
591	30	58.8	243	2	Q9KCQ9_BACHD	Q9kcq9	bacillus ha
592	30	58.8	245	2	Q4RQU6_TETNG	Q4rqu6	tetraodon n
593	30	58.8	246	2	Q4Q1B7_LEIMA	Q4q1b7	leishmania
594	30	58.8	246	2	Q4Q0Q0_LEIMA	Q4q0q0	leishmania
595	30	58.8	246	2	Q5FMN5_LACAC	Q5fmn5	lactobacill
596	30	58.8	250	2	Q7VZV9_BORPE	Q7vzv9	bordetella
597	30	58.8	251	1	RS3A_SCHPO	Q09781	schizosacch
598	30	58.8	252	2	Q71U75_HUMAN	Q71u75	homo sapien
599	30	58.8	255	2	Q5FUC5_GLUOX	Q5fuc5	gluconobact
600	30	58.8	260	1	1433C_TOBAC	P93343	nicotiana t
601	30	58.8	260	2	Q5AQQ6_EMENI	Q5aqq6	aspergillus
602	30	58.8	260	2	Q5KTN5_TOBAC	Q5ktn5	nicotiana t
603	30	58.8	260	2	Q75ZE3_TOBAC	Q75ze3	nicotiana t
604	30	58.8	261	2	Q5XU73_CALMO	Q5xu73	callicebus
605	30	58.8	261	2	Q5VRZ6_ORYSA	Q5vrz6	oryza sativ
606	30	58.8	266	2	Q9SXA4_ARATH	Q9sxa4	arabidopsis
607	30	58.8	269	2	Q50KB3_MACMU	Q50kb3	macaca mula
608	30	58.8	270	2	Q88ND8_PSEPK	Q88nd8	pseudomonas
609	30	58.8	271	2	Q5XII6_RAT	Q5xii6	rattus norv
610	30	58.8	272	2	Q8C7M7_MOUSE	Q8c7m7	mus musculu
611	30	58.8	273	1	ZCHC9_MOUSE	Q8r1j3	mus musculu
612	30	58.8	273	2	Q73XW2_MYCPA	Q73xw2	mycobacteri
613	30	58.8	278	1	Y751_METJA	Q58161	methanococc
614	30	58.8	279	2	Q50KB4_PANTR	Q50kb4	pan troglod
615	30	58.8	284	2	Q4XRJ5_PLACH	Q4xrj5	plasmodium
616	30	58.8	285	2	Q6CE41_YARLI	Q6ce41	yarrowia li
617	30	58.8	285	2	Q4XT80_PLACH	Q4xt80	plasmodium
618	30	58.8	285	2	Q4XVL6_PLACH	Q4xvl6	plasmodium
619	30	58.8	285	2	Q93JU3_PSEST	Q93ju3	pseudomonas
620	30	58.8	287	2	Q4HL90_CAMLA	Q4hl90	campylobact
621	30	58.8	292	2	Q8BYG9_MOUSE	Q8byg9	m mus muscu
622	30	58.8	295	2	Q8N289_HUMAN	Q8n289	homo sapien
623	30	58.8	295	2	Q6NW42_HUMAN	Q6nw42	homo sapien
624	30	58.8	298	1	BIM3_ARATH	Q9fmb6	arabidopsis
625	30	58.8	300	2	Q7A9B7_ECO57	Q7a9b7	escherichia
626	30	58.8	300	2	Q83IV1_SHIFL	Q83iv1	shigella fl
627	30	58.8	300	2	Q8X8E4_ECO57	Q8x8e4	escherichia
628	30	58.8	308	1	YIHR_ECOLI	P32139	escherichia
629	30	58.8	309	1	T2R64_PANPA	Q5y4y9	pan paniscu
630	30	58.8	312	2	Q9C628_ARATH	Q9c628	arabidopsis
631	30	58.8	315	2	Q89X49_BRAJA	Q89x49	bradyrhizob
632	30	58.8	319	2	Q6FKH5_CANGA	Q6fkh5	candida gla
633	30	58.8	319	2	Q6FQD4_CANGA	Q6fqd4	candida gla
634	30	58.8	319	2	Q88JA5_PSEPK	Q88ja5	pseudomonas
635	30	58.8	323	2	Q8NDD2_HUMAN	Q8ndd2	homo sapien
636	30	58.8	333	2	Q8PLY1_XANAC	Q8ply1	xanthomonas
637	30	58.8	335	2	Q51ZE4_MAGGR	Q51ze4	magnaporthe
638	30	58.8	335	2	Q82SN4_NITEU	Q82sn4	nitrosomona
639	30	58.8	336	2	Q7R768_PLAYO	Q7r768	plasmodium
640	30	58.8	337	2	Q5H0Z3_XANOR	Q5h0z3	xanthomonas
641	30	58.8	339	2	Q4UTD5_XANCP	Q4utd5	xanthomonas
642	30	58.8	339	2	Q8PA91_XANCP	Q8pa91	xanthomonas
643	30	58.8	342	2	Q7ULP6_RHOBA	Q7ulp6	rhodopirell
644	30	58.8	344	2	Q8EDV5_SHEON	Q8edv5	shewanella
645	30	58.8	344	2	Q8FS07_COREF	Q8fs07	corynebacte
646	30	58.8	345	2	Q5Z2N2_NOCFA	Q5z2n2	nocardia fa
647	30	58.8	346	2	Q72WI8_DESVH	Q72wi8	desulfovibr
648	30	58.8	346	2	Q9PLF0_CHLMU	Q9plf0	chlamydia m
649	30	58.8	347	2	Q8T8U9_DROME	Q8t8u9	drosophila
650	30	58.8	347	2	Q9VT39_DROME	Q9vt39	drosophila
651	30	58.8	347	2	Q8FR63_COREF	Q8fr63	corynebacte
652	30	58.8	348	2	Q9J2K9_9GAMA	Q9j2k9	rhesus monk
653	30	58.8	348	2	Q9WRS3_9GAMA	Q9wrs3	macaca mula
654	30	58.8	348	2	Q53D18_9GAMA	Q53d18	macaca fusc
655	30	58.8	350	2	Q8UKL4_AGRT5	Q8ukl4	agrobacteri
656	30	58.8	354	2	Q93XF5_MAIZE	Q93xf5	zea mays (m
657	30	58.8	358	2	Q6ZRP1_HUMAN	Q6zrp1	homo sapien
658	30	58.8	359	2	Q7YZ82_PLACH	Q7yz82	plasmodium
659	30	58.8	360	2	Q7Z1C2_PLACH	Q7z1c2	plasmodium
660	30	58.8	363	2	Q9SKD8_ARATH	Q9skd8	arabidopsis
661	30	58.8	363	2	Q9CTP6_MOUSE	Q9ctp6	mus musculu
662	30	58.8	364	2	Q583Y7_9TRYP	Q583y7	trypanosoma
663	30	58.8	375	2	Q6ZXD1_CHICK	Q6zxd1	gallus gall
664	30	58.8	382	2	Q6LHS1_PHOPR	Q6lhs1	photobacter
665	30	58.8	383	2	Q9WXE9_PRERU	Q9wxe9	prevotella
666	30	58.8	390	2	Q8DSU0_STRMU	Q8dsu0	streptococc
667	30	58.8	393	2	Q6MKM6_BDEBA	Q6mkm6	bdellovibri
668	30	58.8	396	2	Q8GSY5_ORYSA	Q8gsy5	oryza sativ
669	30	58.8	397	2	Q9S7R9_ARATH	Q9s7r9	arabidopsis
670	30	58.8	398	2	Q6ZXC7_RAT	Q6zxc7	rattus norv
671	30	58.8	399	2	Q4LEZ5_9ACTN	Q4lez5	actinobacte
672	30	58.8	399	2	Q4LEZ6_9ACTN	Q4lez6	actinobacte
673	30	58.8	399	2	Q6D5M7_ERWCT	Q6d5m7	erwinia car
674	30	58.8	401	2	Q4WGU7_ASPFU	Q4wgu7	aspergillus
675	30	58.8	404	2	Q4I2D6_GIBZE	Q4i2d6	gibberella
676	30	58.8	406	2	Q8N7T8_HUMAN	Q8n7t8	homo sapien
677	30	58.8	407	2	Q5UF06_9PROT	Q5uf06	uncultured
678	30	58.8	408	2	Q7MST7_WOLSU	Q7mst7	wolinella s
679	30	58.8	409	2	Q8SUH7_ENCCU	Q8suh7	encephalito
680	30	58.8	409	2	Q8SUI8_ENCCU	Q8sui8	encephalito
681	30	58.8	409	2	Q7R6P2_GIALA	Q7r6p2	giardia lam
682	30	58.8	410	2	Q65RR0_MANSM	Q65rr0	mannheimia
683	30	58.8	413	2	Q92UU6_RHIME	Q92uu6	rhizobium m
684	30	58.8	413	2	Q8BUC6_MOUSE	Q8buc6	mus musculu
685	30	58.8	418	2	Q61DN5_CAEBR	Q61dn5	caenorhabdi
686	30	58.8	418	2	Q9D2Y0_MOUSE	Q9d2y0	mus musculu
687	30	58.8	419	2	Q5WMS9_ORYSA	Q5wms9	oryza sativ
688	30	58.8	422	2	Q6NJM3_CORDI	Q6njm3	corynebacte

689	30	58.8	423	2	Q6MQ58_BDEBA	Q6mq58	bdellovibri
690	30	58.8	428	2	Q5U2P2_RAT	Q5u2p2	rattus norv
691	30	58.8	429	1	GLYA_METJA	Q58992	methanococc
692	30	58.8	430	2	Q8N4F1_HUMAN	Q8n4f1	homo sapien
693	30	58.8	430	2	Q4TKW7_9SPHN	Q4tkw7	erythrobact
694	30	58.8	431	2	Q5DX21_HUMAN	Q5dx21	homo sapien
695	30	58.8	432	2	Q6LSG0_PHOPR	Q6lsg0	photobacter
696	30	58.8	437	2	Q6NKZ9_ARATH	Q6nkz9	arabidopsis
697	30	58.8	437	2	Q9RZJ9_DEIRA	Q9rzj9	deinococcus
698	30	58.8	440	2	Q9RGD0_MICAE	Q9rgd0	microcystis
699	30	58.8	440	2	Q6N417_RHOPA	Q6n417	rhodopseudo
700	30	58.8	443	2	Q84YE8_SORBI	Q84ye8	sorghum bic
701	30	58.8	447	2	Q7Q1K3_ANOGA	Q7q1k3	anopheles g
702	30	58.8	448	2	Q71TS8_PASMU	Q71ts8	pasteurella
703	30	58.8	448	2	Q65SD4_MANSM	Q65sd4	mannheimia
704	30	58.8	448	2	Q9CMC5_PASMU	Q9cmc5	pasteurella
705	30	58.8	448	2	Q98CK3_RHILO	Q98ck3	rhizobium l
706	30	58.8	449	2	Q7VN45_HAEDU	Q7vn45	haemophilus
707	30	58.8	456	2	Q6CUX7_KLULA	Q6cux7	kluyveromyc
708	30	58.8	458	1	NIFN_AZOVI	P10336	azotobacter
709	30	58.8	460	2	Q6NAI4_RHOPA	Q6na14	rhodopseudo
710	30	58.8	461	2	Q8L109_9MICO	Q8l109	bogoriella
711	30	58.8	464	2	Q4S5S7_TETNG	Q4s5s7	tetraodon n
712	30	58.8	465	2	Q4TMT9_9SPHN	Q4tmt9	erythrobact
713	30	58.8	465	2	Q5K2P4_PROAT	Q5k2p4	protopterus
714	30	58.8	473	2	Q94789_TRICO	Q94789	trichostron
715	30	58.8	475	2	Q6MKF1_BDEBA	Q6mkf1	bdellovibri
716	30	58.8	476	2	Q71UZ5_PSEST	Q71uz5	pseudomonas
717	30	58.8	476	2	Q8FML5_COREF	Q8fml5	corynebacte
718	30	58.8	478	2	Q4FV56_9GAMM	Q4fv56	psychrobact
719	30	58.8	480	1	THII_PASMU	P57849	pasteurella
720	30	58.8	481	2	O65676_ARATH	O65676	arabidopsis
721	30	58.8	482	2	Q5AXG5_EMENI	Q5axg5	aspergillus
722	30	58.8	484	2	Q75BS4_ASHGO	Q75bs4	ashbya goss
723	30	58.8	486	2	Q5NBL6_ORYSA	Q5nbl6	oryza sativ
724	30	58.8	488	2	Q4FXI1_LEIMA	Q4fxi1	leishmania
725	30	58.8	488	2	Q6AF62_LEIXX	Q6af62	leifsonia x
726	30	58.8	495	2	Q4IZU3_AZOVI	Q4izu3	azotobacter
727	30	58.8	496	2	Q620Z5_CAEBR	Q620z5	caenorhabdi
728	30	58.8	497	2	Q8SA99_MAIZE	Q8sa99	zea mays (m
729	30	58.8	497	2	Q7W1B2_BORPA	Q7w1b2	bordetella
730	30	58.8	497	2	Q7WP17_BORBR	Q7wp17	bordetella
731	30	58.8	498	2	Q4N524_THEPA	Q4n524	theileria p
732	30	58.8	501	2	Q96QU6_HUMAN	Q96qu6	homo sapien
733	30	58.8	501	2	Q8WUL4_HUMAN	Q8wul4	homo sapien
734	30	58.8	501	2	Q96LX5_HUMAN	Q96lx5	homo sapien
735	30	58.8	506	1	DHH1_YEAST	P39517	saccharomyc
736	30	58.8	507	2	Q6FQU5_CANGA	Q6fqu5	candida gla
737	30	58.8	509	2	Q8ESH0_OCEIH	Q8esh0	oceanobacil
738	30	58.8	510	1	PUR9_DEIRA	Q9rw01	d bifunctio
739	30	58.8	512	2	P92039_HAECO	P92039	haemonchus
740	30	58.8	513	1	CATB_PSEAE	Q59635	pseudomonas
741	30	58.8	513	2	Q98B69_RHILO	Q98b69	rhizobium l
742	30	58.8	515	2	Q6WMW1_DROER	Q6wmw1	drosophila
743	30	58.8	516	2	Q57ZF4_9TRYP	Q57zf4	trypanosoma
744	30	58.8	517	2	Q8S396_ARATH	Q8s396	arabidopsis
745	30	58.8	522	2	Q83543_9RHAB	Q83543	mokola viru
746	30	58.8	523	2	Q9H856_HUMAN	Q9h856	homo sapien
747	30	58.8	523	2	Q9JPE5_NEIME	Q9jpe5	neisseria m
748	30	58.8	524	1	G6PI_CHLMU	Q9pk16	chlamydia m
749	30	58.8	524	2	Q9VRM8_DROME	Q9vrm8	drosophila
750	30	58.8	525	2	Q69ZA5_MOUSE	Q69za5	mus musculu
751	30	58.8	526	2	Q86A13_DICDI	Q86a13	dictyosteli
752	30	58.8	529	2	Q4IGI3_GIBZE	Q4igi3	gibberella
753	30	58.8	532	2	Q6STH5_ARATH	Q6sth5	arabidopsis
754	30	58.8	532	2	Q8LD16_ARATH	Q8ld16	arabidopsis
755	30	58.8	534	2	Q6N963_RHOPA	Q6n963	rhodopseudo
756	30	58.8	535	2	Q9F703_STRTR	Q9f703	streptococc
757	30	58.8	535	2	Q822S9_CHLCV	Q822s9	chlamydophi
758	30	58.8	538	2	Q8C9K6_MOUSE	Q8c9k6	mus musculu
759	30	58.8	540	2	Q89CB2_BRAJA	Q89cb2	bradyrhizob
760	30	58.8	541	2	Q89BJ9_BRAJA	Q89bj9	bradyrhizob
761	30	58.8	549	2	Q7V4I7_PROMM	Q7v4i7	prochloroco
762	30	58.8	550	2	Q9LK00_ARATH	Q9lk00	arabidopsis
763	30	58.8	551	2	Q881D5_PSESM	Q881d5	pseudomonas
764	30	58.8	552	2	Q4I870_GIBZE	Q4i870	gibberella
765	30	58.8	566	1	CBIO4_LACPL	Q88zz2	lactobacill
766	30	58.8	572	2	Q6HCX5_BACHK	Q6hcx5	bacillus th
767	30	58.8	572	2	Q72ZI9_BACC1	Q72zi9	bacillus ce
768	30	58.8	572	2	Q81L39_BACAN	Q81l39	bacillus an
769	30	58.8	572	2	Q633P1_BACCZ	Q633p1	bacillus ce
770	30	58.8	573	2	Q817J3_BACCR	Q817j3	bacillus ce
771	30	58.8	578	2	O93800_ALTAL	O93800	alternaria
772	30	58.8	585	2	Q9M255_ARATH	Q9m255	arabidopsis
773	30	58.8	589	1	SYR_TREPA	O83803	treponema p
774	30	58.8	592	2	Q6BZ49_DEBHA	Q6bz49	debaryomyce
775	30	58.8	592	2	Q5NI13_FRATT	Q5ni13	francisella
776	30	58.8	593	2	Q8WPK5_9UROC	Q8wpk5	oikopleura
777	30	58.8	594	2	Q59099_ALCEU	Q59099	alcaligenes
778	30	58.8	604	2	O60201_ASPOR	O60201	aspergillus
779	30	58.8	608	2	Q6AS34_DESPS	Q6as34	desulfotale
780	30	58.8	610	2	Q19848_CAEEL	Q19848	caenorhabdi
781	30	58.8	624	2	Q55X46_CRYNE	Q55x46	cryptococcu
782	30	58.8	624	2	Q5KMT6_CRYNE	Q5kmt6	cryptococcu
783	30	58.8	629	2	Q7ZU52_BRARE	Q7zu52	brachydanio
784	30	58.8	629	2	Q9DEY8_BRARE	Q9dey8	brachydanio
785	30	58.8	631	2	Q4RM10_TETNG	Q4rm10	tetraodon n
786	30	58.8	633	1	IPAA_SHIFL	P18010	shigella fl
787	30	58.8	633	2	Q9HP10_HALSA	Q9hp10	halobacteri
788	30	58.8	633	2	Q6XVZ2_SHIFL	Q6xvz2	shigella fl
789	30	58.8	648	2	Q8NJ02_NEUCR	Q8nj02	neurospora
790	30	58.8	654	2	Q873H9_NEUCR	Q873h9	neurospora
791	30	58.8	669	2	Q5V4P7_HALMA	Q5v4p7	haloarcula
792	30	58.8	669	2	Q9V707_DROME	Q9v707	drosophila
793	30	58.8	669	2	Q4QGP9_LEIMA	Q4qgp9	leishmania
794	30	58.8	670	2	Q5RJF5_XANCV	Q5rjf5	xanthomonas
795	30	58.8	671	2	Q9LB25_RHOCE	Q9lb25	rhodospiril
796	30	58.8	671	2	Q4S3P7_TETNG	Q4s3p7	tetraodon n
797	30	58.8	693	2	Q8ML86_DROME	Q8ml86	drosophila
798	30	58.8	694	2	Q5V478_HALMA	Q5v478	haloarcula
799	30	58.8	694	2	Q51XW4_MAGGR	Q51xw4	magnaporthe
800	30	58.8	697	2	Q7NB55_MYCGA	Q7nb55	mycoplasma
801	30	58.8	698	2	Q8K245_MOUSE	Q8k245	mus musculu
802	30	58.8	698	2	Q8C0K8_MOUSE	Q8c0k8	mus musculu
803	30	58.8	698	2	Q8BXW8_MOUSE	Q8bxw8	mus musculu
804	30	58.8	698	2	Q8BVI8_MOUSE	Q8bvi8	mus musculu
805	30	58.8	718	1	NOL11_PONPY	Q5rb52	pongo pygma
806	30	58.8	719	1	NOL11_HUMAN	Q9h8h0	homo sapien
807	30	58.8	733	2	Q6N460_RHOPA	Q6n460	rhodopseudo
808	30	58.8	734	2	Q9GJY3_SHEEP	Q9gjy3	ovis aries
809	30	58.8	740	2	Q4TQF1_9SPHN	Q4tqf1	erythrobact
810	30	58.8	747	2	Q9BIE6_LEIDO	Q9bie6	leishmania
811	30	58.8	749	2	O83812_TREPA	O83812	treponema p
812	30	58.8	751	2	Q9A952_CAUCR	Q9a952	caulobacter
813	30	58.8	752	2	Q8TPB3_METAC	Q8tpb3	methanosarc
814	30	58.8	757	2	Q82I66_STRAW	Q82i66	streptomyce
815	30	58.8	767	2	Q830H3_ENTFA	Q830h3	enterococcu
816	30	58.8	772	2	Q61CT2_CAEBR	Q61ct2	caenorhabdi
817	30	58.8	777	2	Q6AK66_DESPS	Q6ak66	desulfotale
818	30	58.8	781	2	Q82WV1_NITEU	Q82wv1	nitrosomona
819	30	58.8	784	2	Q4KN73_BORBR	Q4kn73	bordetella
820	30	58.8	784	2	Q7WNX4_BORBR	Q7wnx4	bordetella
821	30	58.8	796	2	Q5H5L8_XANOR	Q5h5l8	xanthomonas
822	30	58.8	800	2	Q6INK0_XENLA	Q6ink0	xenopus lae
823	30	58.8	805	2	Q9P9J0_HALSA	Q9p9j0	halobacteri
824	30	58.8	806	2	Q4ICT4_GIBZE	Q4ict4	gibberella
825	30	58.8	815	2	Q4UEG8_THEAN	Q4ueg8	theileria a
826	30	58.8	819	2	Q6I6F7_EUBMA	Q6i6f7	eublepharis
827	30	58.8	824	2	Q4PBA0_USTMA	Q4pba0	ustilago ma
828	30	58.8	844	2	Q5B210_EMENI	Q5b210	aspergillus
829	30	58.8	847	2	Q84NR1_ORYSA	Q84nr1	oryza sativ
830	30	58.8	851	2	Q4Q8A0_LEIMA	Q4q8a0	leishmania
831	30	58.8	852	2	Q7CSB9_AGRT5	Q7csb9	agrobacteri
832	30	58.8	856	2	Q4NIR6_9MICC	Q4nir6	arthrobacte
833	30	58.8	868	1	SYL_PSESM	Q87vx3	pseudomonas
834	30	58.8	868	2	Q4ZN90_PSESY	Q4zn90	pseudomonas

835	30	58.8	868	2	Q4K5H6_PSEF5	Q4k5h6	pseudomonas
836	30	58.8	868	2	Q4SF53_TETNG	Q4sf53	tetraodon n
837	30	58.8	873	1	SYL_PSEAE	Q9hx33	pseudomonas
838	30	58.8	873	2	Q4Q6U7_LEIMA	Q4q6u7	leishmania
839	30	58.8	873	2	Q9LP01_ARATH	Q9lp01	arabidopsis
840	30	58.8	885	2	Q4J3Q1_AZOVI	Q4j3q1	azotobacter
841	30	58.8	888	1	YGCB_ECOLI	P38036	escherichia
842	30	58.8	893	2	Q5TS49_ANOGA	Q5ts49	anopheles g
843	30	58.8	893	2	Q4Q414_LEIMA	Q4q414	leishmania
844	30	58.8	896	2	Q5QTY8_IDILO	Q5qty8	idiomarina
845	30	58.8	919	2	Q5U4W9_XENLA	Q5u4w9	xenopus lae
846	30	58.8	923	2	Q8UAI8_AGRT5	Q8uai8	agrobacteri
847	30	58.8	924	2	Q4QBQ5_LEIMA	Q4qbq5	leishmania
848	30	58.8	950	2	Q4FRP3_9GAMM	Q4frp3	psychrobact
849	30	58.8	963	2	Q4RQW0_TETNG	Q4rqw0	tetraodon n
850	30	58.8	983	1	EPHA3_CHICK	P29318	gallus gall
851	30	58.8	983	1	EPHA3_HUMAN	P29320	homo sapien
852	30	58.8	983	1	EPHA3_MOUSE	P29319	mus musculu
853	30	58.8	983	2	Q6P4R6_HUMAN	Q6p4r6	homo sapien
854	30	58.8	984	1	EPHA3_RAT	O08680	rattus norv
855	30	58.8	984	2	Q9XCD4_THEFU	Q9xcd4	thermomonos
856	30	58.8	984	2	Q8BRB1_MOUSE	Q8brb1	mus musculu
857	30	58.8	984	2	Q8C3U1_MOUSE	Q8c3u1	mus musculu
858	30	58.8	993	2	Q5SQ95_HUMAN	Q5sq95	homo sapien
859	30	58.8	993	2	Q5SS97_HUMAN	Q5ss97	homo sapien
860	30	58.8	993	2	Q5ST31_HUMAN	Q5st31	homo sapien
861	30	58.8	998	2	Q8IXT1_HUMAN	Q8ixt1	homo sapien
862	30	58.8	998	2	Q9SAJ3_ARATH	Q9saj3	arabidopsis
863	30	58.8	1004	2	Q4QHQ7_LEIMA	Q4qhq7	leishmania
864	30	58.8	1006	2	Q4NXH1_9DELT	Q4nxh1	anaeromyxob
865	30	58.8	1008	2	Q5JZY3_HUMAN	Q5jzy3	homo sapien
866	30	58.8	1009	2	Q24749_DROVI	Q24749	drosophila
867	30	58.8	1010	2	Q7QP15_GIALA	Q7qp15	giardia lam
868	30	58.8	1013	2	Q5PB92_ANAMM	Q5pb92	anaplasma m
869	30	58.8	1016	2	Q91779_XENLA	Q91779	xenopus lae
870	30	58.8	1021	2	Q9LF01_ARATH	Q9lf01	arabidopsis
871	30	58.8	1035	1	POLY_DROME	P10401	drosophila
872	30	58.8	1055	2	Q5N861_ORYSA	Q5n861	oryza sativ
873	30	58.8	1055	2	Q6WG80_ORYSA	Q6wg80	oryza sativ
874	30	58.8	1055	2	Q7XYH6_ORYSA	Q7xyh6	oryza sativ
875	30	58.8	1063	2	Q5SQ96_HUMAN	Q5sq96	homo sapien
876	30	58.8	1063	2	Q5SS98_HUMAN	Q5ss98	homo sapien
877	30	58.8	1063	2	Q5ST30_HUMAN	Q5st30	homo sapien
878	30	58.8	1065	1	NOLG_RHIME	P25197	rhizobium m
879	30	58.8	1082	2	Q4N4P7_THEPA	Q4n4p7	theileria p
880	30	58.8	1085	2	Q6CJA6_KLULA	Q6cja6	kluyveromyc
881	30	58.8	1098	2	Q96Q02_HUMAN	Q96q02	homo sapien
882	30	58.8	1113	1	PER3_MOUSE	O70361	mus musculu
883	30	58.8	1115	2	O89119_MOUSE	O89119	mus musculu
884	30	58.8	1123	2	Q5NH84_FRATT	Q5nh84	francisella
885	30	58.8	1148	2	Q5YQW7_NOCFA	Q5yqw7	nocardia fa
886	30	58.8	1148	2	Q4SKJ1_TETNG	Q4skj1	tetraodon n
887	30	58.8	1157	2	Q6FWT1_CANGA	Q6fwt1	candida gla
888	30	58.8	1158	2	Q8IU40_DICDI	Q8iu40	dictyosteli
889	30	58.8	1158	2	Q54KF1_DICDI	Q54kf1	dictyosteli
890	30	58.8	1186	2	Q7PY35_ANOGA	Q7py35	anopheles g
891	30	58.8	1189	2	Q8KQU7_VIBCH	Q8kqu7	vibrio chol
892	30	58.8	1189	2	Q8RKW7_PRORE	Q8rkw7	providencia
893	30	58.8	1199	2	Q5AU22_EMENI	Q5au22	aspergillus
894	30	58.8	1202	2	Q97B44_THEVO	Q97b44	thermoplasm
895	30	58.8	1269	2	Q57WX5_9TRYP	Q57wx5	trypanosoma
896	30	58.8	1278	2	Q4IRJ1_GIBZE	Q4irj1	gibberella
897	30	58.8	1286	1	AIDA_ECOLI	Q03155	escherichia
898	30	58.8	1315	1	CLSPN_MOUSE	Q80yr7	mus musculu
899	30	58.8	1324	2	Q7XUD8_ORYSA	Q7xud8	oryza sativ
900	30	58.8	1336	2	Q6CBP7_YARLI	Q6cbp7	yarrowia li
901	30	58.8	1382	2	Q4PAR4_USTMA	Q4par4	ustilago ma
902	30	58.8	1417	2	Q4LXY2_9BURK	Q4lxy2	burkholderi
903	30	58.8	1463	2	O44384_DROME	O44384	drosophila
904	30	58.8	1468	2	Q4PB36_USTMA	Q4pb36	ustilago ma
905	30	58.8	1483	2	Q6AHZ1_HUMAN	Q6ahz1	homo sapien
906	30	58.8	1484	1	K1219_MOUSE	Q8bqz4	mus musculu
907	30	58.8	1484	2	O15044_HUMAN	O15044	homo sapien
908	30	58.8	1536	2	Q5PB97_ANAMM	Q5pb97	anaplasma m
909	30	58.8	1589	2	Q8XZ53_RALSO	Q8xz53	ralstonia s
910	30	58.8	1613	2	Q5DZK7_VIBF1	Q5dzk7	vibrio fisc
911	30	58.8	1649	2	Q746C7_THET2	Q746c7	thermus the
912	30	58.8	1662	2	P71431_LEPDI	P71431	leptothrix
913	30	58.8	1666	2	Q7R3J9_GIALA	Q7r3j9	giardia lam
914	30	58.8	1723	2	Q4SD22_TETNG	Q4sd22	tetraodon n
915	30	58.8	1746	2	Q8WY19_HUMAN	Q8wy19	homo sapien
916	30	58.8	1762	2	Q4PB79_USTMA	Q4pb79	ustilago ma
917	30	58.8	1808	2	Q9EWA2_9ACTO	Q9ewa2	streptomyce
918	30	58.8	1898	2	Q8EKM6_SHEON	Q8ekm6	shewanella
919	30	58.8	1900	2	Q4PDX0_USTMA	Q4pdx0	ustilago ma
920	30	58.8	1978	2	Q9K0S7_NEIMB	Q9k0s7	neisseria m
921	30	58.8	1995	2	Q9JY23_NEIMB	Q9jy23	neisseria m
922	30	58.8	2012	1	DSCAM_HUMAN	O60469	homo sapien
923	30	58.8	2013	2	Q8VHZ8_RAT	Q8vhz8	rattus norv
924	30	58.8	2013	2	Q9ERC8_MOUSE	Q9erc8	mus musculu
925	30	58.8	2023	2	Q59GH3_HUMAN	Q59gh3	homo sapien
926	30	58.8	2024	2	Q53CM6_BRARE	Q53cm6	brachydanio
927	30	58.8	2026	2	Q9JPJ4_NEIME	Q9jpj4	neisseria m
928	30	58.8	2113	2	Q8XC71_ECO57	Q8xc71	escherichia
929	30	58.8	2217	2	Q6FNY7_CANGA	Q6fny7	candida gla
930	30	58.8	2224	1	DAB_DROME	P98081	drosophila
931	30	58.8	2332	2	Q6PMW3_9PICO	Q6pmw3	foot-and-mo
932	30	58.8	2333	2	Q6PN04_9PICO	Q6pn04	foot-and-mo
933	30	58.8	2388	2	Q7R5H2_GIALA	Q7r5h2	giardia lam
934	30	58.8	2472	2	Q14214_HUMAN	Q14214	homo sapien
935	30	58.8	2517	2	Q5AZ32_EMENI	Q5az32	aspergillus
936	30	58.8	2605	2	Q8ID88_PLAF7	Q8id88	plasmodium
937	30	58.8	2614	2	O97054_DICDI	O97054	dictyosteli
938	30	58.8	2614	2	Q54K81_DICDI	Q54k81	dictyosteli
939	30	58.8	2766	1	PDZK3_RAT	Q9qzr8	rattus norv
940	30	58.8	2909	2	Q8MY78_ASTPE	Q8my78	asterina pe
941	30	58.8	3867	2	Q53QQ2_HUMAN	Q53qq2	homo sapien
942	30	58.8	4034	2	Q7R5J5_GIALA	Q7r5j5	giardia lam
943	30	58.8	4833	2	Q4RNG0_TETNG	Q4rng0	tetraodon n
944	30	58.8	5175	2	Q8I0L3_CAEEL	Q8i0l3	caenorhabdi
945	30	58.8	5198	2	O76518_CAEEL	O76518	caenorhabdi
946	30	58.8	6669	1	NEBU_HUMAN	P20929	homo sapien
947	30	58.8	7771	2	Q6W5P7_9ACTO	Q6w5p7	streptomyce
948	29.5	57.8	114	2	Q96736_ADEG8	Q96736	avian adeno
949	29	56.9	41	2	Q38531_BPT7	Q38531	bacteriopha
950	29	56.9	51	2	Q86DI4_LEITR	Q86di4	leishmania
951	29	56.9	51	2	Q86DI5_9TRYP	Q86di5	leishmania
952	29	56.9	51	2	Q86DI6_9TRYP	Q86di6	leishmania
953	29	56.9	51	2	Q8MLY1_LEIMA	Q8mly1	leishmania
954	29	56.9	59	1	YDBF_SCHPO	Q10365	schizosacch
955	29	56.9	67	1	VLYS_BPT3	P10307	bacteriopha
956	29	56.9	67	1	VLYS_BPT7	P03802	bacteriopha
957	29	56.9	67	2	Q6WY16_BPT7	Q6wy16	bacteriopha
958	29	56.9	67	2	Q6WY68_BPT7	Q6wy68	bacteriopha
959	29	56.9	67	2	Q858J7_9CAUD	Q858j7	yersinia pe
960	29	56.9	67	2	Q8LT23_BPT7	Q8lt23	bacteriopha
961	29	56.9	67	2	Q8LT33_BPT7	Q8lt33	bacteriopha
962	29	56.9	67	2	Q8LTY3_BPT7	Q8lty3	bacteriopha
963	29	56.9	67	2	Q8LTY4_BPT7	Q8lty4	bacteriopha
964	29	56.9	67	2	Q9T0Z8_9CAUD	Q9t0z8	bacteriopha
965	29	56.9	67	2	Q8W5T7_BPT3	Q8w5t7	bacteriopha
966	29	56.9	67	2	Q6WYM3_BPT7	Q6wym3	bacteriopha
967	29	56.9	72	2	Q8YJU2_ANASP	Q8yju2	anabaena sp
968	29	56.9	81	2	Q6ILB5_DROME	Q6ilb5	drosophila
969	29	56.9	82	2	Q5GSF8_WOLTR	Q5gsf8	wolbachia s
970	29	56.9	83	1	ACPX_STRGA	P12884	streptomyce
971	29	56.9	97	2	Q4WNZ4_ASPFU	Q4wnz4	aspergillus
972	29	56.9	98	2	Q8MSD4_DROME	Q8msd4	drosophila
973	29	56.9	98	2	Q7X1L8_9BACT	Q7x1l8	leptospiril
974	29	56.9	98	2	Q877K3_VIBPA	Q877k3	vibrio para
975	29	56.9	100	2	Q4PM48_IXOSC	Q4pm48	ixodes scap
976	29	56.9	101	2	Q743Q7_MYCPA	Q743q7	mycobacteri
977	29	56.9	102	1	RS10_MYCPE	Q8eub2	mycoplasma
978	29	56.9	113	1	Y1926_PYRKO	Q5jet9	pyrococcus
979	29	56.9	118	2	Q5TY99_ANOGA	Q5ty99	anopheles g
980	29	56.9	118	2	Q64GH0_LEGPN	Q64gh0	legionella

981	29	56.9	121	2	Q6K4C5_ORYSA	Q6k4c5 oryza sativ
982	29	56.9	123	1	MSRA_THEVU	Q9ajf7 thermoactin
983	29	56.9	123	2	Q9IV90_9HIV1	Q9iv90 human immun
984	29	56.9	124	2	Q53NN1_ORYSA	Q53nn1 oryza sativ
985	29	56.9	127	2	Q5ACG4_CANAL	Q5acg4 candida alb
986	29	56.9	138	2	Q5N4V6_SYNP6	Q5n4v6 synechococc
987	29	56.9	138	2	Q9CPT6_MOUSE	Q9cpt6 m mus muscu
988	29	56.9	139	2	Q8F6L3_LEPIN	Q8f6l3 leptospira
989	29	56.9	140	2	Q8CBN0_MOUSE	Q8cbn0 mus musculu
990	29	56.9	145	2	Q87JB8_VIBPA	Q87jb8 vibrio para
991	29	56.9	145	2	Q6V0N9_CHICK	Q6v0n9 gallus gall
992	29	56.9	146	1	LUQ1_APLCA	Q00676 aplysia cal
993	29	56.9	150	2	Q9F1P7_BURCE	Q9f1p7 burkholderi
994	29	56.9	150	2	Q9LAN4_BURCE	Q9lan4 burkholderi
995	29	56.9	150	2	Q4LZ10_9BURK	Q4lz10 burkholderi
996	29	56.9	150	2	Q62G76_BURMA	Q62g76 burkholderi
997	29	56.9	150	2	Q9ZF82_BURPS	Q9zf82 burkholderi
998	29	56.9	152	2	Q6FUH0_CANGA	Q6fuh0 candida gla
999	29	56.9	152	2	Q4LWC1_9BURK	Q4lwc1 burkholderi
1000	29	56.9	155	2	Q8D5I1_VIBVU	Q8d5i1 vibrio vuln

ALIGNMENTS

RESULT 1
Q8VIJ0_MOUSE
ID Q8VIJ0_MOUSE PRELIMINARY; PRT; 108 AA.
AC Q8VIJ0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-DNA light chain (Fragment).
GN Name=Igk-V19-14; Synonyms=Vk19;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C3H/HeJ-lpr/lpr;
RX MEDLINE=96409289; PubMed=8814271;
RA Wloch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL Eur. J. Immunol. 26:2225-2233(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2499887;
RA Baccala R., Quang T.V., Gilbert M., Ternynck T., Avrameas S.;
RT "Two murine natural polyreactive autoantibodies are encoded by
RT nonmutated germ-line genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
RA Tillman D.M., Jou N.T., Hill R.J., Marion T.N.;
RT "Both IgM and IgG anti-DNA antibodies are the products of clonally
RT selective B cell stimulation in (NZB x NZW)F1 mice.";
RL J. Exp. Med. 176:761-779(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91115823; PubMed=1703527;
RA Goshorn S.C., Retzel E., Jemmerson R.;
RT "Common structural features among monoclonal antibodies binding the
RT same antigenic region of cytochrome c.";
RL J. Biol. Chem. 266:2134-2142(1991).
DR EMBL; U59155; AAB02917.1; -; mRNA.
DR PIR; A33933; A33933.
DR PIR; A37262; A37262.
DR PIR; PH1072; PH1072.
DR HSSP; P01634; 1IGC.
DR SMR; Q8VIJ0; 1-108.
DR Ensembl; ENSMUSG00000053690; Mus musculus.
DR MGI; MGI:1330830; Igk-V19-14.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Query Match 84.3%; Score 43; DB 2; Length 108;
Best Local Similarity 81.8%; Pred. No. 0.84;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||:|||:||
Db 24 KASQNVGTNVA 34

RESULT 2
KV5A_MOUSE
ID KV5A_MOUSE STANDARD; PRT; 149 AA.
AC P01633;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-V region MPC11 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE OF 1-71.
RX MEDLINE=83001944; PubMed=6288267; DOI=10.1016/0092-8674(82)90184-2;
RA Kelley D.E., Coleclough C., Perry R.P.;
RT "Functional significance and evolutionary development of the 5'-
RT terminal regions of immunoglobulin variable-region genes.";
RL Cell 29:681-689(1982).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 41-149.
RX MEDLINE=80176554; PubMed=6245773;
RA Rabbitts T.H., Hamlyn P.H., Matthyssens G., Roe B.A.;
RT "The variability, arrangement, and rearrangement of immunoglobulin
RT genes.";
RL Can. J. Biochem. 58:176-187(1980).
RN [3]
RP PROTEIN SEQUENCE OF 30-149.
RX MEDLINE=78186617; PubMed=418775;
RA Smith G.P.;
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
RT myeloma MPC 11.";
RL Biochem. J. 171:337-347(1978).
CC -!- MISCELLANEOUS: The mature chain has 12 additional residues at its
CC amino end, due to a tandem duplication of 36 nucleotides after the
CC codon for residue 36. Residue 42 corresponds to the N-terminal
CC residue of typical kappa chains.
CC ---
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ---
DR EMBL; J00561; AAA38776.1; -; Genomic_DNA.
DR PIR; A90823; KVMS11.
DR HSSP; P01634; 1IGC.
DR SMR; P01633; 42-149.
DR Ensembl; ENSMUSG00000061362; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.

```
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Repeat; Signal.
FT   SIGNAL       1     29
FT   CHAIN       30    149       Ig kappa chain V-V region MPC11.
FT   REPEAT      26     35
FT   REPEAT      38     47
FT   REGION      42     64       Framework-1.
FT   REGION      65     75       Complementarity-determining-1.
FT   REGION      76     90       Framework-2.
FT   REGION      91     97       Complementarity-determining-2.
FT   REGION      98    129       Framework-3.
FT   REGION     130    138       Complementarity-determining-3.
FT   REGION     139    148       Framework-4.
FT   NON_TER    149    149
SQ   SEQUENCE   149 AA;  16434 MW;  B0480C87B682AC3E CRC64;

  Query Match             82.4%;  Score 42;  DB 1;  Length 149;
  Best Local Similarity   81.8%;  Pred. No. 1.9;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||| |:||
Db         65 KASQDVSTTVA 75


RESULT 3
Q58EU4_MOUSE
ID   Q58EU4_MOUSE PRELIMINARY;      PRT;   238 AA.
AC   Q58EU4;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Igk-C protein.
GN   Name=Igk-C;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RG   NIH MGC Project;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC091754; AAH91754.1; -; mRNA.
DR   SMR; Q58EU4; 25-238.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   238 AA;  26440 MW;  AB2B2BA90B9F7D5D CRC64;

  Query Match             78.4%;  Score 40;  DB 2;  Length 238;
  Best Local Similarity   81.8%;  Pred. No. 8.5;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||| |:||
Db         48 KASQDVTTAVA 58


RESULT 4
Q9YDV9_AERPE
ID   Q9YDV9_AERPE PRELIMINARY;      PRT;   110 AA.
AC   Q9YDV9;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein APE0810.
GN   OrderedLocusNames=APE0810;
OS   Aeropyrum pernix.
OC   Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC   Desulfurococcaceae; Aeropyrum.
OX   NCBI_TaxID=56636;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=K1;
RX   MEDLINE=99310339; PubMed=10382966;
RA   Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA   Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA   Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA   Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA   Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
RA   Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT   "Complete genome sequence of an aerobic hyper-thermophilic
RT   crenarchaeon, Aeropyrum pernix K1.";
RL   DNA Res. 6:83-101(1999).
DR   EMBL; BA000002; BAA79788.1; -; Genomic_DNA.
DR   PIR; D72673; D72673.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   110 AA;  12572 MW;  D1A1898896CF8F34 CRC64;

  Query Match             72.5%;  Score 37;  DB 2;  Length 110;
  Best Local Similarity   72.7%;  Pred. No. 16;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              | |||:| |||
Db         65 KLSQDLGQSVA 75


RESULT 5
O34578_BACSU
ID   O34578_BACSU PRELIMINARY;      PRT;   254 AA.
AC   O34578; Q796M8;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein yjnA.
GN   Name=yjnA; OrderedLocusNames=BSU12400;
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
```

```
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=168;
RX   MEDLINE=98240225; PubMed=9579062;
RA   Rivolta C., Soldo B., Lazarevic V., Joris B., Mauel C., Karamata D.;
RT   "A 35.7 kb DNA fragment from the Bacillus subtilis chromosome
RT   containing a putative 12.3 kb operon involved in hexuronate catabolism
RT   and a perfectly symmetrical hypothetical catabolite-responsive
RT   element.";
RL   Microbiology 144:877-884(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=168;
RX   MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA   Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA   Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA   Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA   Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA   Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA   Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T.,
RA   Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA   Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA   Ghim S.-Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA   Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA   Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,
RA   Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA   Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
RA   Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA   Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C.,
RA   Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA   Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA   Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA   Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA   Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA   Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA   Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
RA   Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA   Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA   Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA   Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA   Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA   Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,
RA   Yoshikawa H., Danchin A.;
RT   "The complete genome sequence of the Gram-positive bacterium Bacillus
RT   subtilis.";
RL   Nature 390:249-256(1997).
DR   EMBL; AF015825; AAC46336.1; -; Genomic_DNA.
DR   EMBL; Z99110; CAB13097.1; -; Genomic_DNA.
DR   PIR; E69853; E69853.
DR   InterPro; IPR002781; DUF81.
DR   Pfam; PF01925; DUF81; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   254 AA;  27135 MW;  C1513F06D214EC3D CRC64;

  Query Match             72.5%;  Score 37;  DB 2;  Length 254;
  Best Local Similarity   72.7%;  Pred. No. 40;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||| ||| :|
Db        178 KASQIVGTDIA 188


RESULT 6
Q8BK10_MOUSE
ID   Q8BK10_MOUSE PRELIMINARY;      PRT;   409 AA.
AC   Q8BK10;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched
DE   library, clone:5730457F11 product:weakly similar to PUTATIVE N-
DE   ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE (EC 3.5.1.25) (GLCNAC 6-P
DE   DEACETYLASE).
GN   Name=5730457F11Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Whole body;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
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RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK077584; BAC36877.1; -; mRNA.
DR   HSSP; O34450; 1UN7.
DR   MEROPS; M38.979; -.
DR   Ensembl; ENSMUSG00000036820; Mus musculus.
DR   MGI; MGI:2443978; 5730457F11Rik.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008448; F:N-acetylglucosamine-6-phosphate deacetylase. . .; IEA.
DR   GO; GO:0006044; P:N-acetylglucosamine metabolism; IEA.
DR   InterPro; IPR006680; Amidohydro_1.
DR   InterPro; IPR011550; Amidohydro_like.
DR   InterPro; IPR003764; NagA.
DR   Pfam; PF01979; Amidohydro_1; 1.
DR   ProDom; PD001248; Amidohydro_like; 1.
DR   TIGRFAMs; TIGR00221; nagA; 1.
SQ   SEQUENCE   409 AA;  43519 MW;  204931474779CAC6 CRC64;

  Query Match             72.5%;  Score 37;  DB 2;  Length 409;
  Best Local Similarity   63.6%;  Pred. No. 66;
  Matches    7;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||::|||: ||
Db         82 KATEDVGSGVA 92


RESULT 7
Q8JZV7_MOUSE
ID   Q8JZV7_MOUSE PRELIMINARY;      PRT;   409 AA.
AC   Q8JZV7;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   RIKEN cDNA 5730457F11 (Mus musculus cDNA, RIKEN full-length enriched
DE   library, clone:G430059K10 product:weakly similar to PUTATIVE N-
DE   ACETYLGLUCOSAMINE-6-PHOSPHATE DEACETYLASE) (EC 3.5.1.25) (GLCNAC 6-P
DE   DEACETYLASE).
GN   Name=5730457F11Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Liver;
RA   Strausberg R.;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC037005; AAH37005.1; -; mRNA.
DR   EMBL; AK090009; BAC41042.1; -; mRNA.
DR   HSSP; O34450; 1UN7.
DR   MEROPS; M38.979; -.
DR   Ensembl; ENSMUSG00000036820; Mus musculus.
DR   MGI; MGI:2443978; 5730457F11Rik.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008448; F:N-acetylglucosamine-6-phosphate deacetylase. . .; IEA.
DR   GO; GO:0006044; P:N-acetylglucosamine metabolism; IEA.
DR   InterPro; IPR006680; Amidohydro_1.
DR   InterPro; IPR011550; Amidohydro_like.
DR   InterPro; IPR003764; NagA.
DR   Pfam; PF01979; Amidohydro_1; 1.
DR   ProDom; PD001248; Amidohydro_like; 1.
DR   TIGRFAMs; TIGR00221; nagA; 1.
SQ   SEQUENCE   409 AA;  43501 MW;  914930464779CAC7 CRC64;

  Query Match             72.5%;  Score 37;  DB 2;  Length 409;
  Best Local Similarity   63.6%;  Pred. No. 66;
  Matches    7;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||::|||: ||
Db         82 KATEDVGSGVA 92


RESULT 8
Q18361_CAEEL
ID   Q18361_CAEEL PRELIMINARY;      PRT;   520 AA.
AC   Q18361;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein C33A12.6.
GN   ORFNames=C33A12.6;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   -!- SIMILARITY: Belongs to the UDP-glycosyltransferase family.
DR   EMBL; Z68493; CAA92791.1; -; Genomic_DNA.
DR   PIR; T19661; T19661.
DR   Ensembl; C33A12.6; Caenorhabditis elegans.
DR   WormBase; WBGene00007885; C33A12.6.
DR   WormPep; C33A12.6; CE05352.
DR   GO; GO:0016758; F:transferase activity, transferring hexosyl . . .; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR002213; UDP_glucos_trans.
DR   Pfam; PF00201; UDPGT; 1.
DR   PROSITE; PS00375; UDPGT; 1.
KW   Complete proteome; Glycosyltransferase; Hypothetical protein;
KW   Transferase.
SQ   SEQUENCE   520 AA;  58191 MW;  BE15F2C32BEE71AA CRC64;

  Query Match             72.5%;  Score 37;  DB 2;  Length 520;
  Best Local Similarity   63.6%;  Pred. No. 85;
  Matches    7;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||:|||:||: |
Db        110 KAAQDMGTAFA 120


RESULT 9
KV5I_MOUSE
ID   KV5I_MOUSE     STANDARD;      PRT;   115 AA.
AC   P01642;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-V region L7 precursor (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=81220975; PubMed=6264318;
RA   Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT   "Differences between germ-line and rearranged immunoglobulin V kappa
RT   coding sequences suggest a localized mutation mechanism.";
RL   Nature 291:668-670(1981).
CC   -!- MISCELLANEOUS: There appears to be two possible splice junctions
CC       at the 3' end of the intron. The alternate would code for a
CC       protein lacking residues 17-19.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A01925; KVMSL7.
DR   PDB; 1C08; X-ray; A=22-115.
DR   PDB; 1IC4; X-ray; L=22-115.
DR   PDB; 1IC5; X-ray; L=22-115.
DR   PDB; 1IC7; X-ray; L=22-115.
DR   PDB; 1J1O; X-ray; L=22-115.
DR   PDB; 1J1P; X-ray; L=22-115.
DR   PDB; 1J1X; X-ray; L=22-114.
DR   Ensembl; ENSMUSG00000029975; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
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KW   3D-structure; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21   >115       Ig kappa chain V-V region L7.
FT   REGION       21     43       Framework-1.
FT   REGION       44     54       Complementarity-determining-1.
FT   REGION       55     69       Framework-2.
FT   REGION       70     76       Complementarity-determining-2.
FT   REGION       77    108       Framework-3.
FT   REGION      109   >115       Complementarity-determining-3.
FT   DISULFID     43    108       By similarity.
FT   NON_TER     115    115
FT   STRAND       24     27
FT   STRAND       30     33
FT   TURN         35     36
FT   STRAND       39     45
FT   TURN         50     51
FT   STRAND       53     58
FT   TURN         60     61
FT   STRAND       65     69
FT   TURN         70     72
FT   STRAND       73     74
FT   TURN         76     77
FT   TURN         80     81
FT   STRAND       82     87
FT   TURN         88     89
FT   STRAND       90     95
FT   HELIX       100    102
FT   STRAND      104    110
SQ   SEQUENCE   115 AA;  12615 MW;  C17BEC758C577E00 CRC64;

  Query Match             70.6%;  Score 36;  DB 1;  Length 115;
  Best Local Similarity   60.0%;  Pred. No. 28;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              :||| :|||:
Db         44 RASQSIGTSI 53


RESULT 10
CYB51_SCHPO
ID   CYB51_SCHPO    STANDARD;      PRT;   124 AA.
AC   O94391;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Probable cytochrome b5 1.
GN   ORFNames=SPBC29A10.16c;
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=972;
RX   MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,
RA   Sgouros J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Duesterhoeft A., Fritzc C., Holzer E., Moestl D.,
RA   Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
RA   Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).
CC   -!- FUNCTION: Membrane bound hemoprotein which function as an electron
CC       carrier for several membrane bound oxygenases (By similarity).
CC   -!- SUBCELLULAR LOCATION: Microsomal membrane. Bound to the
CC       cytoplasmic side of the endoplasmic reticulum (By similarity).
CC   -!- SIMILARITY: Belongs to the cytochrome b5 family.
CC   -!- SIMILARITY: Contains 1 cytochrome b5 heme-binding domain.
CC   ---------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------------
DR   EMBL; AL034463; CAA22444.1; -; Genomic_DNA.
DR   PIR; T40071; T40071.
DR   HSSP; P04166; 1EUE.
DR   GeneDB_Spombe; SPBC29A10.16c; -.
DR   InterPro; IPR001199; Cyt_B5.
DR   Pfam; PF00173; Cyt-b5; 1.
DR   PRINTS; PR00363; CYTOCHROMEB5.
DR   ProDom; PD000612; Cyt_B5; 1.
DR   PROSITE; PS50255; CYTOCHROME_B5_2; 1.
KW   Complete proteome; Electron transport; Endoplasmic reticulum; Heme;
KW   Iron; Metal-binding; Microsome; Transmembrane; Transport.
FT   TRANSMEM     100    120       Potential.
FT   DOMAIN         3     79       Cytochrome b5 heme-binding.
FT   METAL         38     38       Iron (heme axial ligand) (By similarity).
FT   METAL         62     62       Iron (heme axial ligand) (By similarity).
SQ   SEQUENCE   124 AA;  13910 MW;  299D12CB693831D4 CRC64;

  Query Match             70.6%;  Score 36;  DB 1;  Length 124;
  Best Local Similarity   63.6%;  Pred. No. 30;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              || ||:| |:|
Db         55 KAYQDIGHSIA 65


RESULT 11
KV5G_MOUSE
ID   KV5G_MOUSE     STANDARD;      PRT;   130 AA.
AC   P01639; P01640;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-V region MOPC 41 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=79221900; PubMed=111146;
RA   Seidman J.G., Max E.E., Leder P.;
RT   "A kappa-immunoglobulin gene is formed by site-specific recombination
RT   without further somatic mutation.";
RL   Nature 280:370-375(1979).
RN   [2]
RP   PROTEIN SEQUENCE OF 1-33.
RX   MEDLINE=77148916; PubMed=403522;
RA   Burstein Y., Schechter I.;
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RT   "Amino acid sequence of the NH2-terminal extra piece segments of the
RT   precursors of mouse immunoglobulin lambda1-type and kappa-type light
RT   chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
RN   [3]
RP   PROTEIN SEQUENCE OF 23-130.
RX   MEDLINE=67056897; PubMed=4162931;
RA   Gray W.R., Dreyer W.J., Hood L.E.;
RT   "Mechanism of antibody synthesis: size differences between mouse kappa
RT   chains.";
RL   Science 155:465-467(1967).
CC   -!- MISCELLANEOUS: This precursor was synthesized in a cell-free
CC       system directed by mRNA isolated from myeloma polysomes.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A93211; KVMSM4.
DR   HSSP; P01594; 1JV5.
DR   SMR; P01639; 23-130.
DR   Ensembl; ENSMUSG00000062548; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    130       Ig kappa chain V-V region MOPC 41.
FT   REGION       23     45       Framework-1.
FT   REGION       46     56       Complementarity-determining-1.
FT   REGION       57     71       Framework-2.
FT   REGION       72     78       Complementarity-determining-2.
FT   REGION       79    110       Framework-3.
FT   REGION      111    119       Complementarity-determining-3.
FT   REGION      120    129       Framework-4.
FT   DISULFID     45    110       By similarity.
FT   VARIANT       1      2       Missing (in 25% of the molecules).
FT   NON_TER     130    130
SQ   SEQUENCE   130 AA;  14311 MW;  5EFE0FE71D5F1BEC CRC64;

  Query Match             70.6%;  Score 36;  DB 1;  Length 130;
  Best Local Similarity   60.0%;  Pred. No. 32;
  Matches    6;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              :||||:|:|:
Db         46 RASQDIGSSL 55


RESULT 12
O61933_CAEEL
ID   O61933_CAEEL PRELIMINARY;      PRT;   317 AA.
AC   O61933;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein R09A1.3.
GN   ORFNames=R09A1.3;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; AF068711; AAC17777.1; -; Genomic_DNA.
DR   PIR; T33277; T33277.
DR   Ensembl; R09A1.3; Caenorhabditis elegans.
DR   WormBase; WBGene00019973; R09A1.3.
DR   WormPep; R09A1.3; CE18129.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   317 AA;  35559 MW;  87127052557A517D CRC64;

  Query Match             70.6%;  Score 36;  DB 2;  Length 317;
  Best Local Similarity   63.6%;  Pred. No. 82;
  Matches    7;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              | | |:||| |
Db         37 KRSMDIGTSTA 47


RESULT 13
Q4LRF1_9BURK
ID   Q4LRF1_9BURK PRELIMINARY;      PRT;   373 AA.
AC   Q4LRF1;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein precursor.
GN   ORFNames=Bcen2424DRAFT_2994;
OS   Burkholderia cenocepacia HI2424.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX   NCBI_TaxID=331272;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=HI2424;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT   HI2424.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=HI2424;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT   HI2424.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAHL01000024; EAM18665.1; -; Genomic_DNA.
KW   Hypothetical protein; Signal.
FT   SIGNAL        1     26       Potential.
SQ   SEQUENCE   373 AA;  37914 MW;  A1A27B6F1A3191B5 CRC64;

  Query Match             70.6%;  Score 36;  DB 2;  Length 373;
  Best Local Similarity   70.0%;  Pred. No. 98;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              | ||| |||:
Db        347 KVSQDSGTSI 356


RESULT 14
Q4XXF0_PLACH
ID   Q4XXF0_PLACH PRELIMINARY;      PRT;   501 AA.
AC   Q4XXF0;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
```

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DE   Hypothetical protein.
GN   ORFNames=PC104863.00.0;
OS   Plasmodium chabaudi.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5825;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA   Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA   James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA   Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA   Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C.,
RA   Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT   "A comprehensive survey of the Plasmodium life cycle by genomic,
RT   transcriptomic, and proteomic analyses.";
RL   Science 307:82-86(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAJ01002457; CAH78411.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   501 AA;  56871 MW;  1D57A2403BEF888D CRC64;

  Query Match             70.6%;  Score 36;  DB 2;  Length 501;
  Best Local Similarity   87.5%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGT 8
              |||||:||
Db        401 KASQDLGT 408


RESULT 15
HEMA_PI3B
ID   HEMA_PI3B      STANDARD;      PRT;   572 AA.
AC   P06167;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Hemagglutinin-neuraminidase (EC 3.2.1.18).
GN   Name=HN;
OS   Bovine parainfluenza 3 virus (BPIV-3).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Respirovirus.
OX   NCBI_TaxID=11215;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC RNA].
RC   STRAIN=910N;
RX   MEDLINE=87174819; PubMed=3031615;
RA   Suzu S., Sakai Y., Shioda T., Shibuta H.;
RT   "Nucleotide sequence of the bovine parainfluenza 3 virus genome: the
RT   genes of the F and HN glycoproteins.";
RL   Nucleic Acids Res. 15:2945-2958(1987).
CC   -!- FUNCTION: Attaches the virus to sialic acid-containing cell
CC       receptors and thereby initiating infection. Binding of HN protein
CC       to the receptor induces a conformational change that allows the F
CC       protein to trigger virion/cell membranes fusion (By similarity).
CC   -!- FUNCTION: Neuraminidase activity ensures the efficient spread of
CC       the virus by dissociating the mature virions from the neuraminic
CC       acid containing glycoproteins (By similarity).
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-,
CC       alpha-(2->8)- glycosidic linkages of terminal sialic residues in
CC       oligosaccharides, glycoproteins, glycolipids, colominic acid and
CC       synthetic substrates.
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC   -!- SIMILARITY: Belongs to the paramyxoviruses hemagglutinin-
CC       neuraminidase family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; Y00114; CAA68298.1; -; Genomic_RNA.
DR   EMBL; D84095; BAA12218.1; -; Genomic_RNA.
DR   SMR; P06167; 142-572.
DR   InterPro; IPR000665; Hem-neuramndse.
DR   Pfam; PF00423; HN; 1.
KW   Envelope protein; Glycoprotein; Hemagglutinin; Hydrolase;
KW   Signal-anchor; Structural protein; Transmembrane.
FT   TOPO_DOM      1     30       Cytoplasmic (Potential).
FT   TRANSMEM     31     51       Potential.
FT   TOPO_DOM     52    572       Extracellular (Potential).
FT   CARBOHYD    308    308       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    351    351       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    448    448       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    523    523       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    570    570       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   572 AA;  64590 MW;  DDF84E90C4EC87B4 CRC64;

  Query Match             70.6%;  Score 36;  DB 1;  Length 572;
  Best Local Similarity   60.0%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              | | |:|||:
Db         82 KTSDDIGTSI 91


RESULT 16
Q65689_PI3B
ID   Q65689_PI3B PRELIMINARY;      PRT;   572 AA.
AC   Q65689;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hemagglutinin-neuraminidase protein.
OS   Bovine parainfluenza 3 virus (BPIV-3).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Respirovirus.
OX   NCBI_TaxID=11215;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=95287485; PubMed=7769692;
RA   Breker-Klassen M.M., Yoo D., Mittal S.K., Sorden S.D., Haines D.M.,
RA   Babiuk L.A.;
RT   "Recombinant type 5 adenoviruses expressing bovine parainfluenza virus
RT   type 3 glycoproteins protect Sigmodon hispidus cotton rats from bovine
RT   parainfluenza virus type 3 infection.";
RL   J. Virol. 69:4308-4315(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=96405248; PubMed=8809388;
RA   Breker-Klassen M.M., Yoo D., Babiuk L.A.;
RT   "Comparisons of the F and HN gene sequences of different strains of
RT   bovine parainfluenza virus type 3: relationship to phenotype and
RT   pathogenicity.";
RL   Can. J. Vet. Res. 60:228-236(1996).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Breker-Klassen M.M.;
RT   "The immunobiology of bovine parainfluenza virus type 3 F and HN
RT   glycoproteins.";
RL   Thesis (1995), Veterinary Infectious Disease Organizatn, University of
RL   Saskatchewan Unpublished.
DR   EMBL; U31671; AAB03692.1; -; Genomic_DNA.
DR   SMR; Q65689; 142-572.
DR   GO; GO:0004308; F:exo-alpha-sialidase activity; IEA.
DR   GO; GO:0019058; P:viral infectious cycle; IEA.
DR   InterPro; IPR000665; Hem-neuramndse.
DR   Pfam; PF00423; HN; 1.
KW   Envelope protein; Hemagglutinin; Hydrolase; Transmembrane.
SQ   SEQUENCE   572 AA;  64668 MW;  D708557A0CFA8B1C CRC64;

  Query Match             70.6%;  Score 36;  DB 2;  Length 572;
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  Best Local Similarity   60.0%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              | | |:|||:
Db         82 KTSDDIGTSI 91


RESULT 17
CATA_CAUCR
ID   CATA_CAUCR     STANDARD;      PRT;   737 AA.
AC   O31066;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase).
GN   Name=katG; OrderedLocusNames=CC3043;
OS   Caulobacter crescentus.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC   Caulobacteraceae; Caulobacter.
OX   NCBI_TaxID=155892;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=ATCC 19089 / CB15;
RX   MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA   Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA   Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA   Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA   DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA   Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA   Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA   Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA   Fraser C.M.;
RT   "Complete genome sequence of Caulobacter crescentus.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 1-494.
RC   STRAIN=ATCC 19089 / CB15;
RX   MEDLINE=98012985; PubMed=9352936;
RA   Steinman H.M., Fareed F., Weinstein L.;
RT   "Catalase-peroxidase of Caulobacter crescentus: function and role in
RT   stationary-phase survival.";
RL   J. Bacteriol. 179:6831-6836(1997).
CC   -!- FUNCTION: Bifunctional, exhibiting both a catalase and broad-
CC       spectrum peroxidase activities.
CC   -!- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
CC   -!- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per dimer
CC       (By similarity).
CC   -!- INDUCTION: By hydrogen peroxide.
CC   -!- SIMILARITY: Belongs to the peroxidase family. Bacterial
CC       peroxidase/catalase subfamily.
CC   ---------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------------
DR   EMBL; AE005967; AAK25005.1; -; Genomic_DNA.
DR   EMBL; AF027168; AAC45850.1; -; Genomic_DNA.
DR   PIR; A87626; A87626.
DR   PIR; T45480; T45480.
DR   HSSP; Q939D2; 1MWV.
DR   TIGR; CC3043; -.
DR   InterPro; IPR000763; ctase/prase.
DR   InterPro; IPR002016; Peroxidase.
DR   Pfam; PF00141; peroxidase; 2.
DR   PRINTS; PR00460; BPEROXIDASE.
DR   PRINTS; PR00458; PEROXIDASE.
DR   TIGRFAMs; TIGR00198; cat_per_HPI; 1.
DR   PROSITE; PS00435; PEROXIDASE_1; 1.
DR   PROSITE; PS00436; PEROXIDASE_2; 1.
DR   PROSITE; PS50873; PEROXIDASE_4; 1.
KW   Complete proteome; Heme; Hydrogen peroxide; Iron; Metal-binding;
KW   Organic radical; Oxidoreductase; Peroxidase.
FT   ACT_SITE    106    106       Proton acceptor (By similarity).
FT   ACT_SITE    319    319       Tryptophan radical intermediate (By
FT                                similarity).
FT   METAL       268    268       Iron (heme axial ligand) (By similarity).
FT   SITE        102    102       Transition state stabilizer (By
FT                                similarity).
SQ   SEQUENCE   737 AA;  80166 MW;  D900742D04E02E97 CRC64;

  Query Match             70.6%;  Score 36;  DB 1;  Length 737;
  Best Local Similarity   70.0%;  Pred. No. 2e+02;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              ||::| ||||
Db        550 KAAKDAGTSV 559


RESULT 18
Q5AAV6_CANAL
ID   Q5AAV6_CANAL PRELIMINARY;      PRT;   978 AA.
AC   Q5AAV6;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein PUT3.
GN   Name=PUT3; ORFNames=CaO19.13584, CaO19.6203;
OS   Candida albicans SC5314.
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX   NCBI_TaxID=237561;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=SC5314;
RX   PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA   Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA   Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA   Davis R.W., Scherer S.;
RT   "The diploid genome sequence of Candida albicans.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=SC5314;
RA   Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA   Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA   Jones T., Scherer S., Agabian N.;
RT   "Annotation of the Genome of Candida albicans.";
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AACQ01000038; EAK99799.1; -; Genomic_DNA.
DR   EMBL; AACQ01000037; EAK99886.1; -; Genomic_DNA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0006350; P:transcription; IEA.
KW   DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;
KW   Transcription; Transcription regulation; Zinc.
SQ   SEQUENCE   978 AA;  109909 MW;  765D44EEC099B8F6 CRC64;

  Query Match             70.6%;  Score 36;  DB 2;  Length 978;
  Best Local Similarity   88.9%;  Pred. No. 2.7e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ASQDVGTSV 10
              || ||||||
Db        951 ASPDVGTSV 959


RESULT 19
Q5B2F2_EMENI
ID   Q5B2F2_EMENI PRELIMINARY;      PRT;  1579 AA.
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AC   Q5B2F2;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=AN5278.2;
OS   Aspergillus nidulans FGSC A4.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Emericella.
OX   NCBI_TaxID=227321;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FGSC A4;
RA   Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA   Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA   Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA   Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA   Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA   Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA   Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA   Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA   Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA   Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA   Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA   Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA   Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA   Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA   Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA   Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA   Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA   Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA   Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA   Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA   Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA   Lander E.;
RT   "Genome Sequence of Aspergillus nidulans.";
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AACD01000093; EAA62438.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   1579 AA;  178352 MW;  C310124CB1CF388C CRC64;

  Query Match            70.6%;  Score 36;  DB 2;  Length 1579;
  Best Local Similarity  63.6%;  Pred. No. 4.6e+02;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              || :| |||:|
Db        196 KAERDKGTSIA 206


RESULT 20
Q4YNQ6_PLABE
ID   Q4YNQ6_PLABE PRELIMINARY;      PRT;  2491 AA.
AC   Q4YNQ6;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=PB108442.00.0;
OS   Plasmodium berghei.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5821;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA   Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA   James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA   Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA   Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C.,
RA   Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT   "A comprehensive survey of the Plasmodium life cycle by genomic,
RT   transcriptomic, and proteomic analyses.";
RL   Science 307:82-86(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAI01003293; CAI00354.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   2491 AA;  279011 MW;  09E709B81AF9F358 CRC64;

  Query Match            70.6%;  Score 36;  DB 2;  Length 2491;
  Best Local Similarity  87.5%;  Pred. No. 7.4e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGT 8
              |||||:||
Db       2432 KASQDLGT 2439


RESULT 21
Q7RNQ6_PLAYO
ID   Q7RNQ6_PLAYO PRELIMINARY;      PRT;  2598 AA.
AC   Q7RNQ6;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   Name=PY01759;
OS   Plasmodium yoelii yoelii.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=73239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=17XNL;
RX   MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA   Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA   Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA   Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA   Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA   Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA   Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA   Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA   van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA   Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA   Carucci D.J.;
RT   "Genome sequence and comparative analysis of the model rodent malaria
RT   parasite Plasmodium yoelii yoelii.";
RL   Nature 419:512-519(2002).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABL01000473; EAA21125.1; -; Genomic_DNA.
DR   GO; GO:0005488; F:binding; IEA.
DR   InterPro; IPR011989; ARM-like.
DR   InterPro; IPR000225; Armadillo.
DR   InterPro; IPR000362; Fumarate_lyase.
DR   PROSITE; PS50176; ARM_REPEAT; 1.
DR   PROSITE; PS00163; FUMARATE_LYASES; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   2598 AA;  289931 MW;  F2DEE98B4404D54E CRC64;

  Query Match            70.6%;  Score 36;  DB 2;  Length 2598;
  Best Local Similarity  87.5%;  Pred. No. 7.8e+02;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGT 8
              |||||:||
Db       2498 KASQDLGT 2505


RESULT 22
Q6Z997_ORYSA
ID   Q6Z997_ORYSA PRELIMINARY;      PRT;    83 AA.
```

```
AC   Q6Z997;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein P0682A06.37.
GN   Name=P0682A06.37;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP004705; BAD05477.1; -; Genomic_DNA.
DR   Gramene; Q6Z997; -.
KW   Hypothetical protein.
SQ   SEQUENCE   83 AA;  9121 MW;  EC1E9401D7F0BDAC CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 83;
  Best Local Similarity   70.0%;  Pred. No. 32;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ASQDVGTSVA 11
              | |::|||||
Db         38 AGQELGTSVA 47


RESULT 23
ATPF_STRMU
ID   ATPF_STRMU     STANDARD;      PRT;   165 AA.
AC   P95785;
DT   01-NOV-1997 (Rel. 35, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   ATP synthase B chain (EC 3.6.3.14).
GN   Name=atpF; OrderedLocusNames=SMU.1532;
OS   Streptococcus mutans.
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=1309;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=GS-5;
RX   MEDLINE=97149283; PubMed=8996091; DOI=10.1016/S0378-1119(96)00502-1;
RA   Smith A.J., Quivey R.G., Faustoferri R.C.;
RT   "Cloning and nucleotide sequence analysis of the Streptococcus mutans
RT   membrane-bound, proton-translocating ATPase operon.";
RL   Gene 183:87-96(1996).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=UA159 / ATCC 700610 / Serotype c;
RX   MEDLINE=22295063; PubMed=12397186; DOI=10.1073/pnas.172501299;
RA   Ajdic D.J., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
RA   Carson M.B., Primeaux C., Tian R., Kenton S., Jia H.G., Lin S.P.,
RA   Qian Y., Li S., Zhu H., Najar F.Z., Lai H., White J., Roe B.A.,
RA   Ferretti J.J.;
RT   "Genome sequence of Streptococcus mutans UA159, a cariogenic dental
RT   pathogen.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).
CC   -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(In) = ADP + phosphate +
CC       H(+)(Out).
CC   -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
CC       core - and CF(0) - the membrane proton channel. CF(1) has five
CC       subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)
CC       has three main subunits: a, b and c.
CC   -!- SIMILARITY: Belongs to the ATPase B chain family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U31170; AAD13379.1; -; Genomic_DNA.
DR   EMBL; AE014985; AAN59182.1; -; Genomic_DNA.
DR   PIR; JC5737; JC5737.
DR   InterPro; IPR005864; ATP_synthF0_B.
DR   InterPro; IPR002146; ATPsynt_B/B'sub.
DR   Pfam; PF00430; ATP-synt_B; 1.
DR   TIGRFAMs; TIGR01144; ATP_synt_b; 1.
KW   CF(0); Complete proteome; Hydrogen ion transport; Ion transport;
KW   Transmembrane; Transport.
FT   TRANSMEM      7     27       Potential.
FT   CONFLICT     41     41       A -> T (in Ref. 1).
SQ   SEQUENCE   165 AA;  17922 MW;  B1DADD506F487413 CRC64;

  Query Match             68.6%;  Score 35;  DB 1;  Length 165;
  Best Local Similarity   63.6%;  Pred. No. 67;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||:||: || |
Db        110 KANQDIATSKA 120


RESULT 24
Q5HWH8_CAMJR
ID   Q5HWH8_CAMJR PRELIMINARY;      PRT;   250 AA.
AC   Q5HWH8;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Major antigenic peptide PEB3.
GN   OrderedLocusNames=CJE0337;
OS   Campylobacter jejuni (strain RM1221).
OC   Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC   Campylobacteraceae; Campylobacter.
OX   NCBI_TaxID=195099;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15660156; DOI=10.1371/journal.pbio.0030015;
RA   Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
RA   Ravel J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
RA   Dodson R.J., Durkin A.S., Madupu R., Sullivan S.A., Shetty J.U.,
RA   Ayodeji M.A., Shvartsbeyn A., Schatz M.C., Badger J.H., Fraser C.M.,
RA   Nelson K.E.;
RT   "Major structural differences and novel potential virulence mechanisms
RT   from the genomes of multiple Campylobacter species.";
RL   PLoS Biol. 3:72-85(2005).
DR   EMBL; CP000025; AAW34927.1; -; Genomic_DNA.
DR   TIGR; CJE0337; -.
DR   InterPro; IPR011587; MBP_prokaryotic.
DR   ProDom; PD008688; MBP_prokaryotic; 1.
KW   Complete proteome.
SQ   SEQUENCE   250 AA;  27522 MW;  A111949630A04065 CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 250;
  Best Local Similarity   54.5%;  Pred. No. 1e+02;
  Matches    6;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |:: |:||:||
Db        194 KSNPDIGTAVA 204


RESULT 25
Q9PIK7_CAMJE
ID   Q9PIK7_CAMJE PRELIMINARY;      PRT;   250 AA.
AC   Q9PIK7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Major antigenic peptide PEB3.
GN   Name=peb3; OrderedLocusNames=Cj0289c;
```

```
OS   Campylobacter jejuni.
OC   Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC   Campylobacteraceae; Campylobacter.
OX   NCBI_TaxID=197;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NCTC 11168;
RX   MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
RA   Parkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M.,
RA   Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
RA   Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA   Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA   Whitehead S., Barrell B.G.;
RT   "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT   reveals hypervariable sequences.";
RL   Nature 403:665-668(2000).
DR   EMBL; AL139074; CAB72756.1; -; Genomic_DNA.
DR   PIR; G81447; G81447.
DR   InterPro; IPR011587; MBP_prokaryotic.
DR   ProDom; PD008688; MBP_prokaryotic; 1.
KW   Complete proteome.
SQ   SEQUENCE   250 AA;  27536 MW;  B2A9AF0630A04065 CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 250;
  Best Local Similarity   54.5%;  Pred. No. 1e+02;
  Matches    6;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |:: |:||:||
Db        194 KSNPDIGTAVA 204


RESULT 26
UB72_DEIRA
ID   UB72_DEIRA     STANDARD;      PRT;   298 AA.
AC   Q9RV58;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Protein DR1172.
GN   OrderedLocusNames=DR1172;
OS   Deinococcus radiodurans.
OC   Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC   Deinococcaceae; Deinococcus.
OX   NCBI_TaxID=1299;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RX   MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;
RA   White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA   Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA   Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA   Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,
RA   Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA   Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,
RA   Fraser C.M.;
RT   "Genome sequence of the radioresistant bacterium Deinococcus
RT   radiodurans R1.";
RL   Science 286:1571-1577(1999).
RN   [2]
RP   PROTEIN SEQUENCE OF 1-15.
RC   STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;
RA   Joshi B.S., Apte S.K., Schmid R., Altendorf K.;
RL   Submitted (JUN-2003) to Swiss-Prot.
CC   -!- SIMILARITY: Belongs to the LEA type 1 family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AE001966; AAF10747.1; -; Genomic_DNA.
DR   PIR; B75429; B75429.
DR   TIGR; DR1172; -.
DR   InterPro; IPR000074; ApoA1_A4_E.
DR   InterPro; IPR004238; LEA.
DR   Pfam; PF02987; LEA_4; 3.
KW   Complete proteome; Direct protein sequencing; Repeat.
FT   REPEAT       48    117       LEA-like 1.
FT   REPEAT      128    197       LEA-like 2.
FT   REPEAT      201    270       LEA-like 3.
FT   COMPBIAS     67    267       Ala-rich.
SQ   SEQUENCE   298 AA;  30930 MW;  0F542B1A010F4CB2 CRC64;

  Query Match             68.6%;  Score 35;  DB 1;  Length 298;
  Best Local Similarity   77.8%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 ASQDVGTSV 10
              |:||||:||
Db         49 AAQDVGSSV 57


RESULT 27
Q9TNJ1_9MARC
ID   Q9TNJ1_9MARC PRELIMINARY;      PRT;   311 AA.
AC   Q9TNJ1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   DNA-directed RNA polymerase (EC 2.7.7.6) beta'-2 chain
DE   (Fragment).
GN   Name=rpoC2;
OS   Haplomitrium mnioides.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
OC   Jungermanniopsida; Metzgeriidae; Haplomitriales; Haplomitriaceae;
OC   Haplomitrium.
OX   NCBI_TaxID=56921;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99404147; PubMed=10474899;
RA   Nishiyama T., Kato M.;
RT   "Molecular phylogenetic analysis among bryophytes and tracheophytes
RT   based on combined data of plastid coded genes and the 18S rRNA gene.";
RL   Mol. Biol. Evol. 16:1027-1036(1999).
DR   EMBL; AB013679; BAA83455.1; -; Genomic_DNA.
DR   HSSP; Q9KWU6; 1HQM.
DR   GO; GO:0009507; C:chloroplast; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006350; P:transcription; IEA.
DR   InterPro; IPR007066; RNA_pol_Rpb1_3.
DR   InterPro; IPR007083; RNA_pol_Rpb1_4.
DR   InterPro; IPR007081; RNA_pol_Rpb1_5.
DR   Pfam; PF04983; RNA_pol_Rpb1_3; 1.
DR   Pfam; PF05000; RNA_pol_Rpb1_4; 1.
DR   Pfam; PF04998; RNA_pol_Rpb1_5; 1.
KW   Chloroplast; DNA-directed RNA polymerase.
FT   NON_TER     311    311
SQ   SEQUENCE   311 AA;  34628 MW;  60CAE0033F51F78B CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 311;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 SQDVGTSVA 11
              :||:|||:|
Db        260 NQDIGTSLA 268


RESULT 28
Q60ZB5_CAEBR
ID   Q60ZB5_CAEBR PRELIMINARY;      PRT;   314 AA.
```

```
AC   Q60ZB5;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein CBG17889 (Fragment).
GN   Name=CBG17889;
OS   Caenorhabditis briggsae.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6238;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RG   The C.briggsae Sequencing Consortium;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAC01000087; CAE71047.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   314 AA;  35353 MW;  6530419B535CA52E CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 314;
  Best Local Similarity   72.7%;  Pred. No. 1.3e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              | | ||||| |
Db         35 KRSVDVGTSTA 45


RESULT 29
Q5HP41_STAEQ
ID   Q5HP41_STAEQ PRELIMINARY;      PRT;   374 AA.
AC   Q5HP41;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Peptidase T-like protein.
GN   OrderedLocusNames=SERP1072;
OS   Staphylococcus epidermidis (strain ATCC 35984 / RP62A).
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=176279;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RA   Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA   Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA   Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA   Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,
RA   Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA   Hance I.R., Nelson K.E., Fraser C.M.;
RT   "Insights on evolution of virulence and resistance from the complete
RT   genome analysis of an early methicillin-resistant Staphylococcus
RT   aureus strain and a biofilm-producing methicillin-resistant
RT   Staphylococcus epidermidis strain.";
RL   J. Bacteriol. 187:2426-2438(2005).
DR   EMBL; CP000029; AAW54438.1; -; Genomic_DNA.
DR   TIGR; SERP1072; -.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0046983; F:protein dimerization activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR002933; Peptidase_M20.
DR   InterPro; IPR010162; Pept_M20B_pepT.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   TIGRFAMs; TIGR01883; PepT-like; 1.
DR   PROSITE; PS00758; ARGE_DAPE_CPG2_1; UNKNOWN_1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; UNKNOWN_1.
KW   Complete proteome.
SQ   SEQUENCE   374 AA;  40277 MW;  5FC72F83F16C0A35 CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 374;
  Best Local Similarity   77.8%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 ASQDVGTSV 10
              ||:||||:|
Db        168 ASKDVGTTV 176


RESULT 30
Q8CP46_STAEP
ID   Q8CP46_STAEP PRELIMINARY;      PRT;   374 AA.
AC   Q8CP46;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Tripeptidase.
GN   OrderedLocusNames=SE1193;
OS   Staphylococcus epidermidis.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=1282;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=ATCC 12228;
RX   PubMed=12950922; DOI=10.1046/j.1365-2958.2003.03671.x;
RA   Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA   Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA   Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT   "Genome-based analysis of virulence genes in a non-biofilm-forming
RT   Staphylococcus epidermidis strain (ATCC 12228).";
RL   Mol. Microbiol. 49:1577-1593(2003).
DR   EMBL; AE016748; AAO04792.1; -; Genomic_DNA.
DR   HSSP; P26311; 1FNO.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0046983; F:protein dimerization activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR001261; ArgE_dapE.
DR   InterPro; IPR011650; M20_dimer.
DR   InterPro; IPR010162; Pept_M20B_pepT.
DR   InterPro; IPR002933; Peptidase_M20.
DR   Pfam; PF07687; M20_dimer; 1.
DR   Pfam; PF01546; Peptidase_M20; 1.
DR   TIGRFAMs; TIGR01883; PepT-like; 1.
DR   PROSITE; PS00758; ARGE_DAPE_CPG2_1; UNKNOWN_1.
DR   PROSITE; PS00759; ARGE_DAPE_CPG2_2; UNKNOWN_1.
KW   Complete proteome.
SQ   SEQUENCE   374 AA;  40261 MW;  42702664E53C0A35 CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 374;
  Best Local Similarity   77.8%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 ASQDVGTSV 10
              ||:||||:|
Db        168 ASKDVGTTV 176


RESULT 31
Q566R3_RAT
ID   Q566R3_RAT  PRELIMINARY;      PRT;   407 AA.
AC   Q566R3;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein RGD1311086_predicted.
GN   Name=RGD1311086_predicted;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
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OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC093381; AAH93381.1; -; mRNA.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   InterPro; IPR000467; G_patch.
DR   Pfam; PF01585; G-patch; 1.
DR   SMART; SM00443; G_patch; 1.
DR   PROSITE; PS50174; G_PATCH; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   407 AA;  46073 MW;  7A2C233451EAA800 CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 407;
  Best Local Similarity   77.8%;  Pred. No. 1.8e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTS 9
              | |:|||||
Db        186 KGSKDVGTS 194


RESULT 32
Q5B779_EMENI
ID   Q5B779_EMENI PRELIMINARY;      PRT;   416 AA.
AC   Q5B779;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=AN3601.2;
OS   Aspergillus nidulans FGSC A4.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Emericella.
OX   NCBI_TaxID=227321;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FGSC A4;
RA   Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA   Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA   Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA   Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA   Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA   Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA   Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA   Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA   Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA   Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA   Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA   Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA   Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA   Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA   Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA   Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA   Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA   Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA   Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA   Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA   Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA   Lander E.;
RT   "Genome Sequence of Aspergillus nidulans.";
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AACD01000061; EAA59809.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   416 AA;  46773 MW;  5CD12C4AD132FEDA CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 416;
  Best Local Similarity   66.7%;  Pred. No. 1.8e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ASQDVGTSV 10
              || |:|||:
Db         99 ASNDIGTSI 107


RESULT 33
Q4QIV2_LEIMA
ID   Q4QIV2_LEIMA PRELIMINARY;      PRT;   494 AA.
AC   Q4QIV2;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=LmjF06.1240;
OS   Leishmania major.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX   NCBI_TaxID=5664;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Friedlin;
RA   Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA   Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S.,
RA   Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CT005245; CAJ02171.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   494 AA;  52681 MW;  6365304AD7F5F7C4 CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 494;
  Best Local Similarity   45.5%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              :: ||:|:|:|
Db        409 RSGQDIGSSIA 419


RESULT 34
Q5UWB5_HALMA
ID   Q5UWB5_HALMA PRELIMINARY;      PRT;   501 AA.
AC   Q5UWB5;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   3-octaprenyl-4-hydroxybenzoate carboxy-lyase.
GN   Name=ubiD; OrderedLocusNames=rrnB0267;
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OS   Haloarcula marismortui (Halobacterium marismortui).
OC   Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC   Halobacteriaceae; Haloarcula.
OX   NCBI_TaxID=2238;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 43049;
RX   PubMed=15520287; DOI=10.1101/gr.2700304;
RA   Baliga N.S., Bonneau R., Facciotti M.T., Pan M., Glusman G.,
RA   Deutsch E.W., Shannon P., Chiu Y., Weng R.S., Gan R.R., Hung P.,
RA   Date S.V., Marcotte E., Hood L., Ng W.V.;
RT   "Genome sequence of Haloarcula marismortui: a halophilic archaeon from
RT   the Dead Sea.";
RL   Genome Res. 14:2221-2234(2004).
DR   EMBL; AY596298; AAV48438.1; -; Genomic_DNA.
DR   GO; GO:0016829; F:lyase activity; IEA.
DR   InterPro; IPR002830; carboxylyase.
DR   Pfam; PF01977; UbiD; 1.
KW   Complete proteome; Lyase.
SQ   SEQUENCE   501 AA;  55248 MW;  D3C5153247B8FB21 CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 501;
  Best Local Similarity   72.7%;  Pred. No. 2.2e+02;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              | | ||||| |
Db        438 KGSADVGTSKA 448


RESULT 35
Q8R0V4_MOUSE
ID   Q8R0V4_MOUSE PRELIMINARY;      PRT;   661 AA.
AC   Q8R0V4;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Gpatc1 protein (Fragment).
GN   Name=Gpatc1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Liver;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Liver;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC026394; AAH26394.1; -; mRNA.
DR   MGI; MGI:1914721; Gpatc1.
FT   NON_TER       1       1
SQ   SEQUENCE   661 AA;  73786 MW;  F67C8B55F1410A3D CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 661;
  Best Local Similarity   87.5%;  Pred. No. 2.9e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGT 8
              || |||||
Db        132 KAGQDVGT 139


RESULT 36
Q5HLJ7_STAEQ
ID   Q5HLJ7_STAEQ PRELIMINARY;      PRT;   801 AA.
AC   Q5HLJ7;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Nitrite reductase [NAD(P)H], large subunit (EC 1.6.6.4).
GN   Name=nirB; OrderedLocusNames=SERP1990;
OS   Staphylococcus epidermidis (strain ATCC 35984 / RP62A).
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=176279;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15774886; DOI=10.1128/JB.187.7.2426-2438.2005;
RA   Gill S.R., Fouts D.E., Archer G.L., Mongodin E.F., DeBoy R.T.,
RA   Ravel J., Paulsen I.T., Kolonay J.F., Brinkac L.M., Beanan M.J.,
RA   Dodson R.J., Daugherty S.C., Madupu R., Angiuoli S.V., Durkin A.S.,
RA   Haft D.H., Vamathevan J.J., Khouri H., Utterback T.R., Lee C.,
RA   Dimitrov G., Jiang L., Qin H., Weidman J., Tran K., Kang K.H.,
RA   Hance I.R., Nelson K.E., Fraser C.M.;
RT   "Insights on evolution of virulence and resistance from the complete
RT   genome analysis of an early methicillin-resistant Staphylococcus
RT   aureus strain and a biofilm-producing methicillin-resistant
RT   Staphylococcus epidermidis strain.";
RL   J. Bacteriol. 187:2426-2438(2005).
DR   EMBL; CP000029; AAW52910.1; -; Genomic_DNA.
DR   TIGR; SERP1990; -.
DR   GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000759; Adrndx_reductase.
DR   InterPro; IPR001327; FAD_pyr_redox.
DR   InterPro; IPR007419; Fer2_BFD.
DR   InterPro; IPR000205; NAD_BS.
DR   InterPro; IPR006066; Nir_Si.
DR   InterPro; IPR006067; Nir_Sir_4Fe4S.
DR   InterPro; IPR005117; NiR_SiR_beta_fer.
DR   InterPro; IPR000103; Pyridine_redox_2.
DR   InterPro; IPR001100; Pyr_redox.
DR   Pfam; PF04324; Fer2_BFD; 1.
DR   Pfam; PF01077; NIR_SIR; 1.
DR   Pfam; PF03460; NIR_SIR_ferr; 1.
DR   PRINTS; PR00419; ADXRDTASE.
DR   PRINTS; PR00368; FADPNR.
DR   PRINTS; PR00411; PNDRDTASEI.
DR   PRINTS; PR00469; PNDRDTASEII.
DR   PRINTS; PR00397; SIROHAEM.
DR   ProDom; PD000139; FAD_pyr_redox; 1.
DR   PROSITE; PS00365; NIR_SIR; 1.
KW   Complete proteome; Oxidoreductase.
SQ   SEQUENCE   801 AA;  89140 MW;  C234B97EB8D6FFAF CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 801;
  Best Local Similarity   54.5%;  Pred. No. 3.6e+02;
  Matches    6;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |  :| |||:|
Db        398 KGDEDAGTSIA 408
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RESULT 37
Q8CN69_STAEP
ID   Q8CN69_STAEP PRELIMINARY;      PRT;   801 AA.
AC   Q8CN69;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Nitrite reductase.
GN   OrderedLocusNames=SE1978;
OS   Staphylococcus epidermidis.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=1282;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=ATCC 12228;
RX   PubMed=12950922; DOI=10.1046/j.1365-2958.2003.03671.x;
RA   Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
RA   Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
RA   Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
RT   "Genome-based analysis of virulence genes in a non-biofilm-forming
RT   Staphylococcus epidermidis strain (ATCC 12228).";
RL   Mol. Microbiol. 49:1577-1593(2003).
DR   EMBL; AE016750; AAO05619.1; -; Genomic_DNA.
DR   HSSP; Q94655; 1ONF.
DR   GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR000759; Adrndx_reductase.
DR   InterPro; IPR007419; BFD_Fer2_bd.
DR   InterPro; IPR001327; FAD_pyr_redox.
DR   InterPro; IPR000205; NAD_BS.
DR   InterPro; IPR006066; Nir_Si.
DR   InterPro; IPR006067; Nir_Sir_4Fe4S.
DR   InterPro; IPR005117; NiR_SiR_beta_fer.
DR   InterPro; IPR001100; Pyr_redox.
DR   Pfam; PF04324; Fer2_BFD; 1.
DR   Pfam; PF01077; NIR_SIR; 1.
DR   Pfam; PF03460; NIR_SIR_ferr; 1.
DR   Pfam; PF00070; Pyr_redox; 1.
DR   PRINTS; PR00419; ADXRDTASE.
DR   PRINTS; PR00368; FADPNR.
DR   PRINTS; PR00411; PNDRDTASEI.
DR   PRINTS; PR00397; SIROHAEM.
DR   ProDom; PD000139; FAD_pyr_redox; 1.
DR   PROSITE; PS00365; NIR_SIR; 1.
KW   Complete proteome.
SQ   SEQUENCE   801 AA;  89125 MW;  A3BBFF6FA887729A CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 801;
  Best Local Similarity   54.5%;  Pred. No. 3.6e+02;
  Matches    6;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |  :| |||:|
Db        398 KGDEDAGTSIA 408


RESULT 38
Q9DBM1_MOUSE
ID   Q9DBM1_MOUSE PRELIMINARY;      PRT;   930 AA.
AC   Q9DBM1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Mus musculus adult male liver cDNA, RIKEN full-length enriched
DE   library, clone:1300003A17 product:hypothetical D111/G-patch domain
DE   containing protein, full insert sequence.
GN   Name=Gpatc1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
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RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK004868; BAB23629.1; -; mRNA.
DR   Ensembl; ENSMUSG00000063808; Mus musculus.
DR   MGI; MGI:1914721; Gpatc1.
DR   GO; GO:0005622; C:intracellular; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   InterPro; IPR011666; DUF1604.
DR   InterPro; IPR000467; G_patch.
DR   Pfam; PF07713; DUF1604; 1.
DR   Pfam; PF01585; G-patch; 1.
DR   SMART; SM00443; G_patch; 1.
DR   PROSITE; PS50174; G_PATCH; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   930 AA;  103007 MW;  62D383B72424EF73 CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 930;
  Best Local Similarity   87.5%;  Pred. No. 4.2e+02;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGT 8
              || |||||
Db        401 KAGQDVGT 408


RESULT 39
Q74ZC6_ASHGO
ID   Q74ZC6_ASHGO PRELIMINARY;      PRT;  1158 AA.
AC   Q74ZC6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   AGR273Cp.
GN   Name=AGR273C;
OS   Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX   NCBI_TaxID=33169;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=ATCC 10895;
RX   PubMed=15001715; DOI=10.1126/science.1095781;
RA   Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,
RA   Mohr C., Poehlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
RA   Gaffney T.D., Philippsen P.;
RT   "The Ashbya gossypii genome as a tool for mapping the ancient
RT   Saccharomyces cerevisiae genome.";
RL   Science 304:304-307(2004).
DR   EMBL; AE016820; AAS54763.1; -; Genomic_DNA.
DR   AGD; AGR273C; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0030261; P:chromosome condensation; IEA.
DR   GO; GO:0007067; P:mitosis; IEA.
DR   InterPro; IPR011989; ARM-like.
DR   InterPro; IPR007673; Cnd1.
DR   InterPro; IPR000357; HEAT.
DR   Pfam; PF02985; HEAT; 3.
DR   PIRSF; PIRSF017127; Condensin_D2; 1.
KW   Complete proteome; DNA condensation.
SQ   SEQUENCE   1158 AA;  130314 MW;  5E773F8FCC5C329C CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 1158;
  Best Local Similarity   63.6%;  Pred. No. 5.4e+02;
  Matches    7;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              | | | |||:|
Db        582 KGSNDEGTSIA 592


RESULT 40
Q55J08_CRYNE
ID   Q55J08_CRYNE PRELIMINARY;      PRT;  2245 AA.
AC   Q55J08;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=CNBL1770;
OS   Cryptococcus neoformans var. neoformans B-3501A.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC   Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX   NCBI_TaxID=283643;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=B-3501A;
RA   Fung E., Hyman R.W., Rowley D., Bruno D., Miranda M., Fukushima M.,
RA   Wickes B.L., Fu J., Davis R.W.;
RT   "Cryptococcus neoformans serotype D sequencing.";
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAEY01000057; EAL17662.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   2245 AA;  248551 MW;  A8088229EB26A2A9 CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 2245;
  Best Local Similarity   77.8%;  Pred. No. 1.1e+03;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTS 9
              |:| |||||
Db       1021 KSSSDVGTS 1029


RESULT 41
Q5KCP4_CRYNE
ID   Q5KCP4_CRYNE PRELIMINARY;      PRT;  2245 AA.
AC   Q5KCP4;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=CNH01780;
OS   Cryptococcus neoformans var. neoformans JEC21.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC   Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX   NCBI_TaxID=214684;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=JEC21;
RA   Loftus B., Amedeo P., Roncaglia P., Vamathevan J., Utterback T.,
RA   Van Aken S., Fraser C.;
RL   Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=JEC21;
RX   PubMed=15653466; DOI=10.1126/science.1103773;
RA   Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D.,
RA   Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E.,
RA   Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J.,
RA   D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J.,
RA   Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I.,
RA   Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E.,
RA   Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L.,
RA   Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A.,
RA   Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R.,
RA   Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W.,
RA   Fraser C.M., Hyman R.W.;
RT   "The genome of the basidiomycetous yeast and human pathogen
RT   Cryptococcus neoformans.";
RL   Science 307:1321-1324(2005).
```

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DR   EMBL; AE017348; AAW45045.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   2245 AA;  248426 MW;  2BF43DFA85560943 CRC64;

  Query Match             68.6%;  Score 35;  DB 2;  Length 2245;
  Best Local Similarity   77.8%;  Pred. No. 1.1e+03;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTS 9
              |:| |||||
Db       1021 KSSSDVGTS 1029


RESULT 42
Q8CEY4_MOUSE
ID   Q8CEY4_MOUSE PRELIMINARY;      PRT;    83 AA.
AC   Q8CEY4;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Mus musculus adult male tongue cDNA, RIKEN full-length enriched
DE   library, clone:2310035N23 product:hypothetical protein, full insert
DE   sequence. (Fragment).
GN   Name=1200004M23Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Tongue;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Tongue;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Tongue;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Tongue;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Tongue;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Tongue;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK009639; BAC25263.1; -; mRNA.
DR   Ensembl; ENSMUSG00000043488; Mus musculus.
DR   MGI; MGI:1914707; 1200004M23Rik.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   83 AA;  8553 MW;  68BEA4987BA886E0 CRC64;

  Query Match             66.7%;  Score 34;  DB 2;  Length 83;
  Best Local Similarity   100.0%;  Pred. No. 52;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 QDVGTSV 10
              |||||||
Db          8 QDVGTSV 14


RESULT 43
Q5TTA0_ANOGA
ID   Q5TTA0_ANOGA PRELIMINARY;      PRT;   120 AA.
AC   Q5TTA0;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   ENSANGP00000010179 (Fragment).
GN   ORFNames=ENSANGG00000007690;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RT   "Anopheles gambiae re-annotation.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
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RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008881; EAL40640.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13562 MW;  EACE14639F7F3CD2 CRC64;

  Query Match             66.7%;  Score 34;  DB 2;  Length 120;
  Best Local Similarity   54.5%;  Pred. No. 78;
  Matches    6;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              : | :||||:|
Db         98 RGSDEVGTSIA 108


RESULT 44
GREA_PSESM
ID   GREA_PSESM     STANDARD;      PRT;   158 AA.
AC   Q87WP5;
DT   29-MAR-2004 (Rel. 43, Created)
DT   29-MAR-2004 (Rel. 43, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Transcription elongation factor greA (Transcript cleavage factor
DE   greA).
GN   Name=greA; OrderedLocusNames=PSPTO4500;
OS   Pseudomonas syringae (pv. tomato).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=323;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=DC3000;
RX   MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA   Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA   Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA   Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA   Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA   Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA   Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA   Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
RA   Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA   Bender C.L., White O., Fraser C.M., Collmer A.;
RT   "The complete genome sequence of the Arabidopsis and tomato pathogen
RT   Pseudomonas syringae pv. tomato DC3000.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
CC   -!- FUNCTION: Necessary for efficient RNA polymerase transcription
CC       elongation past template-encoded arresting sites. The arresting
CC       sites in DNA have the property of trapping a certain fraction of
CC       elongating RNA polymerases that pass through, resulting in locked
CC       ternary complexes. Cleavage of the nascent transcript by cleavage
CC       factors such as greA or greB allows the resumption of elongation
CC       from the new 3'terminus. GreA releases sequences of 2 to 3
CC       nucleotides (By similarity).
CC   -!- SIMILARITY: Belongs to the greA/greB family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; AE016853; AAO57948.1; -; Genomic_DNA.
DR   HSSP; P21346; 1GRJ.
DR   TIGR; PSPTO4500; -.
DR   HAMAP; MF_00105; -; 1.
DR   InterPro; IPR006359; GreA.
DR   InterPro; IPR012243; GreA_GreB.
DR   InterPro; IPR001437; GreA_GreB_reg.
DR   Pfam; PF01272; GreA_GreB; 1.
DR   Pfam; PF03449; GreA_GreB_N; 1.
DR   PIRSF; PIRSF006092; GreA; 1.
DR   ProDom; PD004918; GreA_GreB; 1.
DR   TIGRFAMs; TIGR01462; greA; 1.
DR   PROSITE; PS00829; GREAB_1; 1.
DR   PROSITE; PS00830; GREAB_2; 1.
KW   Coiled coil; Complete proteome; DNA-binding; Transcription;
KW   Transcription regulation.
FT   COILED       45     72       Potential.
SQ   SEQUENCE   158 AA;  17392 MW;  DACAF1177A3E086C CRC64;

  Query Match             66.7%;  Score 34;  DB 1;  Length 158;
  Best Local Similarity   66.7%;  Pred. No. 1e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTS 9
              | |||:||:
Db         28 KLSQDIGTA 36


RESULT 45
Q4ZNQ2_PSESY
ID   Q4ZNQ2_PSESY PRELIMINARY;      PRT;   158 AA.
AC   Q4ZNQ2;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Prokaryotic transcription elongation factor GreA.
GN   ORFNames=Psyr_4190;
OS   Pseudomonas syringae pv. syringae B728a.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=205918;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=B728a;
RG   DOE Joint Genome Institute;
RA   Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Trong S.,
RA   Nolan M., Goltsman E., Thiel J., Malfatti S., Lapidus A., Detter J.C.,
RA   Land M., Richardson P.M., Kyrpides N.C., Ivanova N.;
RT   "Comparison of two complete genome sequences of Pseudomonas syringae
RT   pv. syringae B728a and pv. tomato DC3000.";
RL   Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=B728a;
RA   Loper J.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=B728a;
RA   Feil H., Feil W.S., Lindow S.E.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CP000075; AAY39220.1; -; Genomic_DNA.
DR   GO; GO:0003746; F:translation elongation factor activity; IEA.
KW   Elongation factor.
SQ   SEQUENCE   158 AA;  17418 MW;  4AA4027FCF5B87AD CRC64;

  Query Match             66.7%;  Score 34;  DB 2;  Length 158;
  Best Local Similarity   66.7%;  Pred. No. 1e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTS 9
              | |||:||:
Db         28 KLSQDIGTA 36


RESULT 46
Q4KIG6_PSEF5
ID   Q4KIG6_PSEF5 PRELIMINARY;      PRT;   158 AA.
AC   Q4KIG6;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
```

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DE   Transcription elongation factor GreA.
GN   Name=greA; ORFNames=PFL_0832;
OS   Pseudomonas fluorescens (strain Pf-5).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=220664;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Pf-5;
RX   PubMed=15980861; DOI=10.1038/nbt1110;
RA   Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
RA   Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA   Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA   Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
RA   Khouri H.M., Pierson E., Pierson L. III, Thomashow L., Loper J.;
RT   "Complete genome sequence of the plant commensal Pseudomonas
RT   fluorescens Pf-5.";
RL   Nat. Biotechnol. 23:873-878(2005).
DR   EMBL; CP000076; AAY96232.1; -; Genomic_DNA.
KW   Elongation factor.
SQ   SEQUENCE   158 AA;  17312 MW;  3395608644DB029C CRC64;

  Query Match             66.7%;  Score 34;  DB 2;  Length 158;
  Best Local Similarity   66.7%;  Pred. No. 1e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTS 9
              | |||:||:
Db         28 KLSQDIGTA 36


RESULT 47
Q7QCN2_ANOGA
ID   Q7QCN2_ANOGA PRELIMINARY;      PRT;   181 AA.
AC   Q7QCN2;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ENSANGP00000010766 (Fragment).
GN   ORFNames=ENSANGG00000008277;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RT   "Anopheles gambiae re-annotation.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008859; EAA07730.2; -; Genomic_DNA.
DR   InterPro; IPR000727; T_SNARE.
DR   PROSITE; PS50192; T_SNARE; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   181 AA;  19790 MW;  713EC114DF49F7C4 CRC64;

  Query Match             66.7%;  Score 34;  DB 2;  Length 181;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ASQDVGTSV 10
              |:||:|| |
Db        140 AAQDIGTKV 148


RESULT 48
Q8TU86_METAC
ID   Q8TU86_METAC PRELIMINARY;      PRT;   182 AA.
AC   Q8TU86;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Molybdenum cofactor biosynthesis protein B.
GN   Name=moaB; OrderedLocusNames=MA0187;
OS   Methanosarcina acetivorans.
OC   Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC   Methanosarcinaceae; Methanosarcina.
OX   NCBI_TaxID=2214;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C2A / ATCC 35395 / DSM 2834;
RX   MEDLINE=21929760; PubMed=11932238; DOI=10.1101/gr.223902;
RA   Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA   FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA   Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA   Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA   Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA   Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA   Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA   Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA   Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA   Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA   Metcalf W.W., Birren B.;
RT   "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT   and physiological diversity.";
RL   Genome Res. 12:532-542(2002).
DR   EMBL; AE010676; AAM03640.1; -; Genomic_DNA.
DR   HSSP; P30746; 1MKZ.
DR   GO; GO:0006777; P:Mo-molybdopterin cofactor biosynthesis; IEA.
DR   InterPro; IPR001453; MoCF_bios.
DR   Pfam; PF00994; MoCF_biosynth; 1.
DR   ProDom; PD002460; MoCF_biosynth; 1.
DR   TIGRFAMs; TIGR00177; molyb_syn; 1.
KW   Complete proteome.
SQ   SEQUENCE   182 AA;  19604 MW;  7D4E2014881B15F6 CRC64;

  Query Match             66.7%;  Score 34;  DB 2;  Length 182;
  Best Local Similarity   60.0%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              |: :|:||||
Db        127 KSLEDIGTSV 136


RESULT 49
Q82CD8_STRAW
ID   Q82CD8_STRAW PRELIMINARY;      PRT;   212 AA.
AC   Q82CD8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=SAV5412;
OS   Streptomyces avermitilis.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=33903;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX   MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA   Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA   Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA   Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT   "Genome sequence of an industrial microorganism Streptomyces
RT   avermitilis: deducing the ability of producing secondary
```

```
RT   metabolites.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
RX   MEDLINE=22608306; PubMed=12692562; DOI=10.1038/nbt820;
RA   Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA   Sakaki Y., Hattori M., Omura S.;
RT   "Complete genome sequence and comparative analysis of the industrial
RT   microorganism Streptomyces avermitilis.";
RL   Nat. Biotechnol. 21:526-531(2003).
DR   EMBL; BA000030; BAC73124.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   212 AA;  23457 MW;  27BBEB761841437E CRC64;

  Query Match             66.7%;  Score 34;  DB 2;  Length 212;
  Best Local Similarity   70.0%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              |  ||||| |
Db        144 KVGQDVGTPV 153


RESULT 50
Q5VNG3_ORYSA
ID   Q5VNG3_ORYSA PRELIMINARY;      PRT;   213 AA.
AC   Q5VNG3;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical protein P0491D10.18.
GN   Name=P0491D10.18;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
RT   clone:P0491D10.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP004791; BAD69016.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   213 AA;  22432 MW;  DA6D62DAA3ADBD27 CRC64;

  Query Match             66.7%;  Score 34;  DB 2;  Length 213;
  Best Local Similarity   70.0%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ASQDVGTSVA 11
              |  |||||:|
Db          8 AGDDVGTSMA 17


Search completed: March 23, 2006, 02:02:27
Job time : 141.773 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:05:22 ; Search time 23.8082 Seconds
(without alignments)
38.198 Million cell updates/sec

Title: US-10-755-382-20
Perfect score: 51
Sequence: 1 KASQDVGTSVA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	51	100.0	11	1	US-08-318-157B-20	Sequence 20, Appl
2	51	100.0	11	2	US-09-253-794-20	Sequence 20, Appl
3	51	100.0	106	1	US-08-318-157B-4	Sequence 4, Appli
4	51	100.0	106	1	US-08-318-157B-19	Sequence 19, Appl
5	51	100.0	106	2	US-09-253-794-4	Sequence 4, Appli
6	51	100.0	106	2	US-09-253-794-19	Sequence 19, Appl
7	44	86.3	107	2	US-08-838-682-19	Sequence 19, Appl
8	44	86.3	107	2	US-08-895-914-19	Sequence 19, Appl
9	44	86.3	107	2	US-09-357-710A-19	Sequence 19, Appl
10	44	86.3	107	2	US-09-357-707-19	Sequence 19, Appl
11	44	86.3	107	2	US-09-357-708-19	Sequence 19, Appl
12	44	86.3	249	1	US-08-797-689-18	Sequence 18, Appl
13	44	86.3	249	2	US-09-984-186-18	Sequence 18, Appl
14	43	84.3	11	1	US-08-602-725-6	Sequence 6, Appli
15	43	84.3	11	2	US-08-646-265A-118	Sequence 118, App
16	43	84.3	11	2	US-09-406-535-8	Sequence 8, Appli
17	43	84.3	11	2	US-09-508-413A-8	Sequence 8, Appli
18	43	84.3	11	2	US-10-226-795-18	Sequence 18, Appl
19	43	84.3	102	2	US-09-905-243-80	Sequence 80, Appl
20	43	84.3	104	2	US-09-508-413A-16	Sequence 16, Appl
21	43	84.3	107	2	US-08-767-128-32	Sequence 32, Appl
22	43	84.3	107	2	US-08-646-265A-130	Sequence 130, App
23	43	84.3	107	2	US-08-646-265A-131	Sequence 131, App
24	43	84.3	107	2	US-09-406-535-4	Sequence 4, Appli
25	43	84.3	107	2	US-09-905-243-77	Sequence 77, Appl
26	43	84.3	109	1	US-08-602-725-30	Sequence 30, Appl
27	43	84.3	110	1	US-08-602-725-2	Sequence 2, Appli
28	43	84.3	123	1	US-08-398-613A-20	Sequence 20, Appl
29	43	84.3	123	1	US-08-398-612A-20	Sequence 20, Appl
30	43	84.3	123	1	US-08-398-611A-20	Sequence 20, Appl
31	43	84.3	123	1	US-08-491-334A-20	Sequence 20, Appl
32	43	84.3	123	2	US-09-027-449-17	Sequence 17, Appl
33	43	84.3	123	2	US-08-804-444A-17	Sequence 17, Appl
34	43	84.3	123	2	US-09-026-985-17	Sequence 17, Appl
35	43	84.3	123	2	US-09-121-952A-17	Sequence 17, Appl
36	43	84.3	123	2	US-09-234-340A-17	Sequence 17, Appl
37	43	84.3	123	2	US-09-355-014-17	Sequence 17, Appl
38	43	84.3	126	2	US-08-646-265A-43	Sequence 43, Appl
39	43	84.3	126	2	US-08-646-265A-47	Sequence 47, Appl
40	43	84.3	126	2	US-08-646-265A-51	Sequence 51, Appl
41	43	84.3	126	2	US-08-646-265A-53	Sequence 53, Appl
42	43	84.3	126	2	US-08-646-265A-57	Sequence 57, Appl
43	43	84.3	126	2	US-08-646-265A-59	Sequence 59, Appl
44	43	84.3	126	2	US-08-646-265A-63	Sequence 63, Appl
45	43	84.3	126	2	US-08-646-265A-65	Sequence 65, Appl
46	43	84.3	126	2	US-08-646-265A-69	Sequence 69, Appl
47	43	84.3	126	2	US-08-646-265A-73	Sequence 73, Appl
48	43	84.3	126	2	US-08-646-265A-75	Sequence 75, Appl
49	43	84.3	126	2	US-08-646-265A-77	Sequence 77, Appl
50	43	84.3	126	2	US-08-646-265A-81	Sequence 81, Appl
51	43	84.3	126	2	US-08-646-265A-85	Sequence 85, Appl
52	43	84.3	126	2	US-08-646-265A-87	Sequence 87, Appl
53	43	84.3	126	2	US-08-646-265A-91	Sequence 91, Appl
54	43	84.3	127	2	US-08-646-265A-27	Sequence 27, Appl
55	43	84.3	132	1	US-08-602-725-38	Sequence 38, Appl
56	43	84.3	145	2	US-10-226-795-17	Sequence 17, Appl
57	43	84.3	237	1	US-08-398-612A-28	Sequence 28, Appl
58	43	84.3	237	1	US-08-398-611A-28	Sequence 28, Appl
59	43	84.3	237	1	US-08-491-334A-28	Sequence 28, Appl
60	43	84.3	237	2	US-09-027-449-25	Sequence 25, Appl
61	43	84.3	237	2	US-08-804-444A-25	Sequence 25, Appl
62	43	84.3	237	2	US-09-026-985-25	Sequence 25, Appl
63	43	84.3	237	2	US-09-121-952A-25	Sequence 25, Appl
64	43	84.3	237	2	US-09-234-340A-25	Sequence 25, Appl
65	43	84.3	237	2	US-09-355-014-25	Sequence 25, Appl
66	43	84.3	238	1	US-08-398-613A-28	Sequence 28, Appl
67	43	84.3	269	2	US-08-646-265A-109	Sequence 109, App
68	42	82.4	11	1	US-08-318-970B-14	Sequence 14, Appl
69	42	82.4	11	1	US-08-649-272A-1	Sequence 1, Appli
70	42	82.4	11	2	US-09-105-799-1	Sequence 1, Appli
71	42	82.4	11	2	US-09-269-921-3	Sequence 3, Appli
72	42	82.4	11	2	US-09-269-332-59	Sequence 59, Appl
73	42	82.4	107	1	US-08-491-845-4	Sequence 4, Appli
74	42	82.4	107	1	US-08-491-845-12	Sequence 12, Appl
75	42	82.4	109	1	US-07-934-373C-5	Sequence 5, Appli
76	42	82.4	109	2	US-08-437-642B-5	Sequence 5, Appli
77	42	82.4	109	2	US-08-146-206C-5	Sequence 5, Appli
78	42	82.4	109	2	US-09-705-686-5	Sequence 5, Appli
79	42	82.4	109	2	US-09-705-392A-5	Sequence 5, Appli
80	42	82.4	109	2	US-09-705-398-5	Sequence 5, Appli
81	42	82.4	109	4	PCT-US93-07832-5	Sequence 5, Appli
82	42	82.4	126	2	US-09-355-925-6	Sequence 6, Appli
83	42	82.4	126	2	US-09-269-921-106	Sequence 106, App
84	42	82.4	126	2	US-09-269-921-107	Sequence 107, App
85	42	82.4	131	2	US-09-269-921-104	Sequence 104, App
86	42	82.4	250	1	US-08-133-804-2	Sequence 2, Appli
87	42	82.4	250	1	US-08-461-184-8	Sequence 8, Appli
88	42	82.4	250	1	US-08-463-675-8	Sequence 8, Appli
89	42	82.4	250	1	US-08-464-589-8	Sequence 8, Appli
90	42	82.4	250	1	US-08-461-838-2	Sequence 2, Appli
91	42	82.4	250	1	US-08-461-386-2	Sequence 2, Appli
92	42	82.4	622	1	US-08-356-786-16	Sequence 16, Appl
93	40	78.4	106	2	US-09-189-129-4	Sequence 4, Appli
94	40	78.4	106	2	US-09-824-286-4	Sequence 4, Appli
95	40	78.4	107	1	US-07-634-278-50	Sequence 50, Appl
96	40	78.4	107	1	US-07-634-278-51	Sequence 51, Appl
97	40	78.4	107	1	US-08-477-728-50	Sequence 50, Appl
98	40	78.4	107	1	US-08-477-728-51	Sequence 51, Appl
99	40	78.4	107	1	US-08-474-040-50	Sequence 50, Appl
100	40	78.4	107	1	US-08-474-040-51	Sequence 51, Appl

101	40	78.4	107	1	US-08-487-200-50	Sequence 50, Appl
102	40	78.4	107	1	US-08-487-200-51	Sequence 51, Appl
103	40	78.4	107	2	US-08-484-537-50	Sequence 50, Appl
104	40	78.4	107	2	US-08-484-537-51	Sequence 51, Appl
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108	40	78.4	108	2	US-09-013-872-21	Sequence 21, Appl
109	40	78.4	108	2	US-09-184-198-20	Sequence 20, Appl
110	40	78.4	108	2	US-09-184-198-21	Sequence 21, Appl
111	40	78.4	108	2	US-09-633-653-20	Sequence 20, Appl
112	40	78.4	108	2	US-09-633-653-21	Sequence 21, Appl
113	39	76.5	11	1	US-08-318-970B-15	Sequence 15, Appl
114	39	76.5	107	1	US-07-934-373C-41	Sequence 41, Appl
115	39	76.5	107	1	US-07-934-373C-43	Sequence 43, Appl
116	39	76.5	107	2	US-08-437-642B-41	Sequence 41, Appl
117	39	76.5	107	2	US-08-437-642B-43	Sequence 43, Appl
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120	39	76.5	109	2	US-08-437-642B-1	Sequence 1, Appli
121	39	76.5	109	2	US-08-146-206C-1	Sequence 1, Appli
122	39	76.5	109	2	US-09-705-686-1	Sequence 1, Appli
123	39	76.5	109	2	US-09-705-392A-1	Sequence 1, Appli
124	39	76.5	109	2	US-09-705-392A-27	Sequence 27, Appl
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128	39	76.5	109	2	US-09-705-392A-35	Sequence 35, Appl
129	39	76.5	109	2	US-09-705-398-1	Sequence 1, Appli
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131	39	76.5	110	1	US-08-497-312-23	Sequence 23, Appl
132	39	76.5	110	1	US-08-497-312-25	Sequence 25, Appl
133	39	76.5	214	2	US-09-679-397-1	Sequence 1, Appli
134	39	76.5	214	2	US-09-680-148-1	Sequence 1, Appli
135	39	76.5	214	2	US-09-304-465A-1	Sequence 1, Appli
136	39	76.5	214	2	US-10-356-974-1	Sequence 1, Appli
137	39	76.5	237	1	US-08-463-587A-25	Sequence 25, Appl
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143	38	74.5	108	2	US-09-184-198-25	Sequence 25, Appl
144	38	74.5	108	2	US-09-633-653-25	Sequence 25, Appl
145	38	74.5	108	2	US-09-232-290-18	Sequence 18, Appl
146	37	72.5	105	2	US-09-065-059-17	Sequence 17, Appl
147	37	72.5	105	2	US-08-913-555-17	Sequence 17, Appl
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149	37	72.5	110	2	US-10-096-246A-13	Sequence 13, Appl
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151	37	72.5	239	2	US-10-092-246-33	Sequence 33, Appl
152	37	72.5	239	2	US-10-096-246A-32	Sequence 32, Appl
153	37	72.5	239	2	US-10-096-246A-33	Sequence 33, Appl
154	37	72.5	240	2	US-10-092-246-34	Sequence 34, Appl
155	37	72.5	240	2	US-10-092-246-35	Sequence 35, Appl
156	37	72.5	240	2	US-10-092-246-36	Sequence 36, Appl
157	37	72.5	240	2	US-10-092-246-37	Sequence 37, Appl
158	37	72.5	240	2	US-10-096-246A-34	Sequence 34, Appl
159	37	72.5	240	2	US-10-096-246A-35	Sequence 35, Appl
160	37	72.5	240	2	US-10-096-246A-36	Sequence 36, Appl
161	37	72.5	240	2	US-10-096-246A-37	Sequence 37, Appl
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163	37	72.5	244	2	US-09-940-391-1	Sequence 1, Appli
164	37	72.5	257	2	US-10-092-246-2	Sequence 2, Appli
165	37	72.5	257	2	US-10-096-246A-2	Sequence 2, Appli
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167	36	70.6	92	1	US-08-273-146-53	Sequence 53, Appl
168	36	70.6	96	1	US-08-276-852-113	Sequence 113, App
169	36	70.6	96	1	US-08-899-575-113	Sequence 113, App
170	36	70.6	96	1	US-08-899-575-113	Sequence 113, App
171	36	70.6	96	4	PCT-US95-08743-113	Sequence 113, App
172	36	70.6	107	1	US-08-888-366-14	Sequence 14, Appl
173	36	70.6	107	1	US-08-888-366-20	Sequence 20, Appl
174	36	70.6	107	1	US-08-888-366-26	Sequence 26, Appl
175	36	70.6	107	2	US-08-766-350B-47	Sequence 47, Appl
176	36	70.6	108	2	US-09-726-219A-267	Sequence 267, App
177	36	70.6	108	2	US-09-196-522-267	Sequence 267, App
178	36	70.6	109	1	US-08-713-939A-74	Sequence 74, Appl
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180	36	70.6	109	2	US-09-550-374-74	Sequence 74, Appl
181	36	70.6	109	2	US-09-943-906-74	Sequence 74, Appl
182	36	70.6	109	2	US-10-435-602-74	Sequence 74, Appl
183	36	70.6	143	1	US-08-653-402B-8	Sequence 8, Appli
184	36	70.6	231	2	US-09-248-796A-19015	Sequence 19015, A
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189	35	68.6	107	1	US-08-232-081B-40	Sequence 40, Appl
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192	35	68.6	107	2	US-08-525-539A-81	Sequence 81, Appl
193	35	68.6	107	2	US-09-648-067A-10	Sequence 10, Appl
194	35	68.6	107	2	US-09-648-067A-12	Sequence 12, Appl
195	35	68.6	107	2	US-09-602-812A-1	Sequence 1, Appli
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199	35	68.6	147	1	US-08-653-402B-4	Sequence 4, Appli
200	35	68.6	239	1	US-07-956-399-4	Sequence 4, Appli
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203	35	68.6	243	1	US-08-461-386-6	Sequence 6, Appli
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205	35	68.6	355	2	US-08-875-811-57	Sequence 57, Appl
206	35	68.6	374	2	US-09-710-279-1664	Sequence 1664, Ap
207	35	68.6	389	2	US-09-134-001C-3161	Sequence 3161, Ap
208	35	68.6	534	1	US-08-356-786-10	Sequence 10, Appl
209	35	68.6	801	2	US-09-710-279-90	Sequence 90, Appl
210	35	68.6	802	2	US-09-134-001C-3741	Sequence 3741, Ap
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213	34	66.7	126	2	US-08-479-285-28	Sequence 28, Appl
214	34	66.7	126	2	US-09-503-653A-28	Sequence 28, Appl
215	34	66.7	241	1	US-08-235-838-5	Sequence 5, Appli
216	34	66.7	241	1	US-08-465-473B-5	Sequence 5, Appli
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220	34	66.7	617	2	US-08-840-713-37	Sequence 37, Appl
221	34	66.7	637	1	US-08-235-838-14	Sequence 14, Appl
222	34	66.7	637	1	US-08-465-473B-14	Sequence 14, Appl
223	34	66.7	711	1	US-08-235-838-7	Sequence 7, Appli
224	34	66.7	711	1	US-08-465-473B-7	Sequence 7, Appli
225	33	64.7	11	1	US-08-476-176B-53	Sequence 53, Appl
226	33	64.7	11	2	US-08-127-721A-53	Sequence 53, Appl
227	33	64.7	11	2	US-08-485-246A-53	Sequence 53, Appl
228	33	64.7	11	2	US-09-798-689-32	Sequence 32, Appl
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236	33	64.7	107	2	US-08-554-840-4	Sequence 4, Appli
237	33	64.7	107	2	US-08-127-721A-4	Sequence 4, Appli
238	33	64.7	107	2	US-08-485-246A-4	Sequence 4, Appli
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241	33	64.7	107	2	US-08-925-339-3	Sequence 3, Appli
242	33	64.7	107	2	US-08-925-339-4	Sequence 4, Appli
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244	33	64.7	107	2	US-09-332-595-2	Sequence 2, Appli
245	33	64.7	107	2	US-09-332-595-3	Sequence 3, Appli
246	33	64.7	107	2	US-09-332-595-4	Sequence 4, Appli

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251	33	64.7	124	2	US-09-802-096-4	Sequence 4, Appli
252	33	64.7	124	2	US-09-802-077-4	Sequence 4, Appli
253	33	64.7	124	2	US-09-925-179-4	Sequence 4, Appli
254	33	64.7	126	1	US-08-202-047-13	Sequence 13, Appl
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257	33	64.7	126	1	US-08-202-047-19	Sequence 19, Appl
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259	33	64.7	126	2	US-08-964-690-15	Sequence 15, Appl
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263	33	64.7	127	1	US-08-476-176B-8	Sequence 8, Appli
264	33	64.7	127	1	US-08-476-176B-10	Sequence 10, Appl
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266	33	64.7	127	2	US-08-127-721A-8	Sequence 8, Appli
267	33	64.7	127	2	US-08-127-721A-10	Sequence 10, Appl
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269	33	64.7	127	2	US-08-485-246A-8	Sequence 8, Appli
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272	33	64.7	131	1	US-08-822-028-14	Sequence 14, Appl
273	33	64.7	131	2	US-08-964-690-5	Sequence 5, Appli
274	33	64.7	131	2	US-08-479-285-14	Sequence 14, Appl
275	33	64.7	131	2	US-09-503-653A-14	Sequence 14, Appl
276	33	64.7	234	2	US-09-049-672A-6	Sequence 6, Appli
277	33	64.7	240	1	US-08-800-198-8	Sequence 8, Appli
278	33	64.7	240	2	US-09-296-595-8	Sequence 8, Appli
279	33	64.7	283	2	US-09-952-689-5	Sequence 5, Appli
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282	33	64.7	572	1	US-08-185-949B-81	Sequence 81, Appl
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285	32	62.7	14	1	US-08-837-941-26	Sequence 26, Appl
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288	32	62.7	95	2	US-09-036-579-72	Sequence 72, Appl
289	32	62.7	95	2	US-09-550-374-72	Sequence 72, Appl
290	32	62.7	95	2	US-09-943-906-72	Sequence 72, Appl
291	32	62.7	95	2	US-10-435-602-72	Sequence 72, Appl
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293	32	62.7	108	2	US-08-752-693A-2	Sequence 2, Appli
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296	32	62.7	109	2	US-09-550-374-73	Sequence 73, Appl
297	32	62.7	109	2	US-09-943-906-73	Sequence 73, Appl
298	32	62.7	109	2	US-10-435-602-73	Sequence 73, Appl
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302	32	62.7	132	1	US-08-452-164A-55	Sequence 55, Appl
303	32	62.7	132	2	US-08-976-183A-36	Sequence 36, Appl
304	32	62.7	132	2	US-08-976-183A-37	Sequence 37, Appl
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309	32	62.7	237	1	US-08-926-789-16	Sequence 16, Appl
310	32	62.7	241	1	US-08-224-591-18	Sequence 18, Appl
311	32	62.7	241	1	US-08-926-789-18	Sequence 18, Appl
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314	32	62.7	245	2	US-09-956-087-5	Sequence 5, Appli
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317	32	62.7	265	2	US-09-420-592A-5	Sequence 5, Appli
318	32	62.7	265	2	US-09-985-442-5	Sequence 5, Appli
319	32	62.7	265	2	US-09-983-580-5	Sequence 5, Appli
320	32	62.7	438	2	US-10-104-047-3166	Sequence 3166, Ap
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322	32	62.7	466	2	US-09-902-540-11407	Sequence 11407, A
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324	32	62.7	471	2	US-09-970-532-2	Sequence 2, Appli
325	32	62.7	490	2	US-09-949-016-6218	Sequence 6218, Ap
326	32	62.7	610	2	US-09-902-540-13312	Sequence 13312, A
327	31	60.8	11	2	US-09-192-854-170	Sequence 170, App
328	31	60.8	11	2	US-09-511-939-298	Sequence 298, App
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330	31	60.8	25	1	US-08-997-362-17	Sequence 17, Appl
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332	31	60.8	25	2	US-09-095-855-17	Sequence 17, Appl
333	31	60.8	25	2	US-08-705-347A-17	Sequence 17, Appl
334	31	60.8	25	2	US-09-324-542-17	Sequence 17, Appl
335	31	60.8	25	2	US-09-205-426-17	Sequence 17, Appl
336	31	60.8	25	2	US-09-200-643-17	Sequence 17, Appl
337	31	60.8	106	2	US-08-635-109-8	Sequence 8, Appli
338	31	60.8	106	2	US-08-844-215-11	Sequence 11, Appl
339	31	60.8	107	1	US-08-888-366-22	Sequence 22, Appl
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343	31	60.8	145	2	US-08-766-350B-2	Sequence 2, Appli
344	31	60.8	145	2	US-08-766-350B-58	Sequence 58, Appl
345	31	60.8	166	1	US-08-997-080-109	Sequence 109, App
346	31	60.8	166	1	US-08-997-362-109	Sequence 109, App
347	31	60.8	166	2	US-09-095-855-109	Sequence 109, App
348	31	60.8	166	2	US-09-324-542-109	Sequence 109, App
349	31	60.8	166	2	US-09-205-426-109	Sequence 109, App
350	31	60.8	239	2	US-09-248-796A-20397	Sequence 20397, A
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352	31	60.8	359	2	US-09-646-028-16	Sequence 16, Appl
353	31	60.8	361	2	US-09-646-028-13	Sequence 13, Appl
354	31	60.8	374	2	US-09-646-028-15	Sequence 15, Appl
355	31	60.8	607	2	US-09-248-796A-17281	Sequence 17281, A
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358	31	60.8	1503	2	US-09-949-016-6341	Sequence 6341, Ap
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362	30	58.8	22	1	US-08-837-941-6	Sequence 6, Appli
363	30	58.8	59	2	US-09-621-976-6569	Sequence 6569, Ap
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369	30	58.8	95	2	US-10-194-975-92	Sequence 92, Appl
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374	30	58.8	107	2	US-09-133-119-3	Sequence 3, Appli
375	30	58.8	107	2	US-08-192-093A-3	Sequence 3, Appli
376	30	58.8	107	2	US-08-695-692B-6	Sequence 6, Appli
377	30	58.8	107	2	US-09-647-468-147	Sequence 147, App
378	30	58.8	107	2	US-09-756-301B-3	Sequence 3, Appli
379	30	58.8	107	2	US-09-756-398B-3	Sequence 3, Appli
380	30	58.8	108	2	US-09-155-106-22	Sequence 22, Appl
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382	30	58.8	108	2	US-09-155-106-24	Sequence 24, Appl
383	30	58.8	108	2	US-09-155-106-28	Sequence 28, Appl
384	30	58.8	108	2	US-09-155-106-30	Sequence 30, Appl
385	30	58.8	129	2	US-09-647-468-161	Sequence 161, App
386	30	58.8	155	2	US-09-472-087-20	Sequence 20, Appl
387	30	58.8	155	2	US-09-472-087-112	Sequence 112, App
388	30	58.8	163	2	US-09-107-532A-4269	Sequence 4269, Ap
389	30	58.8	190	2	US-09-248-796A-17539	Sequence 17539, A
390	30	58.8	295	2	US-09-799-345-2	Sequence 2, Appli
391	30	58.8	295	2	US-09-962-276-2	Sequence 2, Appli
392	30	58.8	295	2	US-10-441-282-2	Sequence 2, Appli

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396	30	58.8	364	2	US-09-964-956-64	Sequence 64, Appl
397	30	58.8	377	2	US-09-107-532A-6995	Sequence 6995, Ap
398	30	58.8	424	2	US-09-489-039A-8695	Sequence 8695, Ap
399	30	58.8	482	2	US-09-902-540-16520	Sequence 16520, A
400	30	58.8	506	2	US-09-538-092-117	Sequence 117, App
401	30	58.8	506	2	US-09-487-558B-90	Sequence 90, Appl
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406	30	58.8	522	2	US-09-502-264-10	Sequence 10, Appl
407	30	58.8	523	2	US-09-549-519-35	Sequence 35, Appl
408	30	58.8	604	2	US-09-197-814-3	Sequence 3, Appli
409	30	58.8	604	2	US-09-920-581-3	Sequence 3, Appli
410	30	58.8	643	2	US-09-543-681A-6345	Sequence 6345, Ap
411	30	58.8	666	2	US-09-771-161A-136	Sequence 136, App
412	30	58.8	772	2	US-09-134-000C-6491	Sequence 6491, Ap
413	30	58.8	913	2	US-09-252-991A-22127	Sequence 22127, A
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416	30	58.8	983	1	US-08-162-809-16	Sequence 16, Appl
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422	30	58.8	983	2	US-09-771-161A-227	Sequence 227, App
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431	29	56.9	11	2	US-09-511-939-316	Sequence 316, App
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436	29	56.9	107	2	US-09-848-798-179	Sequence 179, App
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463	29	56.9	265	2	US-09-962-276-5	Sequence 5, Appli
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466	29	56.9	265	2	US-10-441-282-5	Sequence 5, Appli
467	29	56.9	265	2	US-10-441-282-6	Sequence 6, Appli
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486	29	56.9	466	2	US-10-104-047-2410	Sequence 2410, Ap
487	29	56.9	473	2	US-09-710-279-60	Sequence 60, Appl
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516	29	56.9	853	2	US-08-446-939B-6	Sequence 6, Appli
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522	29	56.9	928	1	US-08-440-815-2	Sequence 2, Appli
523	29	56.9	928	2	US-08-486-449-2	Sequence 2, Appli
524	29	56.9	928	2	US-08-578-684-2	Sequence 2, Appli
525	29	56.9	953	2	US-09-751-389-7	Sequence 7, Appli
526	29	56.9	967	1	US-08-449-645A-30	Sequence 30, Appl
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530	29	56.9	976	1	US-08-702-367A-18	Sequence 18, Appl
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534	29	56.9	986	1	US-08-673-789-3	Sequence 3, Appli
535	29	56.9	986	1	US-08-449-645A-15	Sequence 15, Appl
536	29	56.9	986	1	US-08-702-367A-15	Sequence 15, Appl
537	29	56.9	986	4	PCT-US95-04681-15	Sequence 15, Appl
538	29	56.9	991	1	US-08-449-645A-13	Sequence 13, Appl

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542	29	56.9	994	2	US-08-368-776A-12	Sequence 12, Appl
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545	29	56.9	998	1	US-08-702-367A-17	Sequence 17, Appl
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547	29	56.9	998	2	US-09-949-016-6501	Sequence 6501, Ap
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551	29	56.9	1005	2	US-09-949-016-9901	Sequence 9901, Ap
552	29	56.9	1013	2	US-09-949-016-7991	Sequence 7991, Ap
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555	29	56.9	1104	2	US-08-446-648-36	Sequence 36, Appl
556	29	56.9	1104	2	US-09-982-610-36	Sequence 36, Appl
557	29	56.9	1104	4	PCT-US95-04228-36	Sequence 36, Appl
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561	29	56.9	1555	2	US-09-949-016-6950	Sequence 6950, Ap
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573	28	54.9	14	1	US-08-321-668-22	Sequence 22, Appl
574	28	54.9	14	1	US-08-321-668-23	Sequence 23, Appl
575	28	54.9	14	1	US-08-321-668-24	Sequence 24, Appl
576	28	54.9	14	1	US-08-321-668-27	Sequence 27, Appl
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582	28	54.9	14	1	US-08-321-668-37	Sequence 37, Appl
583	28	54.9	14	1	US-08-321-668-38	Sequence 38, Appl
584	28	54.9	14	1	US-08-321-668-39	Sequence 39, Appl
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594	28	54.9	14	1	US-08-837-941-36	Sequence 36, Appl
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597	28	54.9	14	1	US-08-837-941-39	Sequence 39, Appl
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599	28	54.9	18	2	US-09-556-605-54	Sequence 54, Appl
600	28	54.9	19	2	US-09-556-605-53	Sequence 53, Appl
601	28	54.9	20	2	US-09-556-605-17	Sequence 17, Appl
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606	28	54.9	78	2	US-10-178-213-86	Sequence 86, Appl
607	28	54.9	79	2	US-09-774-639-288	Sequence 288, App
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614	28	54.9	106	1	US-08-950-660-4	Sequence 4, Appli
615	28	54.9	106	2	US-09-157-452B-4	Sequence 4, Appli
616	28	54.9	106	2	US-08-454-899G-10	Sequence 10, Appl
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620	28	54.9	107	1	US-08-488-113B-123	Sequence 123, App
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622	28	54.9	107	1	US-08-107-669D-26	Sequence 26, Appl
623	28	54.9	107	1	US-08-472-788A-26	Sequence 26, Appl
624	28	54.9	107	1	US-08-477-531B-26	Sequence 26, Appl
625	28	54.9	107	1	US-08-646-360-123	Sequence 123, App
626	28	54.9	107	1	US-08-082-842A-26	Sequence 26, Appl
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628	28	54.9	107	2	US-09-136-389-123	Sequence 123, App
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630	28	54.9	107	2	US-09-711-485-123	Sequence 123, App
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632	28	54.9	107	2	US-09-647-468-146	Sequence 146, App
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636	28	54.9	111	1	US-08-477-728-47	Sequence 47, Appl
637	28	54.9	111	1	US-08-474-040-46	Sequence 46, Appl
638	28	54.9	111	1	US-08-474-040-47	Sequence 47, Appl
639	28	54.9	111	1	US-08-487-200-46	Sequence 46, Appl
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645	28	54.9	124	2	US-08-454-899G-71	Sequence 71, Appl
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647	28	54.9	125	2	US-09-647-468-160	Sequence 160, App
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649	28	54.9	128	1	US-08-463-128-10	Sequence 10, Appl
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652	28	54.9	128	1	US-08-436-339A-6	Sequence 6, Appli
653	28	54.9	128	1	US-08-436-339A-10	Sequence 10, Appl
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655	28	54.9	128	2	US-08-454-899G-63	Sequence 63, Appl
656	28	54.9	128	2	US-08-454-899G-67	Sequence 67, Appl
657	28	54.9	129	2	US-09-556-605-2	Sequence 2, Appli
658	28	54.9	133	2	US-09-107-433-3161	Sequence 3161, Ap
659	28	54.9	146	2	US-09-540-236-3232	Sequence 3232, Ap
660	28	54.9	152	2	US-09-621-976-4568	Sequence 4568, Ap
661	28	54.9	167	2	US-09-248-796A-15429	Sequence 15429, A
662	28	54.9	181	2	US-09-513-007-4	Sequence 4, Appli
663	28	54.9	181	2	US-09-134-000C-4633	Sequence 4633, Ap
664	28	54.9	181	2	US-09-970-532-4	Sequence 4, Appli
665	28	54.9	188	2	US-09-603-052-4	Sequence 4, Appli
666	28	54.9	216	2	US-09-510-252-4	Sequence 4, Appli
667	28	54.9	223	2	US-09-710-279-2824	Sequence 2824, Ap
668	28	54.9	226	2	US-09-134-001C-5247	Sequence 5247, Ap
669	28	54.9	237	2	US-09-270-767-41826	Sequence 41826, A
670	28	54.9	266	2	US-09-602-787A-174	Sequence 174, App
671	28	54.9	280	2	US-08-974-022-46	Sequence 46, Appl
672	28	54.9	280	2	US-08-795-445A-46	Sequence 46, Appl
673	28	54.9	280	2	US-08-795-447A-46	Sequence 46, Appl
674	28	54.9	280	2	US-08-974-186-46	Sequence 46, Appl
675	28	54.9	280	2	US-08-795-446B-46	Sequence 46, Appl
676	28	54.9	280	2	US-08-706-945D-132	Sequence 132, App
677	28	54.9	280	2	US-08-577-788C-46	Sequence 46, Appl
678	28	54.9	308	2	US-09-252-991A-30126	Sequence 30126, A
679	28	54.9	311	2	US-09-252-991A-16719	Sequence 16719, A
680	28	54.9	312	2	US-09-583-110-5178	Sequence 5178, Ap
681	28	54.9	313	1	US-08-592-411-15	Sequence 15, Appl
682	28	54.9	314	1	US-08-592-411-17	Sequence 17, Appl
683	28	54.9	314	2	US-09-489-039A-9896	Sequence 9896, Ap
684	28	54.9	322	2	US-09-326-806-3	Sequence 3, Appli

685	28	54.9	341	2	US-09-501-612A-2	Sequence 2, Appli
686	28	54.9	341	2	US-09-328-352-5092	Sequence 5092, Ap
687	28	54.9	341	2	US-09-543-681A-7606	Sequence 7606, Ap
688	28	54.9	341	2	US-10-336-491-2	Sequence 2, Appli
689	28	54.9	342	2	US-09-107-433-3723	Sequence 3723, Ap
690	28	54.9	344	2	US-09-902-540-14026	Sequence 14026, A
691	28	54.9	355	2	US-09-252-991A-22494	Sequence 22494, A
692	28	54.9	365	2	US-09-902-540-10440	Sequence 10440, A
693	28	54.9	375	2	US-09-323-872A-33	Sequence 33, Appl
694	28	54.9	375	2	US-09-072-433-18	Sequence 18, Appl
695	28	54.9	375	2	US-09-710-279-3200	Sequence 3200, Ap
696	28	54.9	380	1	US-08-420-235B-5	Sequence 5, Appli
697	28	54.9	380	2	US-08-793-624-5	Sequence 5, Appli
698	28	54.9	380	4	PCT-US95-10194-5	Sequence 5, Appli
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708	28	54.9	429	2	US-09-107-433-4300	Sequence 4300, Ap
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716	28	54.9	455	1	US-08-837-941-2	Sequence 2, Appli
717	28	54.9	455	1	US-08-126-016-2	Sequence 2, Appli
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724	28	54.9	455	2	US-09-573-986-3	Sequence 3, Appli
725	28	54.9	455	2	US-09-027-287-3	Sequence 3, Appli
726	28	54.9	455	2	US-09-252-656B-3	Sequence 3, Appli
727	28	54.9	455	2	US-08-406-824A-4	Sequence 4, Appli
728	28	54.9	455	2	US-09-523-323-3	Sequence 3, Appli
729	28	54.9	455	2	US-09-756-854-5	Sequence 5, Appli
730	28	54.9	455	2	US-09-557-908-5	Sequence 5, Appli
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741	28	54.9	462	2	US-09-991-326-7	Sequence 7, Appli
742	28	54.9	462	2	US-09-605-703B-2644	Sequence 2644, Ap
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746	28	54.9	465	2	US-09-957-005-11	Sequence 11, Appl
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757	28	54.9	491	1	US-08-390-517A-3	Sequence 3, Appli
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763	28	54.9	528	2	US-09-949-016-7126	Sequence 7126, Ap
764	28	54.9	528	2	US-09-949-016-7127	Sequence 7127, Ap
765	28	54.9	528	2	US-09-949-016-7128	Sequence 7128, Ap
766	28	54.9	528	2	US-09-949-016-7129	Sequence 7129, Ap
767	28	54.9	542	2	US-09-198-452A-1003	Sequence 1003, Ap
768	28	54.9	543	2	US-09-938-956-7	Sequence 7, Appli
769	28	54.9	547	2	US-09-438-185A-933	Sequence 933, App
770	28	54.9	547	2	US-10-104-047-3096	Sequence 3096, Ap
771	28	54.9	548	2	US-09-538-092-1058	Sequence 1058, Ap
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774	28	54.9	553	2	US-09-066-544-2	Sequence 2, Appli
775	28	54.9	553	2	US-08-951-086-2	Sequence 2, Appli
776	28	54.9	553	2	US-09-430-669-2	Sequence 2, Appli
777	28	54.9	554	2	US-09-222-938A-22	Sequence 22, Appl
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779	28	54.9	561	2	US-09-902-540-16262	Sequence 16262, A
780	28	54.9	586	2	US-09-134-001C-4456	Sequence 4456, Ap
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782	28	54.9	599	2	US-09-172-339-2	Sequence 2, Appli
783	28	54.9	599	2	US-09-398-395A-22	Sequence 22, Appl
784	28	54.9	599	2	US-09-887-586A-22	Sequence 22, Appl
785	28	54.9	599	2	US-09-895-752-22	Sequence 22, Appl
786	28	54.9	599	2	US-09-903-012B-22	Sequence 22, Appl
787	28	54.9	599	2	US-09-900-797-22	Sequence 22, Appl
788	28	54.9	599	2	US-09-893-820-22	Sequence 22, Appl
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791	28	54.9	608	2	US-09-949-016-11150	Sequence 11150, A
792	28	54.9	608	2	US-09-949-016-11151	Sequence 11151, A
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794	28	54.9	621	2	US-09-248-796A-19368	Sequence 19368, A
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803	28	54.9	666	2	US-09-228-986-68	Sequence 68, Appl
804	28	54.9	666	2	US-10-101-464A-68	Sequence 68, Appl
805	28	54.9	709	2	US-09-583-110-5113	Sequence 5113, Ap
806	28	54.9	747	2	US-09-724-864-36	Sequence 36, Appl
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808	28	54.9	807	2	US-09-252-991A-18831	Sequence 18831, A
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812	28	54.9	826	2	US-09-248-796A-18843	Sequence 18843, A
813	28	54.9	854	2	US-09-134-000C-4673	Sequence 4673, Ap
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815	28	54.9	870	2	US-09-543-681A-5184	Sequence 5184, Ap
816	28	54.9	903	2	US-09-252-991A-17937	Sequence 17937, A
817	28	54.9	909	2	US-09-013-895A-4	Sequence 4, Appli
818	28	54.9	909	2	US-09-448-868-4	Sequence 4, Appli
819	28	54.9	909	2	US-10-226-296-4	Sequence 4, Appli
820	28	54.9	934	1	US-08-215-805A-80	Sequence 80, Appl
821	28	54.9	942	2	US-10-004-542-2	Sequence 2, Appli
822	28	54.9	942	2	US-10-430-797-2	Sequence 2, Appli
823	28	54.9	948	1	US-08-469-537A-101	Sequence 101, App
824	28	54.9	948	2	US-09-751-389-5	Sequence 5, Appli
825	28	54.9	977	2	US-09-302-812-2	Sequence 2, Appli
826	28	54.9	977	2	US-09-511-477-2	Sequence 2, Appli
827	28	54.9	977	2	US-09-511-507-2	Sequence 2, Appli
828	28	54.9	977	2	US-09-973-451-2	Sequence 2, Appli
829	28	54.9	1033	2	US-09-252-991A-20611	Sequence 20611, A
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833	28	54.9	1098	2	US-08-726-214-10	Sequence 10, Appl
834	28	54.9	1196	2	US-09-107-532A-3944	Sequence 3944, Ap
835	28	54.9	1621	1	US-08-242-677-2	Sequence 2, Appli
836	28	54.9	1670	2	US-09-902-540-15506	Sequence 15506, A
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839	28	54.9	1938	2	US-09-949-016-6609	Sequence 6609, Ap
840	28	54.9	2035	1	US-08-046-585-5	Sequence 5, Appli
841	28	54.9	2035	1	US-08-393-703-5	Sequence 5, Appli
842	28	54.9	2035	4	PCT-US93-11721-5	Sequence 5, Appli
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844	28	54.9	2137	2	US-09-134-001C-4463	Sequence 4463, Ap
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846	28	54.9	2285	2	US-09-932-183A-2	Sequence 2, Appli
847	28	54.9	2410	2	US-09-270-767-44775	Sequence 44775, A
848	28	54.9	3852	2	US-10-025-225-4	Sequence 4, Appli
849	28	54.9	4585	2	US-10-025-225-6	Sequence 6, Appli
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854	27	52.9	11	1	US-08-053-451B-66	Sequence 66, Appl
855	27	52.9	11	1	US-08-053-451B-75	Sequence 75, Appl
856	27	52.9	11	2	US-09-647-468-136	Sequence 136, App
857	27	52.9	11	2	US-09-798-058-8	Sequence 8, Appli
858	27	52.9	14	1	US-08-321-668-30	Sequence 30, Appl
859	27	52.9	14	1	US-08-837-941-30	Sequence 30, Appl
860	27	52.9	20	1	US-08-053-451B-163	Sequence 163, App
861	27	52.9	28	2	US-09-270-767-60561	Sequence 60561, A
862	27	52.9	34	1	US-08-321-668-5	Sequence 5, Appli
863	27	52.9	34	1	US-08-837-941-5	Sequence 5, Appli
864	27	52.9	43	2	US-08-675-499A-10	Sequence 10, Appl
865	27	52.9	43	2	US-08-812-008-10	Sequence 10, Appl
866	27	52.9	47	2	US-09-227-357-656	Sequence 656, App
867	27	52.9	47	2	US-09-973-278-615	Sequence 615, App
868	27	52.9	56	1	US-08-162-102C-39	Sequence 39, Appl
869	27	52.9	61	2	US-09-583-110-4245	Sequence 4245, Ap
870	27	52.9	61	2	US-09-107-433-3952	Sequence 3952, Ap
871	27	52.9	68	2	US-09-107-532A-4596	Sequence 4596, Ap
872	27	52.9	72	2	US-09-227-357-655	Sequence 655, App
873	27	52.9	72	2	US-09-973-278-614	Sequence 614, App
874	27	52.9	73	2	US-09-134-001C-5305	Sequence 5305, Ap
875	27	52.9	76	2	US-09-248-796A-24712	Sequence 24712, A
876	27	52.9	83	2	US-09-270-767-43992	Sequence 43992, A
877	27	52.9	92	2	US-09-134-000C-3938	Sequence 3938, Ap
878	27	52.9	92	2	US-09-311-021-90	Sequence 90, Appl
879	27	52.9	93	2	US-09-288-143-107	Sequence 107, App
880	27	52.9	95	2	US-10-194-975-90	Sequence 90, Appl
881	27	52.9	97	2	US-09-540-236-2688	Sequence 2688, Ap
882	27	52.9	98	2	US-09-248-796A-24649	Sequence 24649, A
883	27	52.9	103	2	US-09-107-532A-4889	Sequence 4889, Ap
884	27	52.9	104	2	US-09-248-796A-26143	Sequence 26143, A
885	27	52.9	107	1	US-07-634-278-103	Sequence 103, App
886	27	52.9	107	1	US-08-477-728-103	Sequence 103, App
887	27	52.9	107	1	US-08-474-040-103	Sequence 103, App
888	27	52.9	107	1	US-08-487-200-103	Sequence 103, App
889	27	52.9	107	1	US-08-480-434-73	Sequence 73, Appl
890	27	52.9	107	1	US-08-290-592E-20	Sequence 20, Appl
891	27	52.9	107	1	US-08-290-592E-21	Sequence 21, Appl
892	27	52.9	107	1	US-08-053-451B-73	Sequence 73, Appl
893	27	52.9	107	1	US-08-053-451B-174	Sequence 174, App
894	27	52.9	107	2	US-08-484-537-103	Sequence 103, App
895	27	52.9	107	2	US-09-647-468-93	Sequence 93, Appl
896	27	52.9	107	2	US-09-647-468-99	Sequence 99, Appl
897	27	52.9	107	2	US-09-647-468-101	Sequence 101, App
898	27	52.9	107	2	US-09-647-468-107	Sequence 107, App
899	27	52.9	107	2	US-09-647-468-109	Sequence 109, App
900	27	52.9	107	2	US-09-647-468-148	Sequence 148, App
901	27	52.9	107	2	US-09-902-540-12267	Sequence 12267, A
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903	27	52.9	107	4	PCT-US95-10053-18	Sequence 18, Appl
904	27	52.9	107	4	PCT-US96-09448-20	Sequence 20, Appl
905	27	52.9	107	4	PCT-US96-09448-21	Sequence 21, Appl
906	27	52.9	109	1	US-08-162-102C-24	Sequence 24, Appl
907	27	52.9	109	2	US-08-920-100B-24	Sequence 24, Appl
908	27	52.9	109	2	US-09-798-058-4	Sequence 4, Appli
909	27	52.9	109	4	PCT-US93-08786-24	Sequence 24, Appl
910	27	52.9	110	2	US-09-949-016-7902	Sequence 7902, Ap
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912	27	52.9	116	2	US-10-104-047-2329	Sequence 2329, Ap
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914	27	52.9	121	2	US-09-393-634-70	Sequence 70, Appl
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917	27	52.9	127	2	US-09-647-468-162	Sequence 162, App
918	27	52.9	127	2	US-09-647-468-179	Sequence 179, App
919	27	52.9	127	2	US-09-647-468-180	Sequence 180, App
920	27	52.9	127	2	US-09-647-468-181	Sequence 181, App
921	27	52.9	127	2	US-09-647-468-182	Sequence 182, App
922	27	52.9	127	2	US-09-647-468-183	Sequence 183, App
923	27	52.9	127	2	US-09-513-999C-7831	Sequence 7831, Ap
924	27	52.9	127	2	US-09-513-999C-7832	Sequence 7832, Ap
925	27	52.9	127	4	PCT-US95-15716-4	Sequence 4, Appli
926	27	52.9	128	2	US-09-450-520A-6	Sequence 6, Appli
927	27	52.9	134	2	US-09-621-976-5076	Sequence 5076, Ap
928	27	52.9	136	1	US-07-634-278-99	Sequence 99, Appl
929	27	52.9	136	1	US-08-477-728-99	Sequence 99, Appl
930	27	52.9	136	1	US-08-474-040-99	Sequence 99, Appl
931	27	52.9	136	1	US-08-487-200-99	Sequence 99, Appl
932	27	52.9	136	2	US-08-484-537-99	Sequence 99, Appl
933	27	52.9	138	1	US-08-480-434-63	Sequence 63, Appl
934	27	52.9	138	1	US-08-053-451B-63	Sequence 63, Appl
935	27	52.9	139	2	US-09-270-767-45065	Sequence 45065, A
936	27	52.9	142	1	US-08-579-940-2	Sequence 2, Appli
937	27	52.9	142	2	US-08-838-692-4	Sequence 4, Appli
938	27	52.9	145	2	US-09-270-767-57695	Sequence 57695, A
939	27	52.9	151	2	US-10-001-887-96	Sequence 96, Appl
940	27	52.9	152	2	US-09-270-767-46868	Sequence 46868, A
941	27	52.9	165	2	US-09-252-991A-24061	Sequence 24061, A
942	27	52.9	178	2	US-09-328-352-4296	Sequence 4296, Ap
943	27	52.9	181	2	US-09-134-000C-3801	Sequence 3801, Ap
944	27	52.9	194	2	US-09-215-221-52	Sequence 52, Appl
945	27	52.9	194	2	US-09-516-914-9	Sequence 9, Appli
946	27	52.9	197	2	US-09-902-540-12160	Sequence 12160, A
947	27	52.9	199	2	US-09-489-039A-8835	Sequence 8835, Ap
948	27	52.9	200	2	US-09-902-540-15542	Sequence 15542, A
949	27	52.9	205	2	US-10-172-527A-23	Sequence 23, Appl
950	27	52.9	209	2	US-09-605-703B-2320	Sequence 2320, Ap
951	27	52.9	214	2	US-09-543-681A-6504	Sequence 6504, Ap
952	27	52.9	215	1	US-08-737-129A-8	Sequence 8, Appli
953	27	52.9	222	2	US-09-148-545-135	Sequence 135, App
954	27	52.9	222	2	US-09-902-540-10672	Sequence 10672, A
955	27	52.9	222	2	US-09-621-011-135	Sequence 135, App
956	27	52.9	229	2	US-09-248-796A-20250	Sequence 20250, A
957	27	52.9	234	2	US-09-049-672A-2	Sequence 2, Appli
958	27	52.9	237	2	US-08-808-148-3	Sequence 3, Appli
959	27	52.9	237	2	US-09-976-594-216	Sequence 216, App
960	27	52.9	240	2	US-09-902-540-11028	Sequence 11028, A
961	27	52.9	242	2	US-09-543-681A-5113	Sequence 5113, Ap
962	27	52.9	242	2	US-09-134-000C-5008	Sequence 5008, Ap
963	27	52.9	244	2	US-09-489-039A-14079	Sequence 14079, A
964	27	52.9	246	2	US-09-238-481-2	Sequence 2, Appli
965	27	52.9	246	2	US-09-572-810A-2	Sequence 2, Appli
966	27	52.9	246	2	US-10-089-019-8	Sequence 8, Appli
967	27	52.9	248	2	US-09-305-390-5	Sequence 5, Appli
968	27	52.9	248	2	US-10-070-634-14	Sequence 14, Appl
969	27	52.9	249	2	US-09-134-001C-4825	Sequence 4825, Ap
970	27	52.9	250	2	US-09-248-796A-22986	Sequence 22986, A
971	27	52.9	253	2	US-09-248-796A-15774	Sequence 15774, A
972	27	52.9	254	2	US-09-252-991A-20551	Sequence 20551, A
973	27	52.9	255	2	US-09-543-681A-4771	Sequence 4771, Ap
974	27	52.9	258	2	US-09-248-796A-19807	Sequence 19807, A
975	27	52.9	259	2	US-09-185-160-9	Sequence 9, Appli
976	27	52.9	259	2	US-09-489-039A-12916	Sequence 12916, A

977	27	52.9	260	2	US-09-902-540-15829	Sequence 15829, A
978	27	52.9	269	2	US-09-902-540-16198	Sequence 16198, A
979	27	52.9	272	2	US-09-538-092-306	Sequence 306, App
980	27	52.9	277	2	US-09-252-991A-18435	Sequence 18435, A
981	27	52.9	285	2	US-09-270-767-37674	Sequence 37674, A
982	27	52.9	285	2	US-09-270-767-52891	Sequence 52891, A
983	27	52.9	291	2	US-09-976-594-326	Sequence 326, App
984	27	52.9	291	6	5194600-2	Patent No. 5194600
985	27	52.9	300	2	US-09-710-279-1900	Sequence 1900, Ap
986	27	52.9	305	2	US-09-248-796A-20071	Sequence 20071, A
987	27	52.9	309	2	US-09-252-991A-30024	Sequence 30024, A
988	27	52.9	313	2	US-09-809-545A-46	Sequence 46, Appl
989	27	52.9	318	2	US-09-120-051D-42	Sequence 42, Appl
990	27	52.9	319	2	US-09-120-051D-38	Sequence 38, Appl
991	27	52.9	321	2	US-09-120-051D-32	Sequence 32, Appl
992	27	52.9	322	2	US-09-120-051D-43	Sequence 43, Appl
993	27	52.9	322	2	US-09-120-051D-61	Sequence 61, Appl
994	27	52.9	322	2	US-09-248-796A-14552	Sequence 14552, A
995	27	52.9	323	2	US-09-120-051D-31	Sequence 31, Appl
996	27	52.9	323	2	US-09-120-051D-33	Sequence 33, Appl
997	27	52.9	323	2	US-09-120-051D-34	Sequence 34, Appl
998	27	52.9	323	2	US-09-120-051D-36	Sequence 36, Appl
999	27	52.9	323	2	US-09-120-051D-60	Sequence 60, Appl
1000	27	52.9	328	1	US-08-225-477B-5	Sequence 5, Appli

ALIGNMENTS

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RESULT 1
US-08-318-157B-20
; Sequence 20, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-20

  Query Match           100.0%;  Score 51;  DB 1;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 0.00082;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db          1 KASQDVGTSVA 11


RESULT 2
US-09-253-794-20
; Sequence 20, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 20:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 11 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-253-794-20

  Query Match           100.0%;  Score 51;  DB 2;  Length 11;
  Best Local Similarity  100.0%;  Pred. No. 0.00082;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
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Db          1 KASQDVGTSVA 11


RESULT 3
US-08-318-157B-4
; Sequence 4, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
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;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-4

  Query Match             100.0%;  Score 51;  DB 1;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.0096;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
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Db         24 KASQDVGTSVA 34


RESULT 4
US-08-318-157B-19
; Sequence 19, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-19

  Query Match             100.0%;  Score 51;  DB 1;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.0096;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db         24 KASQDVGTSVA 34


RESULT 5
US-09-253-794-4
; Sequence 4, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 106 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-253-794-4

  Query Match             100.0%;  Score 51;  DB 2;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.0096;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
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Db         24 KASQDVGTSVA 34
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RESULT 6
US-09-253-794-19
; Sequence 19, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 106 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-253-794-19

  Query Match             100.0%;  Score 51;  DB 2;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.0096;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db         24 KASQDVGTSVA 34


RESULT 7
US-08-838-682-19
; Sequence 19, Application US/08838682
; Patent No. 6107090
;  GENERAL INFORMATION:
;    APPLICANT:  Bander M.D., Neil H.
;    TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF PROSTATE
;    TITLE OF INVENTION:  CANCER
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle LLP
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  14603-1051
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/838,682
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/016,976
;      FILING DATE:  06-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/022,125
;      FILING DATE:  18-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldman, Michael L.
;      REGISTRATION NUMBER:  30,727
;      REFERENCE/DOCKET NUMBER:  19603/1172
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716) 263-1304
;      TELEFAX:  (716) 263-1600
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-838-682-19

  Query Match             86.3%;  Score 44;  DB 2;  Length 107;
  Best Local Similarity   90.0%;  Pred. No. 0.24;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              |||||||||:|
Db         24 KASQDVGTAV 33


RESULT 8
US-08-895-914-19
; Sequence 19, Application US/08895914
; Patent No. 6136311
;  GENERAL INFORMATION:
;    APPLICANT:  Bander, Neil H.
;    TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF CANCER
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle LLP
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  14603-1051
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/895,914
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/016,976
;      FILING DATE:  06-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/022,125
;      FILING DATE:  18-JUL-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/838,682
;      FILING DATE:  09-APR-1997
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldman, Michael L.
;      REGISTRATION NUMBER:  30,727
;      REFERENCE/DOCKET NUMBER:  19603/1173
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716) 263-1304
;      TELEFAX:  (716) 263-1600
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-895-914-19

  Query Match             86.3%;  Score 44;  DB 2;  Length 107;
  Best Local Similarity   90.0%;  Pred. No. 0.24;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              |||||||||:|
Db         24 KASQDVGTAV 33


RESULT 9
US-09-357-710A-19
; Sequence 19, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
;  APPLICANT:  Bander, Neil H.
;  TITLE OF INVENTION:   TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:   Lois M. Kwasigroch: BZL 242/025
;  CURRENT APPLICATION NUMBER: US/09/357,710A
;  CURRENT FILING DATE:  1999-07-20
;  PRIOR APPLICATION NUMBER:   US 08/838,682
;  PRIOR FILING DATE:   1997-04-09
;  PRIOR APPLICATION NUMBER:   US 60/016,976
;  PRIOR FILING DATE:   1996-05-06
;  PRIOR APPLICATION NUMBER:   US 60/022,125
;  PRIOR FILING DATE:   1996-07-18
;  NUMBER OF SEQ ID NOS:   21
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-357-710A-19

  Query Match             86.3%;  Score 44;  DB 2;  Length 107;
  Best Local Similarity   90.0%;  Pred. No. 0.24;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              |||||||||:|
Db         24 KASQDVGTAV 33


RESULT 10
US-09-357-707-19
; Sequence 19, Application US/09357707
; Patent No. 6649163
; GENERAL INFORMATION:
;  APPLICANT: Bander, Neil H.
;  TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
;  FILE REFERENCE: Lois M. Kwasigroch: BZL 242/078
;  CURRENT APPLICATION NUMBER: US/09/357,707
;  CURRENT FILING DATE:  1999-07-20
;  PRIOR APPLICATION NUMBER: US 08/895,914
;  PRIOR FILING DATE: 1997-07-17
;  PRIOR APPLICATION NUMBER: US 08/838,682
;  PRIOR FILING DATE: 1997-04-09
;  PRIOR APPLICATION NUMBER: US 60/016,976
;  PRIOR FILING DATE: 1996-05-06
;  PRIOR APPLICATION NUMBER: US 60/022,125
;  PRIOR FILING DATE: 1996-07-18
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-357-707-19

  Query Match             86.3%;  Score 44;  DB 2;  Length 107;
  Best Local Similarity   90.0%;  Pred. No. 0.24;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              |||||||||:|
Db         24 KASQDVGTAV 33


RESULT 11
US-09-357-708-19
; Sequence 19, Application US/09357708
; Patent No. 6770450
; GENERAL INFORMATION:
;  APPLICANT: Bander, Neil H.
;  TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
;  FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
;  CURRENT APPLICATION NUMBER: US/09/357,708
;  CURRENT FILING DATE:  1999-07-20
;  PRIOR APPLICATION NUMBER: US 08/895,914
;  PRIOR FILING DATE: 1997-07-17
;  PRIOR APPLICATION NUMBER: US 08/838,682
;  PRIOR FILING DATE: 1997-04-09
;  PRIOR APPLICATION NUMBER: US 60/016,976
;  PRIOR FILING DATE: 1996-05-06
;  PRIOR APPLICATION NUMBER: US 60/022,125
;  PRIOR FILING DATE: 1996-07-18
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-357-708-19

  Query Match             86.3%;  Score 44;  DB 2;  Length 107;
  Best Local Similarity   90.0%;  Pred. No. 0.24;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSV 10
              |||||||||:|
Db         24 KASQDVGTAV 33


RESULT 12
US-08-797-689-18
; Sequence 18, Application US/08797689
; Patent No. 5876969
;  GENERAL INFORMATION:
;    APPLICANT:  Fleer, Reinhard
;    APPLICANT:  Fournier, Alain
;    APPLICANT:  Guitton, Jean-Dominique
;    APPLICANT:  Jung, Gerard
;    APPLICANT:  Yeh, Patrice
;    TITLE OF INVENTION:  NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
;    TITLE OF INVENTION:  PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
;    TITLE OF INVENTION:  CONTAINING SAID POLYPEPTIDES
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, 3C43
;      CITY:  Collegeville
```

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;       STATE:  PA
;       COUNTRY:  USA
;       ZIP:  19426
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  Macintosh
;       OPERATING SYSTEM:  System 7.1
;       SOFTWARE:  Word 5.1 (PatentIn)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/797,689
;       FILING DATE:  31-JAN-1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/256,927
;       FILING DATE:  28-JUL-1994
;       APPLICATION NUMBER:  FR 92/01064
;       FILING DATE:  31-JAN-1992
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/FR93/00085
;       FILING DATE:  28-JAN-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Smith Ph.D., Julie K.
;       REGISTRATION NUMBER:  P-38,619
;       REFERENCE/DOCKET NUMBER:  ST92006-US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (610) 454-3839
;       TELEFAX:  (610) 454-3808
;   INFORMATION FOR SEQ ID NO:  18:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  249 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-797-689-18

  Query Match             86.3%;  Score 44;  DB 1;  Length 249;
  Best Local Similarity   90.9%;  Pred. No. 0.6;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||| ||||
Db        166 KASQDVDTSVA 176


RESULT 13
US-09-984-186-18
; Sequence 18, Application US/09984186
; Patent No. 6686179
;   GENERAL INFORMATION:
;       APPLICANT: Fleer, Reinhard
;                  Fournier, Alain
;                  Guitton, Jean-Dominique
;                  Jung, Gerard
;                  Yeh, Patrice
;       TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
;                           PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
;                           CONTAINING SAID POLYPEPTIDES
;       NUMBER OF SEQUENCES: 36
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Rhone-Poulenc Rorer Inc.
;            STREET: 500 Arcola Road, 3C43
;            CITY: Collegeville
;            STATE: PA
;            COUNTRY: USA
;            ZIP: 19426
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: Macintosh
;            OPERATING SYSTEM: System 7.1
;            SOFTWARE: Word 5.1 (PatentIn)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/984,186
;            FILING DATE: 29-Oct-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/797,689
;            FILING DATE: 31-JAN-1997
;            APPLICATION NUMBER: US 08/256,927
;            FILING DATE: 28-JUL-1994
;            APPLICATION NUMBER: FR 92/01064
;            FILING DATE: 31-JAN-1992
;            APPLICATION NUMBER: PCT/FR93/00085
;            FILING DATE: 28-JAN-1993
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Smith Ph.D., Julie K.
;            REGISTRATION NUMBER: P-38,619
;            REFERENCE/DOCKET NUMBER: ST92006-US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (610) 454-3839
;            TELEFAX: (610) 454-3808
;   INFORMATION FOR SEQ ID NO: 18:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 249 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-984-186-18

  Query Match             86.3%;  Score 44;  DB 2;  Length 249;
  Best Local Similarity   90.9%;  Pred. No. 0.6;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||| ||||
Db        166 KASQDVDTSVA 176


RESULT 14
US-08-602-725-6
; Sequence 6, Application US/08602725
; Patent No. 5965710
;  GENERAL INFORMATION:
;    APPLICANT:  BODMER, WALTER F
;    APPLICANT:  DURBIN, HELGA
;    APPLICANT:  SNARY, DAVID
;    APPLICANT:  STEWART, LORNA MD
;    APPLICANT:  YOUNG, SUSAN
;    APPLICANT:  BATES, PAUL A
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES FOR USE IN
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD, 8TH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,725
;      FILING DATE:  02-FEB-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB94/01816
;      FILING DATE:  19-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9317423
;      FILING DATE:  21-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
```

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;       REGISTRATION NUMBER:  36663
;       REFERENCE/DOCKET NUMBER:  1090-8
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  703-816-4091
;       TELEFAX:  703-816-4100
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  11 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:  internal
;     ORIGINAL SOURCE:
;       ORGANISM:  VL chain CDR1
US-08-602-725-6

  Query Match             84.3%;  Score 43;  DB 1;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 0.032;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db          1 KASQNVGTNVA 11


RESULT 15
US-08-646-265A-118
; Sequence 118, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  118:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-118

  Query Match             84.3%;  Score 43;  DB 2;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 0.032;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db          1 KASQNVGTNVA 11


RESULT 16
US-09-406-535-8
; Sequence 8, Application US/09406535
; Patent No. 6376653
; GENERAL INFORMATION:
;  APPLICANT: Connie L. Erickson-Miller
;  APPLICANT: Stephen D. Holmes
;  APPLICANT: James D. Winkler
;  TITLE OF INVENTION: Tie2 Antagonist Antibodies
;  FILE REFERENCE: P50844
;  CURRENT APPLICATION NUMBER: US/09/406,535
;  CURRENT FILING DATE: 1999-09-27
;  EARLIER APPLICATION NUMBER: 60/102,100
;  EARLIER FILING DATE: 1998-09-28
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;    LENGTH: 11
;    TYPE: PRT
;    ORGANISM: Mus musculus
;    FEATURE:
;    NAME/KEY: SITE
;    LOCATION: (1)...(11)
;    OTHER INFORMATION: light chain CDR 1
US-09-406-535-8

  Query Match             84.3%;  Score 43;  DB 2;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 0.032;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db          1 KASQNVGTAVA 11


RESULT 17
US-09-508-413A-8
; Sequence 8, Application US/09508413A
; Patent No. 6667035
; GENERAL INFORMATION:
;  APPLICANT: von Eichel-Streiber, Christoph
;  APPLICANT:  Moos, Michael
;  TITLE OF INVENTION: AMINO ACID SEQUENCES FOR THERAPEUTIC AND
;  TITLE OF INVENTION:  PROPHYLACTIC USE AGAINST DISEASES DUE TO CLOSTRIDIUM
;  TITLE OF INVENTION:  DIFFICILE TOXINS
;  FILE REFERENCE: 415142000200
;  CURRENT APPLICATION NUMBER: US/09/508,413A
;  CURRENT FILING DATE:  2000-03-27
;  PRIOR APPLICATION NUMBER: PCT/EP98/05759
;  PRIOR FILING DATE: 1998-09-10
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;    LENGTH: 11
;    TYPE: PRT
;    ORGANISM: Mus musculus
US-09-508-413A-8

  Query Match             84.3%;  Score 43;  DB 2;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 0.032;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db          1 KASQNVGTNVA 11


RESULT 18
US-10-226-795-18
; Sequence 18, Application US/10226795
; Patent No. 6875433
; GENERAL INFORMATION:
;  APPLICANT: HART, MARY KATE
;  APPLICANT:  WILSON, JULIE
;  TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
;  TITLE OF INVENTION:  REGIONS BINDING TO EBOLA GLYCOPROTEIN
;  FILE REFERENCE: ARMY 166
;  CURRENT APPLICATION NUMBER: US/10/226,795
;  CURRENT FILING DATE:  2002-11-18
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic light
;   OTHER INFORMATION: chain of Mab EGP13C6-1-1 amino acid sequence
US-10-226-795-18

  Query Match             84.3%;  Score 43;  DB 2;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 0.032;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db          1 KASQNVGTAVA 11


RESULT 19
US-09-905-243-80
; Sequence 80, Application US/09905243
; Patent No. 6936698
; GENERAL INFORMATION:
;  APPLICANT: Taylor, Alexander H
;  TITLE OF INVENTION: Monoclonal Antibodies with Reduced
;  TITLE OF INVENTION:  Immunogenicity
;  FILE REFERENCE: P50770
;  CURRENT APPLICATION NUMBER: US/09/905,243
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 09/300,970
;  PRIOR FILING DATE: 1999-04-28
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 80
;   LENGTH: 102
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: murine/human sequence
US-09-905-243-80

  Query Match             84.3%;  Score 43;  DB 2;  Length 102;
  Best Local Similarity   81.8%;  Pred. No. 0.36;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 20
US-09-508-413A-16
; Sequence 16, Application US/09508413A
; Patent No. 6667035
; GENERAL INFORMATION:
;  APPLICANT: von Eichel-Streiber, Christoph
;  APPLICANT:  Moos, Michael
;  TITLE OF INVENTION: AMINO ACID SEQUENCES FOR THERAPEUTIC AND
;  TITLE OF INVENTION:  PROPHYLACTIC USE AGAINST DISEASES DUE TO CLOSTRIDIUM
;  TITLE OF INVENTION:  DIFFICILE TOXINS
;  FILE REFERENCE: 415142000200
;  CURRENT APPLICATION NUMBER: US/09/508,413A
;  CURRENT FILING DATE:  2000-03-27
;  PRIOR APPLICATION NUMBER: PCT/EP98/05759
;  PRIOR FILING DATE: 1998-09-10
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 104
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-508-413A-16

  Query Match             84.3%;  Score 43;  DB 2;  Length 104;
  Best Local Similarity   81.8%;  Pred. No. 0.37;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         22 KASQNVGTNVA 32


RESULT 21
US-08-767-128-32
; Sequence 32, Application US/08767128
; Patent No. 6111079
;  GENERAL INFORMATION:
;    APPLICANT:  WYLIE, DWANE E.
;    APPLICANT:  LOPEZ, OSVALDO
;    APPLICANT:  MURRAY, PETER JOSEPH
;    APPLICANT:  GOEBEL, PETER
;    TITLE OF INVENTION:  LEAD BINDING POLYPEPTIDES AND
;    TITLE OF INVENTION:  NUCLEOTIDES CODING THEREFORE
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant, Gould, Smith, Edell, Welter & Schmidt
;      STREET:  3100 No. 6111079west Center, 90 South Seventh St
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/767,128
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:  04-DEC-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/09258
;      FILING DATE:  05-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/541,373
;      FILING DATE:  10-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/462,798
;      FILING DATE:  05-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carter, Charles G.
;      REGISTRATION NUMBER:  35,093
```

```
;       REFERENCE/DOCKET NUMBER:  8648.49USF1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  612/371-5278
;       TELEFAX:  612/332-9081
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  32:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  107 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     FRAGMENT TYPE:  internal
;     ORIGINAL SOURCE:
US-08-767-128-32

  Query Match             84.3%;  Score 43;  DB 2;  Length 107;
  Best Local Similarity   81.8%;  Pred. No. 0.38;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 22
US-08-646-265A-130
; Sequence 130, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  130:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-130

  Query Match             84.3%;  Score 43;  DB 2;  Length 107;
  Best Local Similarity   81.8%;  Pred. No. 0.38;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 23
US-08-646-265A-131
; Sequence 131, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  131:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-131

  Query Match             84.3%;  Score 43;  DB 2;  Length 107;
  Best Local Similarity   81.8%;  Pred. No. 0.38;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 24
US-09-406-535-4
; Sequence 4, Application US/09406535
```

```
; Patent No. 6376653
; GENERAL INFORMATION:
;  APPLICANT: Connie L. Erickson-Miller
;  APPLICANT: Stephen D. Holmes
;  APPLICANT: James D. Winkler
;  TITLE OF INVENTION: Tie2 Antagonist Antibodies
;  FILE REFERENCE: P50844
;  CURRENT APPLICATION NUMBER: US/09/406,535
;  CURRENT FILING DATE: 1999-09-27
;  EARLIER APPLICATION NUMBER: 60/102,100
;  EARLIER FILING DATE: 1998-09-28
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-406-535-4

  Query Match             84.3%;  Score 43;  DB 2;  Length 107;
  Best Local Similarity   81.8%;  Pred. No. 0.38;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTAVA 34


RESULT 25
US-09-905-243-77
; Sequence 77, Application US/09905243
; Patent No. 6936698
; GENERAL INFORMATION:
;  APPLICANT: Taylor, Alexander H
;  TITLE OF INVENTION: Monoclonal Antibodies with Reduced
;  TITLE OF INVENTION:  Immunogenicity
;  FILE REFERENCE: P50770
;  CURRENT APPLICATION NUMBER: US/09/905,243
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 09/300,970
;  PRIOR FILING DATE: 1999-04-28
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 77
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: murine/chimpanzee sequence
US-09-905-243-77

  Query Match             84.3%;  Score 43;  DB 2;  Length 107;
  Best Local Similarity   81.8%;  Pred. No. 0.38;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 26
US-08-602-725-30
; Sequence 30, Application US/08602725
; Patent No. 5965710
;  GENERAL INFORMATION:
;    APPLICANT:  BODMER, WALTER F
;    APPLICANT:  DURBIN, HELGA
;    APPLICANT:  SNARY, DAVID
;    APPLICANT:  STEWART, LORNA MD
;    APPLICANT:  YOUNG, SUSAN
;    APPLICANT:  BATES, PAUL A
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES FOR USE IN
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD, 8TH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,725
;      FILING DATE:  02-FEB-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB94/01816
;      FILING DATE:  19-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9317423
;      FILING DATE:  21-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36663
;      REFERENCE/DOCKET NUMBER:  1090-8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-816-4091
;      TELEFAX:  703-816-4100
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  109 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:  N-terminal
;    ORIGINAL SOURCE:
;      ORGANISM:  Humanised kappa light chain
US-08-602-725-30

  Query Match             84.3%;  Score 43;  DB 1;  Length 109;
  Best Local Similarity   81.8%;  Pred. No. 0.39;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 27
US-08-602-725-2
; Sequence 2, Application US/08602725
; Patent No. 5965710
;  GENERAL INFORMATION:
;    APPLICANT:  BODMER, WALTER F
;    APPLICANT:  DURBIN, HELGA
;    APPLICANT:  SNARY, DAVID
;    APPLICANT:  STEWART, LORNA MD
;    APPLICANT:  YOUNG, SUSAN
;    APPLICANT:  BATES, PAUL A
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES FOR USE IN
;    TITLE OF INVENTION:  DIAGNOSIS AND TREATMENT OF COLORECTAL CANCER
;    NUMBER OF SEQUENCES:  40
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD, 8TH FLOOR
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,725
;      FILING DATE:  02-FEB-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/GB94/01816
;      FILING DATE:  19-AUG-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9317423
;      FILING DATE:  21-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36663
;      REFERENCE/DOCKET NUMBER:  1090-8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-816-4091
;      TELEFAX:  703-816-4100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  110 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  VL chain
US-08-602-725-2

  Query Match             84.3%;  Score 43;  DB 1;  Length 110;
  Best Local Similarity   81.8%;  Pred. No. 0.39;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         25 KASQNVGTNVA 35


RESULT 28
US-08-398-613A-20
; Sequence 20, Application US/08398613A
; Patent No. 5677426
;  GENERAL INFORMATION:
;    APPLICANT:  Fong, Sherman
;    APPLICANT:  Hebert, Caroline Alice
;    APPLICANT:  Kim, Kyung Jin
;    APPLICANT:  Leong, Steven R.
;    TITLE OF INVENTION:  Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/398,613A
;      FILING DATE:  01-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/205864
;      FILING DATE:  03-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fitts, Renee A.
;      REGISTRATION NUMBER:  35,136
;      REFERENCE/DOCKET NUMBER:  874P1-3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1489
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-398-613A-20

  Query Match             84.3%;  Score 43;  DB 1;  Length 123;
  Best Local Similarity   81.8%;  Pred. No. 0.44;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 29
US-08-398-612A-20
; Sequence 20, Application US/08398612A
; Patent No. 5686070
;  GENERAL INFORMATION:
;    APPLICANT:  Doershuk, Claire M.
;    APPLICANT:  Fong, Sherman
;    APPLICANT:  Hebert, Caroline Alice
;    APPLICANT:  Kim, Kyung Jin
;    APPLICANT:  Leong, Steven R.
;    TITLE OF INVENTION:  Anti-IL-8 Monoclonal Antibodies for
;    TITLE OF INVENTION:  Treatment of Inflammatory Disorders
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/398,612A
;      FILING DATE:  01-MAR-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/398611
;      FILING DATE:  01-Mar-1995
;      APPLICATION NUMBER:  08/205864
;      FILING DATE:  03-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0874P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-398-612A-20
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  Query Match             84.3%;  Score 43;  DB 1;  Length 123;
  Best Local Similarity   81.8%;  Pred. No. 0.44;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 30
US-08-398-611A-20
; Sequence 20, Application US/08398611A
; Patent No. 5702946
;  GENERAL INFORMATION:
;    APPLICANT:  Doershuk, Claire M.
;    APPLICANT:  Fong, Sherman
;    APPLICANT:  Hebert, Caroline Alice
;    APPLICANT:  Kim, Kyung Jin
;    APPLICANT:  Leong, Steven R.
;    TITLE OF INVENTION:  Anti-IL-8 Monoclonal Antibodies for Treatment
;    TITLE OF INVENTION:  of Inflammatory Disorders
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/398,611A
;      FILING DATE:  01-Mar-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/205864
;      FILING DATE:  03-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0874P1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-398-611A-20

  Query Match             84.3%;  Score 43;  DB 1;  Length 123;
  Best Local Similarity   81.8%;  Pred. No. 0.44;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 31
US-08-491-334A-20
; Sequence 20, Application US/08491334A
; Patent No. 5874080
;  GENERAL INFORMATION:
;    APPLICANT:  Hebert, Caroline A.
;    APPLICANT:  Kabakoff, Rhona C.
;    APPLICANT:  Moore, Mark W.
;    TITLE OF INVENTION:  IL-8 Antagonists for Treatment of Inflammatory
;    TITLE OF INVENTION:  Disorders and Asthma
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/491,334A
;      FILING DATE:  27-Jun-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/398611
;      FILING DATE:  01-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/205864
;      FILING DATE:  03-MAR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P0874P2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-5530
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-491-334A-20

  Query Match             84.3%;  Score 43;  DB 1;  Length 123;
  Best Local Similarity   81.8%;  Pred. No. 0.44;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 32
US-09-027-449-17
; Sequence 17, Application US/09027449
; Patent No. 6025158
;  GENERAL INFORMATION:
;    APPLICANT:  Gonzalez, Tania R.
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    TITLE OF INVENTION:  Antibody Fragment-Polymer Conjugates and
;    TITLE OF INVENTION:  Humanized Anti-IL-8 Monoclonal Antibodies
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
```

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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/027,449
;      FILING DATE:  20-Feb-1998
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/074,330
;      FILING DATE:  22-Jan-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/038,664
;      FILING DATE:  21-Feb-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R3-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-027-449-17

  Query Match             84.3%;  Score 43;  DB 2;  Length 123;
  Best Local Similarity   81.8%;  Pred. No. 0.44;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 33
US-08-804-444A-17
; Sequence 17, Application US/08804444A
; Patent No. 6117980
;  GENERAL INFORMATION:
;    APPLICANT:  Gonzalez, Tania N
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    TITLE OF INVENTION:  Humanized Anti-IL-8 Monoclonal Antibodies
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/804,444A
;      FILING DATE:  21-Feb-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-08-804-444A-17

  Query Match             84.3%;  Score 43;  DB 2;  Length 123;
  Best Local Similarity   81.8%;  Pred. No. 0.44;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 34
US-09-026-985-17
; Sequence 17, Application US/09026985
; Patent No. 6133426
;  GENERAL INFORMATION:
;    APPLICANT:  Gonzalez, Tania R.
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    TITLE OF INVENTION:  Antibody Fragment-Polymer Conjugates and
;    TITLE OF INVENTION:  Humanized Anti-IL-8 Monoclonal Antibodies
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/026,985
;      FILING DATE:  20-Feb-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R3-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-026-985-17

  Query Match             84.3%;  Score 43;  DB 2;  Length 123;
  Best Local Similarity   81.8%;  Pred. No. 0.44;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 35
US-09-121-952A-17
; Sequence 17, Application US/09121952A
; Patent No. 6458355
;  GENERAL INFORMATION:
;    APPLICANT:  Genentech, Inc., Hsei, Vanessa
;    APPLICANT:  Koumenis, Iphigenia
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Shahrokh, Zahra
;    APPLICANT:  Zapata, Gerardo A.
;    TITLE OF INVENTION:  METHODS OF TREATING INFLAMMATORY DISEASES
;    TITLE OF INVENTION:  WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
;    NUMBER OF SEQUENCES:  72
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/121,952A
;      FILING DATE:  24-Jul-1998
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/074330
;      FILING DATE:  22-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/075467
;      FILING DATE:  20-FEB-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-121-952A-17

  Query Match             84.3%;  Score 43;  DB 2;  Length 123;
  Best Local Similarity   81.8%;  Pred. No. 0.44;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 36
US-09-234-340A-17
; Sequence 17, Application US/09234340A
; Patent No. 6468532
;  GENERAL INFORMATION:
;    APPLICANT:  Genentech, Inc., Hsei, Vanessa
;    APPLICANT:  Koumenis, Iphigenia
;    APPLICANT:  Leong, Steven R.
;    APPLICANT:  Presta, Leonard G.
;    APPLICANT:  Shahrokh, Zahra
;    APPLICANT:  Zapata, Gerardo A.
;    TITLE OF INVENTION:  METHODS OF TREATING INFLAMMATORY DISEASES
;    TITLE OF INVENTION:  WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/234,340A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/121,952
;      FILING DATE:  24-Jul-1998
;      APPLICATION NUMBER:  60/074330
;      FILING DATE:  22-JAN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/075467
;      FILING DATE:  20-FEB-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Love, Richard B.
;      REGISTRATION NUMBER:  34,659
;      REFERENCE/DOCKET NUMBER:  P1085R4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5530
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  123 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-234-340A-17

  Query Match             84.3%;  Score 43;  DB 2;  Length 123;
  Best Local Similarity   81.8%;  Pred. No. 0.44;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 37
US-09-355-014-17
; Sequence 17, Application US/09355014
; Patent No. 6870033
;  GENERAL INFORMATION:
;       APPLICANT: Genentech, Inc., Hsei, Vanessa
;                  Koumenis, Iphigenia
;                  Leong, Steven R.
;                  Presta, Leonard G.
;                  Shahrokh, Zahra
;                  Zapata, Gerardo A.
;       TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
;                           Humanized Anti-IL-8 Monoclonal Antibodies
;       NUMBER OF SEQUENCES: 72
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Genentech, Inc.
;            STREET: 1 DNA Way
;            CITY: South San Francisco
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94080
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WinPatin (Genentech)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/355,014
;            FILING DATE: 21-Jul-1999
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Love, Richard B.
;            REGISTRATION NUMBER: 34,659
;            REFERENCE/DOCKET NUMBER: P1085R3PCT
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650/225-5530
;            TELEFAX: 650/952-9881
;  INFORMATION FOR SEQ ID NO: 17:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 123 amino acids
;
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```
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-355-014-17

  Query Match             84.3%;  Score 43;  DB 2;  Length 123;
  Best Local Similarity   81.8%;  Pred. No. 0.44;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 38
US-08-646-265A-43
; Sequence 43, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  43:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-43

  Query Match             84.3%;  Score 43;  DB 2;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.45;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 39
```

```
US-08-646-265A-47
; Sequence 47, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  47:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-47

  Query Match             84.3%;  Score 43;  DB 2;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.45;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 40
US-08-646-265A-51
; Sequence 51, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
```

```
;       COUNTRY:  USA
;       ZIP:  20007-5109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/646,265A
;       FILING DATE:  09-SEP-1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO PCT/JP94/01763
;       FILING DATE:  19-OCT-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 5-291078
;       FILING DATE:  19-NOV-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WEGNER, Harold C.
;       REGISTRATION NUMBER:  25,258
;       REFERENCE/DOCKET NUMBER:  53466/184
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)672-5300
;       TELEFAX:  (202)672-5399
;       TELEX:  904136
;   INFORMATION FOR SEQ ID NO:  51:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  126 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-646-265A-51

  Query Match             84.3%;  Score 43;  DB 2;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.45;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 41
US-08-646-265A-53
; Sequence 53, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-53

  Query Match             84.3%;  Score 43;  DB 2;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.45;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 42
US-08-646-265A-57
; Sequence 57, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
```

```
;    MOLECULE TYPE:  protein
US-08-646-265A-57

  Query Match             84.3%;  Score 43;  DB 2;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.45;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 43
US-08-646-265A-59
; Sequence 59, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  59:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-59

  Query Match             84.3%;  Score 43;  DB 2;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.45;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 44
US-08-646-265A-63
; Sequence 63, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  63:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-63

  Query Match             84.3%;  Score 43;  DB 2;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.45;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 45
US-08-646-265A-65
; Sequence 65, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
```

```
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  65:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-65

  Query Match             84.3%;  Score 43;  DB 2;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.45;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
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Db         43 KASQNVGTNVA 53


RESULT 46
US-08-646-265A-69
; Sequence 69, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  69:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-69

  Query Match             84.3%;  Score 43;  DB 2;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.45;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 47
US-08-646-265A-73
; Sequence 73, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  73:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-73
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  Query Match             84.3%;  Score 43;  DB 2;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.45;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 48
US-08-646-265A-75
; Sequence 75, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  75:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-75

  Query Match             84.3%;  Score 43;  DB 2;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.45;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 49
US-08-646-265A-77
; Sequence 77, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  77:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  126 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-77

  Query Match             84.3%;  Score 43;  DB 2;  Length 126;
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  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
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Db         43 KASQNVGTNVA 53


RESULT 50
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; Sequence 81, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/646,265A
;       FILING DATE:  09-SEP-1996
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO PCT/JP94/01763
;       FILING DATE:  19-OCT-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 5-291078
;       FILING DATE:  19-NOV-1993
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  WEGNER, Harold C.
;       REGISTRATION NUMBER:  25,258
;       REFERENCE/DOCKET NUMBER:  53466/184
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (202)672-5300
;       TELEFAX:  (202)672-5399
;       TELEX:  904136
;   INFORMATION FOR SEQ ID NO:  81:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  126 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-646-265A-81

  Query Match             84.3%;  Score 43;  DB 2;  Length 126;
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  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


Search completed: March 23, 2006, 02:08:15
Job time : 32.8082 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:42:16 ; Search time 77.1507 Seconds
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59.573 Million cell updates/sec

Title: US-10-755-382-20
Perfect score: 51
Sequence: 1 KASQDVGTSVA 11

Scoring table: BLOSUM62
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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39	48	94.1	213	4	US-10-281-479A-46	Sequence 46, Appl
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84	43	84.3	11	3	US-09-949-559-4	Sequence 4, Appli
85	43	84.3	11	3	US-09-749-873-118	Sequence 118, App
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88	43	84.3	11	4	US-10-745-102-8	Sequence 8, Appli
89	43	84.3	11	5	US-10-728-420B-4	Sequence 4, Appli
90	43	84.3	11	5	US-10-914-015-4	Sequence 4, Appli
91	43	84.3	102	3	US-09-905-243-80	Sequence 80, Appl
92	43	84.3	102	6	US-11-099-331-80	Sequence 80, Appl
93	43	84.3	104	4	US-10-745-102-16	Sequence 16, Appl
94	43	84.3	107	3	US-09-905-243-77	Sequence 77, Appl
95	43	84.3	107	3	US-09-949-559-9	Sequence 9, Appli
96	43	84.3	107	3	US-09-949-559-11	Sequence 11, Appl
97	43	84.3	107	3	US-09-749-873-130	Sequence 130, App
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99	43	84.3	107	3	US-09-875-221A-9	Sequence 9, Appli
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103	43	84.3	107	6	US-11-099-331-77	Sequence 77, Appl
104	43	84.3	108	3	US-09-949-559-104	Sequence 104, App
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106	43	84.3	123	3	US-09-726-258-17	Sequence 17, Appl
107	43	84.3	126	3	US-09-749-873-43	Sequence 43, Appl
108	43	84.3	126	3	US-09-749-873-47	Sequence 47, Appl
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110	43	84.3	126	3	US-09-749-873-53	Sequence 53, Appl
111	43	84.3	126	3	US-09-749-873-57	Sequence 57, Appl
112	43	84.3	126	3	US-09-749-873-59	Sequence 59, Appl
113	43	84.3	126	3	US-09-749-873-63	Sequence 63, Appl
114	43	84.3	126	3	US-09-749-873-65	Sequence 65, Appl
115	43	84.3	126	3	US-09-749-873-69	Sequence 69, Appl
116	43	84.3	126	3	US-09-749-873-73	Sequence 73, Appl
117	43	84.3	126	3	US-09-749-873-75	Sequence 75, Appl
118	43	84.3	126	3	US-09-749-873-77	Sequence 77, Appl
119	43	84.3	126	3	US-09-749-873-81	Sequence 81, Appl
120	43	84.3	126	3	US-09-749-873-85	Sequence 85, Appl
121	43	84.3	126	3	US-09-749-873-87	Sequence 87, Appl
122	43	84.3	126	3	US-09-749-873-91	Sequence 91, Appl
123	43	84.3	127	3	US-09-749-873-27	Sequence 27, Appl
124	43	84.3	129	4	US-10-365-123-47	Sequence 47, Appl
125	43	84.3	145	4	US-10-226-795-17	Sequence 17, Appl
126	43	84.3	208	4	US-10-634-581-1	Sequence 1, Appli
127	43	84.3	208	5	US-10-634-199-1	Sequence 1, Appli
128	43	84.3	214	3	US-09-949-559-128	Sequence 128, App
129	43	84.3	214	3	US-09-875-221A-128	Sequence 128, App
130	43	84.3	214	4	US-10-310-454-4	Sequence 4, Appli
131	43	84.3	214	5	US-10-728-420B-113	Sequence 113, App
132	43	84.3	214	5	US-10-914-015-113	Sequence 113, App
133	43	84.3	237	3	US-09-726-258-25	Sequence 25, Appl
134	43	84.3	269	3	US-09-749-873-109	Sequence 109, App
135	43	84.3	492	4	US-10-682-845-59	Sequence 59, Appl
136	43	84.3	492	4	US-10-682-845-61	Sequence 61, Appl
137	43	84.3	492	4	US-10-682-845-63	Sequence 63, Appl
138	43	84.3	492	4	US-10-682-845-65	Sequence 65, Appl
139	43	84.3	492	4	US-10-682-845-67	Sequence 67, Appl
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141	43	84.3	492	4	US-10-682-845-71	Sequence 71, Appl
142	43	84.3	492	4	US-10-682-845-73	Sequence 73, Appl
143	43	84.3	492	4	US-10-682-845-75	Sequence 75, Appl
144	43	84.3	492	4	US-10-682-845-77	Sequence 77, Appl
145	43	84.3	492	4	US-10-682-845-79	Sequence 79, Appl
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147	43	84.3	492	4	US-10-682-845-83	Sequence 83, Appl
148	43	84.3	492	4	US-10-682-845-85	Sequence 85, Appl
149	43	84.3	492	4	US-10-682-845-87	Sequence 87, Appl
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152	42	82.4	11	3	US-09-509-098-5	Sequence 5, Appli
153	42	82.4	11	4	US-10-182-018-59	Sequence 59, Appl
154	42	82.4	11	4	US-10-169-003-59	Sequence 59, Appl
155	42	82.4	11	4	US-10-218-253-3	Sequence 3, Appli
156	42	82.4	11	4	US-10-337-981-59	Sequence 59, Appl
157	42	82.4	11	4	US-10-344-733-59	Sequence 59, Appl
158	42	82.4	11	5	US-10-473-977-4	Sequence 4, Appli
159	42	82.4	11	5	US-10-842-011-18	Sequence 18, Appl
160	42	82.4	11	5	US-10-842-011-35	Sequence 35, Appl
161	42	82.4	11	6	US-11-047-996-59	Sequence 59, Appl
162	42	82.4	12	4	US-10-276-939-5	Sequence 5, Appli
163	42	82.4	101	4	US-10-010-729-39	Sequence 39, Appl
164	42	82.4	101	4	US-10-010-729-41	Sequence 41, Appl
165	42	82.4	104	5	US-10-473-977-63	Sequence 63, Appl
166	42	82.4	106	3	US-09-509-098-133	Sequence 133, App
167	42	82.4	107	3	US-09-509-098-130	Sequence 130, App
168	42	82.4	107	3	US-09-509-098-134	Sequence 134, App
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170	42	82.4	107	5	US-10-842-011-42	Sequence 42, Appl
171	42	82.4	107	5	US-10-842-011-47	Sequence 47, Appl
172	42	82.4	107	5	US-10-842-011-49	Sequence 49, Appl
173	42	82.4	107	5	US-10-864-818-3	Sequence 3, Appli
174	42	82.4	108	4	US-10-276-939-1	Sequence 1, Appli
175	42	82.4	109	5	US-10-835-641-5	Sequence 5, Appli
176	42	82.4	126	3	US-09-760-723-6	Sequence 6, Appli
177	42	82.4	126	3	US-09-355-925-6	Sequence 6, Appli
178	42	82.4	126	3	US-09-269-921-106	Sequence 106, App
179	42	82.4	126	3	US-09-269-921-107	Sequence 107, App
180	42	82.4	126	3	US-09-509-098-12	Sequence 12, Appl
181	42	82.4	126	3	US-09-509-098-14	Sequence 14, Appl
182	42	82.4	126	4	US-10-315-125-6	Sequence 6, Appli
183	42	82.4	126	4	US-10-218-253-106	Sequence 106, App
184	42	82.4	126	4	US-10-218-253-107	Sequence 107, App
185	42	82.4	126	4	US-10-428-085-6	Sequence 6, Appli
186	42	82.4	126	4	US-10-474-714-4	Sequence 4, Appli
187	42	82.4	127	5	US-10-842-011-28	Sequence 28, Appl
188	42	82.4	128	2	US-08-779-784-36	Sequence 36, Appl
189	42	82.4	128	4	US-10-010-729-72	Sequence 72, Appl
190	42	82.4	131	3	US-09-269-921-104	Sequence 104, App
191	42	82.4	131	3	US-09-509-098-2	Sequence 2, Appli
192	42	82.4	131	4	US-10-218-253-104	Sequence 104, App
193	42	82.4	214	4	US-10-679-620-84	Sequence 84, Appl
194	42	82.4	214	6	US-11-132-143-84	Sequence 84, Appl
195	42	82.4	245	5	US-10-864-818-1	Sequence 1, Appli
196	42	82.4	250	3	US-09-887-853-2	Sequence 2, Appli
197	42	82.4	250	5	US-10-683-547-2	Sequence 2, Appli
198	42	82.4	333	4	US-10-059-261-61	Sequence 61, Appl
199	42	82.4	333	5	US-10-627-649-61	Sequence 61, Appl
200	42	82.4	478	4	US-10-679-620-72	Sequence 72, Appl
201	42	82.4	478	6	US-11-132-143-72	Sequence 72, Appl
202	42	82.4	509	4	US-10-679-620-90	Sequence 90, Appl
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205	42	82.4	510	4	US-10-679-620-92	Sequence 92, Appl
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212	41	80.4	107	4	US-10-184-300A-5	Sequence 5, Appli
213	41	80.4	107	4	US-10-184-300A-6	Sequence 6, Appli
214	41	80.4	109	5	US-10-723-383-5	Sequence 5, Appli
215	41	80.4	168	4	US-10-360-053-2	Sequence 2, Appli
216	41	80.4	168	4	US-10-360-053-4	Sequence 4, Appli
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218	40	78.4	107	4	US-10-389-155-9	Sequence 9, Appli
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221	40	78.4	107	4	US-10-389-417-10	Sequence 10, Appl
222	40	78.4	107	4	US-10-452-357-52	Sequence 52, Appl
223	40	78.4	107	4	US-10-452-357-53	Sequence 53, Appl
224	40	78.4	109	4	US-10-078-757B-49	Sequence 49, Appl
225	39	76.5	11	4	US-10-410-894-19	Sequence 19, Appl
226	39	76.5	103	4	US-10-379-392-102	Sequence 102, App
227	39	76.5	103	4	US-10-379-392-127	Sequence 127, App
228	39	76.5	103	4	US-10-379-392-133	Sequence 133, App
229	39	76.5	103	4	US-10-379-392-180	Sequence 180, App
230	39	76.5	107	4	US-10-411-037-35	Sequence 35, Appl
231	39	76.5	107	4	US-10-411-026-35	Sequence 35, Appl
232	39	76.5	107	4	US-10-410-962-35	Sequence 35, Appl
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240	39	76.5	107	5	US-10-410-897-35	Sequence 35, Appl
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242	39	76.5	108	3	US-09-971-543-7	Sequence 7, Appli
243	39	76.5	109	4	US-10-410-894-1	Sequence 1, Appli
244	39	76.5	109	4	US-10-379-392-149	Sequence 149, App
245	39	76.5	109	5	US-10-835-641-1	Sequence 1, Appli
246	39	76.5	109	5	US-10-759-731A-1	Sequence 1, Appli

247	39	76.5	109	5	US-10-901-011-1	Sequence 1, Appli
248	39	76.5	109	5	US-10-939-309-1	Sequence 1, Appli
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253	39	76.5	214	4	US-10-316-694-1	Sequence 1, Appli
254	39	76.5	214	4	US-10-356-974-1	Sequence 1, Appli
255	39	76.5	214	4	US-10-364-953-13	Sequence 13, Appl
256	39	76.5	214	4	US-10-423-299-1	Sequence 1, Appli
257	39	76.5	214	4	US-10-659-825-1	Sequence 1, Appli
258	39	76.5	214	5	US-10-877-532-1	Sequence 1, Appli
259	39	76.5	214	5	US-10-949-683-1	Sequence 1, Appli
260	39	76.5	214	6	US-11-084-729-1	Sequence 1, Appli
261	39	76.5	232	5	US-10-511-794-17	Sequence 17, Appl
262	39	76.5	236	5	US-10-723-003-56	Sequence 56, Appl
263	39	76.5	236	6	US-11-004-639-56	Sequence 56, Appl
264	39	76.5	241	5	US-10-511-794-16	Sequence 16, Appl
265	39	76.5	252	3	US-09-971-543-1	Sequence 1, Appli
266	39	76.5	255	5	US-10-511-794-21	Sequence 21, Appl
267	39	76.5	256	5	US-10-901-011-6	Sequence 6, Appli
268	39	76.5	513	4	US-10-182-975-2	Sequence 2, Appli
269	39	76.5	665	5	US-10-723-003-62	Sequence 62, Appl
270	39	76.5	665	6	US-11-004-639-62	Sequence 62, Appl
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272	39	76.5	738	6	US-11-007-886-19	Sequence 19, Appl
273	39	76.5	739	4	US-10-418-836-26	Sequence 26, Appl
274	39	76.5	739	4	US-10-418-836-27	Sequence 27, Appl
275	39	76.5	739	6	US-11-007-886-26	Sequence 26, Appl
276	39	76.5	739	6	US-11-007-886-27	Sequence 27, Appl
277	39	76.5	740	4	US-10-418-836-28	Sequence 28, Appl
278	39	76.5	740	6	US-11-007-886-28	Sequence 28, Appl
279	39	76.5	741	4	US-10-418-836-30	Sequence 30, Appl
280	39	76.5	741	6	US-11-007-886-30	Sequence 30, Appl
281	39	76.5	742	4	US-10-418-836-29	Sequence 29, Appl
282	39	76.5	742	6	US-11-007-886-29	Sequence 29, Appl
283	39	76.5	743	4	US-10-418-836-9	Sequence 9, Appli
284	39	76.5	743	4	US-10-418-836-31	Sequence 31, Appl
285	39	76.5	743	6	US-11-007-886-9	Sequence 9, Appli
286	39	76.5	743	6	US-11-007-886-31	Sequence 31, Appl
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288	38	74.5	11	4	US-10-449-379-102	Sequence 102, App
289	38	74.5	11	4	US-10-688-015-102	Sequence 102, App
290	38	74.5	11	4	US-10-477-377-5	Sequence 5, Appli
291	38	74.5	11	4	US-10-160-505-102	Sequence 102, App
292	38	74.5	103	4	US-10-379-392-182	Sequence 182, App
293	38	74.5	107	4	US-10-160-506-87	Sequence 87, Appl
294	38	74.5	107	4	US-10-449-379-87	Sequence 87, Appl
295	38	74.5	107	4	US-10-688-015-87	Sequence 87, Appl
296	38	74.5	107	4	US-10-160-505-87	Sequence 87, Appl
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299	38	74.5	331	4	US-10-059-261-169	Sequence 169, App
300	38	74.5	331	5	US-10-627-649-169	Sequence 169, App
301	37	72.5	11	4	US-10-467-546-19	Sequence 19, Appl
302	37	72.5	11	4	US-10-396-578-71	Sequence 71, Appl
303	37	72.5	11	5	US-10-842-011-12	Sequence 12, Appl
304	37	72.5	11	5	US-10-666-332-19	Sequence 19, Appl
305	37	72.5	11	6	US-11-074-803-71	Sequence 71, Appl
306	37	72.5	107	4	US-10-300-215-143	Sequence 143, App
307	37	72.5	107	4	US-10-300-215-145	Sequence 145, App
308	37	72.5	107	4	US-10-300-215-169	Sequence 169, App
309	37	72.5	107	4	US-10-467-546-1	Sequence 1, Appli
310	37	72.5	107	4	US-10-467-546-7	Sequence 7, Appli
311	37	72.5	107	4	US-10-467-546-8	Sequence 8, Appli
312	37	72.5	107	5	US-10-842-011-4	Sequence 4, Appli
313	37	72.5	107	5	US-10-666-332-1	Sequence 1, Appli
314	37	72.5	107	5	US-10-666-332-7	Sequence 7, Appli
315	37	72.5	107	5	US-10-666-332-8	Sequence 8, Appli
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320	37	72.5	239	4	US-10-096-246-32	Sequence 32, Appl
321	37	72.5	239	4	US-10-096-246-33	Sequence 33, Appl
322	37	72.5	240	4	US-10-096-246-34	Sequence 34, Appl
323	37	72.5	240	4	US-10-096-246-35	Sequence 35, Appl
324	37	72.5	240	4	US-10-096-246-36	Sequence 36, Appl
325	37	72.5	240	4	US-10-096-246-37	Sequence 37, Appl
326	37	72.5	242	4	US-10-336-210-9	Sequence 9, Appli
327	37	72.5	244	3	US-09-940-391-1	Sequence 1, Appli
328	37	72.5	244	4	US-10-336-210-8	Sequence 8, Appli
329	37	72.5	257	4	US-10-096-246-2	Sequence 2, Appli
330	37	72.5	296	5	US-10-784-305-2	Sequence 2, Appli
331	37	72.5	622	4	US-10-378-832A-2	Sequence 2, Appli
332	36	70.6	11	4	US-10-377-121-23	Sequence 23, Appl
333	36	70.6	11	4	US-10-239-656-39	Sequence 39, Appl
334	36	70.6	11	5	US-10-482-630-38	Sequence 38, Appl
335	36	70.6	11	6	US-11-050-435-44	Sequence 44, Appl
336	36	70.6	96	4	US-10-016-986-113	Sequence 113, App
337	36	70.6	106	4	US-10-308-817-27	Sequence 27, Appl
338	36	70.6	106	4	US-10-453-698-27	Sequence 27, Appl
339	36	70.6	107	4	US-10-308-817-129	Sequence 129, App
340	36	70.6	107	4	US-10-308-817-130	Sequence 130, App
341	36	70.6	107	4	US-10-453-698-129	Sequence 129, App
342	36	70.6	107	4	US-10-453-698-130	Sequence 130, App
343	36	70.6	107	4	US-10-239-656-38	Sequence 38, Appl
344	36	70.6	107	6	US-11-050-435-32	Sequence 32, Appl
345	36	70.6	107	6	US-11-050-435-34	Sequence 34, Appl
346	36	70.6	107	6	US-11-050-435-35	Sequence 35, Appl
347	36	70.6	107	6	US-11-050-435-36	Sequence 36, Appl
348	36	70.6	107	6	US-11-050-435-37	Sequence 37, Appl
349	36	70.6	108	4	US-10-010-729-45	Sequence 45, Appl
350	36	70.6	108	4	US-10-377-121-2	Sequence 2, Appli
351	36	70.6	108	4	US-10-377-121-7	Sequence 7, Appli
352	36	70.6	108	4	US-10-377-121-12	Sequence 12, Appl
353	36	70.6	108	4	US-10-803-622-267	Sequence 267, App
354	36	70.6	108	4	US-10-803-653-267	Sequence 267, App
355	36	70.6	109	3	US-09-943-906-74	Sequence 74, Appl
356	36	70.6	109	4	US-10-435-602-74	Sequence 74, Appl
357	36	70.6	109	4	US-10-377-121-6	Sequence 6, Appli
358	36	70.6	109	5	US-10-482-630-42	Sequence 42, Appl
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360	36	70.6	111	6	US-11-050-435-6	Sequence 6, Appli
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362	36	70.6	130	4	US-10-010-729-71	Sequence 71, Appl
363	36	70.6	144	4	US-10-642-120-4	Sequence 4, Appli
364	36	70.6	144	4	US-10-642-060-4	Sequence 4, Appli
365	36	70.6	144	4	US-10-642-122-4	Sequence 4, Appli
366	36	70.6	144	4	US-10-642-059-4	Sequence 4, Appli
367	36	70.6	144	4	US-10-642-124-4	Sequence 4, Appli
368	36	70.6	144	4	US-10-621-269-4	Sequence 4, Appli
369	36	70.6	144	4	US-10-620-850-4	Sequence 4, Appli
370	36	70.6	144	4	US-10-642-118-4	Sequence 4, Appli
371	36	70.6	144	4	US-10-642-119-4	Sequence 4, Appli
372	36	70.6	144	4	US-10-642-117-4	Sequence 4, Appli
373	36	70.6	144	5	US-10-642-099-4	Sequence 4, Appli
374	36	70.6	144	5	US-10-642-064-4	Sequence 4, Appli
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379	36	70.6	144	5	US-10-642-065-4	Sequence 4, Appli
380	36	70.6	144	5	US-10-642-071-4	Sequence 4, Appli
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382	36	70.6	214	5	US-10-488-074-68	Sequence 68, Appl
383	36	70.6	214	5	US-10-488-074-70	Sequence 70, Appl
384	36	70.6	214	5	US-10-488-074-72	Sequence 72, Appl
385	36	70.6	233	4	US-10-377-121-16	Sequence 16, Appl
386	36	70.6	233	4	US-10-377-121-20	Sequence 20, Appl
387	36	70.6	240	5	US-10-482-630-51	Sequence 51, Appl
388	36	70.6	252	4	US-10-239-656-55	Sequence 55, Appl
389	36	70.6	257	4	US-10-239-656-67	Sequence 67, Appl
390	36	70.6	480	4	US-10-196-793A-59	Sequence 59, Appl
391	36	70.6	499	4	US-10-239-656-73	Sequence 73, Appl
392	36	70.6	507	4	US-10-074-596-11	Sequence 11, Appl

393	36	70.6	510	4	US-10-239-656-49	Sequence 49, Appl
394	36	70.6	737	4	US-10-369-493-17019	Sequence 17019, A
395	36	70.6	1604	3	US-09-746-491-8	Sequence 8, Appli
396	35	68.6	11	4	US-10-268-501-10	Sequence 10, Appl
397	35	68.6	11	4	US-10-608-626-10	Sequence 10, Appl
398	35	68.6	11	4	US-10-239-656-29	Sequence 29, Appl
399	35	68.6	11	5	US-10-719-310-10	Sequence 10, Appl
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405	35	68.6	105	5	US-10-823-810-30	Sequence 30, Appl
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412	35	68.6	107	4	US-10-412-703A-19	Sequence 19, Appl
413	35	68.6	107	4	US-10-412-703A-20	Sequence 20, Appl
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415	35	68.6	107	4	US-10-412-703A-22	Sequence 22, Appl
416	35	68.6	107	4	US-10-412-703A-23	Sequence 23, Appl
417	35	68.6	107	4	US-10-412-703A-24	Sequence 24, Appl
418	35	68.6	107	4	US-10-412-703A-25	Sequence 25, Appl
419	35	68.6	107	4	US-10-412-703A-26	Sequence 26, Appl
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428	35	68.6	107	4	US-10-723-434-23	Sequence 23, Appl
429	35	68.6	107	4	US-10-723-434-24	Sequence 24, Appl
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431	35	68.6	107	5	US-10-719-310-3	Sequence 3, Appli
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435	35	68.6	107	5	US-10-823-253-24	Sequence 24, Appl
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538	33	64.7	107	3	US-09-874-141-4	Sequence 4, Appli

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555	33	64.7	107	5	US-10-923-068-507	Sequence 507, App
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574	33	64.7	124	3	US-09-925-179-4	Sequence 4, Appli
575	33	64.7	124	5	US-10-968-237-4	Sequence 4, Appli
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586	33	64.7	133	3	US-09-874-141-51	Sequence 51, Appl
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607	33	64.7	488	4	US-10-237-852-2	Sequence 2, Appli
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657	32	62.7	95	6	US-11-027-139-72	Sequence 72, Appl
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674	32	62.7	137	4	US-10-425-115-277169	Sequence 277169,
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678	32	62.7	237	3	US-09-924-099-9	Sequence 9, Appli
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694	32	62.7	379	5	US-10-499-353A-583	Sequence 583, App
695	32	62.7	391	5	US-10-739-930-10338	Sequence 10338, A
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697	32	62.7	439	5	US-10-482-951-4	Sequence 4, Appli
698	32	62.7	439	5	US-10-482-951-40	Sequence 40, Appl
699	32	62.7	441	4	US-10-424-599-171663	Sequence 171663,
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950	30	58.8	123	3	US-09-818-683-165	Sequence 165, App
951	30	58.8	123	3	US-09-818-683-165	Sequence 165, App
952	30	58.8	126	4	US-10-362-082-2	Sequence 2, Appli
953	30	58.8	126	4	US-10-656-769-18	Sequence 18, Appl
954	30	58.8	127	4	US-10-478-056-35	Sequence 35, Appl
955	30	58.8	128	4	US-10-443-466A-2	Sequence 2, Appli
956	30	58.8	128	4	US-10-443-466A-41	Sequence 41, Appl
957	30	58.8	128	4	US-10-443-466A-43	Sequence 43, Appl
958	30	58.8	128	4	US-10-443-466A-72	Sequence 72, Appl
959	30	58.8	128	4	US-10-443-466A-74	Sequence 74, Appl
960	30	58.8	128	4	US-10-443-466A-76	Sequence 76, Appl
961	30	58.8	128	4	US-10-443-466A-78	Sequence 78, Appl
962	30	58.8	128	5	US-10-993-395-2	Sequence 2, Appli
963	30	58.8	128	5	US-10-993-395-13	Sequence 13, Appl
964	30	58.8	128	5	US-10-986-498-16	Sequence 16, Appl
965	30	58.8	128	5	US-10-986-498-20	Sequence 20, Appl
966	30	58.8	129	4	US-10-462-062-161	Sequence 161, App
967	30	58.8	131	4	US-10-424-599-218404	Sequence 218404,
968	30	58.8	132	4	US-10-365-123-53	Sequence 53, Appl
969	30	58.8	135	4	US-10-372-481-27	Sequence 27, Appl
970	30	58.8	135	4	US-10-371-797-27	Sequence 27, Appl
971	30	58.8	137	4	US-10-424-599-162046	Sequence 162046,
972	30	58.8	138	4	US-10-156-761-8826	Sequence 8826, Ap
973	30	58.8	140	5	US-10-276-524-28	Sequence 28, Appl
974	30	58.8	141	4	US-10-437-963-120280	Sequence 120280,
975	30	58.8	148	4	US-10-425-115-274537	Sequence 274537,
976	30	58.8	154	4	US-10-425-115-334047	Sequence 334047,

977	30	58.8	155	4	US-10-153-382-35	Sequence 35, Appl
978	30	58.8	155	5	US-10-612-497-20	Sequence 20, Appl
979	30	58.8	155	5	US-10-612-497-112	Sequence 112, App
980	30	58.8	155	5	US-10-776-649-20	Sequence 20, Appl
981	30	58.8	155	5	US-10-776-649-112	Sequence 112, App
982	30	58.8	155	6	US-11-085-368-35	Sequence 35, Appl
983	30	58.8	155	6	US-11-085-368-67	Sequence 67, Appl
984	30	58.8	157	5	US-10-644-277-36	Sequence 36, Appl
985	30	58.8	160	4	US-10-425-115-218078	Sequence 218078,
986	30	58.8	184	4	US-10-425-114-42739	Sequence 42739, A
987	30	58.8	186	6	US-11-065-977A-6	Sequence 6, Appli
988	30	58.8	202	4	US-10-425-114-39956	Sequence 39956, A
989	30	58.8	204	5	US-10-732-923-14432	Sequence 14432, A
990	30	58.8	205	4	US-10-437-963-132634	Sequence 132634,
991	30	58.8	213	5	US-10-450-763-32094	Sequence 32094, A
992	30	58.8	214	5	US-10-635-908-15	Sequence 15, Appl
993	30	58.8	214	5	US-10-635-908-17	Sequence 17, Appl
994	30	58.8	217	4	US-10-424-599-251950	Sequence 251950,
995	30	58.8	218	4	US-10-425-114-40934	Sequence 40934, A
996	30	58.8	226	4	US-10-411-037-42	Sequence 42, Appl
997	30	58.8	226	4	US-10-411-026-42	Sequence 42, Appl
998	30	58.8	226	4	US-10-410-962-42	Sequence 42, Appl
999	30	58.8	226	4	US-10-411-049-42	Sequence 42, Appl
1000	30	58.8	226	4	US-10-410-930-42	Sequence 42, Appl

ALIGNMENTS

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RESULT 1
US-09-253-794-20
; Sequence 20, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 20:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 11 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-253-794-20

  Query Match             100.0%;  Score 51;  DB 3;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.0028;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db          1 KASQDVGTSVA 11


RESULT 2
US-10-680-734-20
; Sequence 20, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 20
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-680-734-20

  Query Match             100.0%;  Score 51;  DB 4;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.0028;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db          1 KASQDVGTSVA 11


RESULT 3
US-10-755-382-20
; Sequence 20, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
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;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 20:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 11 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-755-382-20

  Query Match             100.0%;  Score 51;  DB 5;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.0028;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| |
Db          1 KASQDVGTSVA 11


RESULT 4
US-09-253-794-4
; Sequence 4, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 106 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-253-794-4

  Query Match             100.0%;  Score 51;  DB 3;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| |
Db         24 KASQDVGTSVA 34


RESULT 5
US-09-253-794-19
; Sequence 19, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 106 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-253-794-19

  Query Match             100.0%;  Score 51;  DB 3;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| |
Db         24 KASQDVGTSVA 34


RESULT 6
US-10-680-734-4
; Sequence 4, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
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;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
;   LENGTH: 106
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-680-734-4

  Query Match             100.0%;  Score 51;  DB 4;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db         24 KASQDVGTSVA 34


RESULT 7
US-10-680-734-19
; Sequence 19, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
;   LENGTH: 106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-19

  Query Match             100.0%;  Score 51;  DB 4;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db         24 KASQDVGTSVA 34


RESULT 8
US-10-755-382-4
; Sequence 4, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 106 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-755-382-4

  Query Match             100.0%;  Score 51;  DB 5;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db         24 KASQDVGTSVA 34


RESULT 9
US-10-755-382-19
; Sequence 19, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
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;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 106 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-755-382-19

  Query Match             100.0%;  Score 51;  DB 5;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.034;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db         24 KASQDVGTSVA 34


RESULT 10
US-10-270-073-4
; Sequence 4, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14VK deduced amino acid sequence
US-10-270-073-4

  Query Match             100.0%;  Score 51;  DB 4;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 0.038;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db         24 KASQDVGTSVA 34


RESULT 11
US-10-006-771A-6
; Sequence 6, Application US/10006771A
; Publication No. US20020165360A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen
;  FILE REFERENCE: 002
;  CURRENT APPLICATION NUMBER: US/10/006,771A
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: 60/250,090
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 232
;   TYPE: PRT
;   ORGANISM: Homo sapiens and Mus sp.
US-10-006-771A-6

  Query Match             100.0%;  Score 51;  DB 4;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 0.082;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
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Db         43 KASQDVGTSVA 53


RESULT 12
US-10-377-109-4
; Sequence 4, Application US/10377109
; Publication No. US20040018557A1
; GENERAL INFORMATION:
;  APPLICANT: QU, ZHENGXING
;  APPLICANT:  HANSEN, HANS
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: BISPECIFIC ANTIBODY POINT MUTATIONS FOR ENHANCING RATE
;  TITLE OF INVENTION:  OF CLEARANCE
;  FILE REFERENCE: 018733/1159
;  CURRENT APPLICATION NUMBER: US/10/377,109
;  CURRENT FILING DATE:  2003-03-03
;  PRIOR APPLICATION NUMBER: 60/361,037
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 232
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-377-109-4

  Query Match             100.0%;  Score 51;  DB 4;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 0.082;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db         43 KASQDVGTSVA 53


RESULT 13
US-10-270-073-6
; Sequence 6, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
```

```
 ;  PRIOR APPLICATION NUMBER: 60/341,881
 ;  PRIOR FILING DATE: 2001-12-21
 ;  PRIOR APPLICATION NUMBER: 60/345,641
 ;  PRIOR FILING DATE: 2002-01-08
 ;  PRIOR APPLICATION NUMBER: 60/404,919
 ;  PRIOR FILING DATE: 2002-08-22
 ;  NUMBER OF SEQ ID NOS: 20
 ;  SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ;   LENGTH: 256
 ;   TYPE: PRT
 ;   ORGANISM: Artificial Sequence
 ;   FEATURE:
 ;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ;   OTHER INFORMATION: hMN-14-0 amino acid sequence
US-10-270-073-6

  Query Match           100.0%;  Score 51;  DB 4;  Length 256;
  Best Local Similarity  100.0%;  Pred. No. 0.091;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db        165 KASQDVGTSVA 175


RESULT 14
US-10-270-073-8
; Sequence 8, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 257
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14-1G amino acid sequence
US-10-270-073-8

  Query Match           100.0%;  Score 51;  DB 4;  Length 257;
  Best Local Similarity  100.0%;  Pred. No. 0.092;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db        166 KASQDVGTSVA 176


RESULT 15
US-10-270-071-18
; Sequence 18, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of hMN14VK
US-10-270-071-18

  Query Match           100.0%;  Score 51;  DB 4;  Length 261;
  Best Local Similarity  100.0%;  Pred. No. 0.093;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db        170 KASQDVGTSVA 180


RESULT 16
US-10-270-073-2
; Sequence 2, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14scFv-L5 amino acid sequence
US-10-270-073-2

  Query Match           100.0%;  Score 51;  DB 4;  Length 261;
  Best Local Similarity  100.0%;  Pred. No. 0.093;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db        170 KASQDVGTSVA 180


RESULT 17
US-10-328-190-6
; Sequence 6, Application US/10328190
; Publication No. US20030162709A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID M.
;  TITLE OF INVENTION: METHODS OF GENERATING MULTISPECIFIC, MULTIVALENT AGENTS
;  TITLE OF INVENTION:  FROM VH AND VL DOMAINS
;  FILE REFERENCE: 042418/0115
;  CURRENT APPLICATION NUMBER: US/10/328,190
;  CURRENT FILING DATE:  2003-04-03
;  PRIOR APPLICATION NUMBER: 60/342,103
;  PRIOR FILING DATE: 2001-12-26
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: hMN14-scFv-L5
;   OTHER INFORMATION: protein sequence
US-10-328-190-6

  Query Match             100.0%;  Score 51;  DB 4;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 0.093;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db        170 KASQDVGTSVA 180


RESULT 18
US-10-270-071-20
; Sequence 20, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 262
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of polypeptide 1 of BS1
US-10-270-071-20

  Query Match             100.0%;  Score 51;  DB 4;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 0.094;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db        171 KASQDVGTSVA 181


RESULT 19
US-10-270-071-24
; Sequence 24, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 262
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of polypeptide 1 of BS1.5
US-10-270-071-24

  Query Match             100.0%;  Score 51;  DB 4;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 0.094;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db        171 KASQDVGTSVA 181


RESULT 20
US-10-270-071-28
; Sequence 28, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 262
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of polypeptide 1 of BS2
US-10-270-071-28

  Query Match             100.0%;  Score 51;  DB 4;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 0.094;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db        171 KASQDVGTSVA 181


RESULT 21
US-10-270-071-34
; Sequence 34, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
```

```
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
;   LENGTH: 262
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence for polypetide 1 of BS1.5H (h679XhMN14 bispecific
;   OTHER INFORMATION: diabody)
US-10-270-071-34

  Query Match             100.0%;  Score 51;  DB 4;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 0.094;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db        171 KASQDVGTSVA 181


RESULT 22
US-10-829-388-12
; Sequence 12, Application US/10829388
; Publication No. US20050003403A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN HSING
;  APPLICANT:  MCBRIDE, WILLIAM J.
;  TITLE OF INVENTION: POLYVALENT PROTEIN COMPLEX
;  FILE REFERENCE: 41133-0006US1
;  CURRENT APPLICATION NUMBER: US/10/829,388
;  CURRENT FILING DATE:  2004-04-22
;  PRIOR APPLICATION NUMBER: 60/464,532
;  PRIOR FILING DATE: 2003-04-22
;  PRIOR APPLICATION NUMBER: 60/525,391
;  PRIOR FILING DATE: 2003-11-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
;   LENGTH: 358
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chimeric sequence from multiple species
US-10-829-388-12

  Query Match             100.0%;  Score 51;  DB 5;  Length 358;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db         25 KASQDVGTSVA 35


RESULT 23
US-10-829-388-2
; Sequence 2, Application US/10829388
; Publication No. US20050003403A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN HSING
;  APPLICANT:  MCBRIDE, WILLIAM J.
;  TITLE OF INVENTION: POLYVALENT PROTEIN COMPLEX
;  FILE REFERENCE: 41133-0006US1
;  CURRENT APPLICATION NUMBER: US/10/829,388
;  CURRENT FILING DATE:  2004-04-22
;  PRIOR APPLICATION NUMBER: 60/464,532
;  PRIOR FILING DATE: 2003-04-22
;  PRIOR APPLICATION NUMBER: 60/525,391
;  PRIOR FILING DATE: 2003-11-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 363
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chimeric sequence from multiple species
US-10-829-388-2

  Query Match             100.0%;  Score 51;  DB 5;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db         30 KASQDVGTSVA 40


RESULT 24
US-10-829-388-11
; Sequence 11, Application US/10829388
; Publication No. US20050003403A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN HSING
;  APPLICANT:  MCBRIDE, WILLIAM J.
;  TITLE OF INVENTION: POLYVALENT PROTEIN COMPLEX
;  FILE REFERENCE: 41133-0006US1
;  CURRENT APPLICATION NUMBER: US/10/829,388
;  CURRENT FILING DATE:  2004-04-22
;  PRIOR APPLICATION NUMBER: 60/464,532
;  PRIOR FILING DATE: 2003-04-22
;  PRIOR APPLICATION NUMBER: 60/525,391
;  PRIOR FILING DATE: 2003-11-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
;   LENGTH: 364
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chimeric sequence from multiple species
US-10-829-388-11

  Query Match             100.0%;  Score 51;  DB 5;  Length 364;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||| 
Db        149 KASQDVGTSVA 159


RESULT 25
US-10-829-388-1
; Sequence 1, Application US/10829388
; Publication No. US20050003403A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN HSING
;  APPLICANT:  MCBRIDE, WILLIAM J.
;  TITLE OF INVENTION: POLYVALENT PROTEIN COMPLEX
;  FILE REFERENCE: 41133-0006US1
;  CURRENT APPLICATION NUMBER: US/10/829,388
;  CURRENT FILING DATE:  2004-04-22
;  PRIOR APPLICATION NUMBER: 60/464,532
;  PRIOR FILING DATE: 2003-04-22
;  PRIOR APPLICATION NUMBER: 60/525,391
;  PRIOR FILING DATE: 2003-11-24
```

```
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 370
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chimeric sequence from multiple species
US-10-829-388-1

  Query Match             100.0%;  Score 51;  DB 5;  Length 370;
  Best Local Similarity   100.0%;  Pred. No. 0.14;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db        155 KASQDVGTSVA 165


RESULT 26
US-10-328-190-14
; Sequence 14, Application US/10328190
; Publication No. US20030162709A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID M.
;  TITLE OF INVENTION: METHODS OF GENERATING MULTISPECIFIC, MULTIVALENT AGENTS
;  TITLE OF INVENTION:  FROM VH AND VL DOMAINS
;  FILE REFERENCE: 042418/0115
;  CURRENT APPLICATION NUMBER: US/10/328,190
;  CURRENT FILING DATE:  2003-04-03
;  PRIOR APPLICATION NUMBER: 60/342,103
;  PRIOR FILING DATE: 2001-12-26
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 391
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Protein
;   OTHER INFORMATION: sequence for VL-chain of TS1
US-10-328-190-14

  Query Match             100.0%;  Score 51;  DB 4;  Length 391;
  Best Local Similarity   100.0%;  Pred. No. 0.15;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db        300 KASQDVGTSVA 310


RESULT 27
US-10-006-773-2
; Sequence 2, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
;  FILE REFERENCE: 003
;  CURRENT APPLICATION NUMBER: US/10/006,773
;  CURRENT FILING DATE:  2001-12-10
;  PRIOR APPLICATION NUMBER: 60/250,089
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 443
;   TYPE: PRT
;   ORGANISM: Homo sapiens and Mus sp.
US-10-006-773-2

  Query Match             100.0%;  Score 51;  DB 4;  Length 443;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db         43 KASQDVGTSVA 53


RESULT 28
US-10-006-771A-2
; Sequence 2, Application US/10006771A
; Publication No. US20020165360A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen
;  FILE REFERENCE: 002
;  CURRENT APPLICATION NUMBER: US/10/006,771A
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: 60/250,090
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 443
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-006-771A-2

  Query Match             100.0%;  Score 51;  DB 4;  Length 443;
  Best Local Similarity   100.0%;  Pred. No. 0.17;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db         43 KASQDVGTSVA 53


RESULT 29
US-10-900-928-3
; Sequence 3, Application US/10900928
; Publication No. US20050069552A1
; GENERAL INFORMATION:
;  APPLICANT: Bleck, Gregory T.
;  APPLICANT:  York, Donna
;  APPLICANT:  Collins, Ian
;  TITLE OF INVENTION: Fusion Antibodies
;  FILE REFERENCE: GALA-09135
;  CURRENT APPLICATION NUMBER: US/10/900,928
;  CURRENT FILING DATE:  2004-07-28
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 669
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-900-928-3

  Query Match             100.0%;  Score 51;  DB 5;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 0.26;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||||
Db        480 KASQDVGTSVA 490


RESULT 30
US-10-281-479A-28
; Sequence 28, Application US/10281479A
```

```
; Publication No. US20030133932A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  Oshumi, Jun
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THER
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 21085.0029U6
;  CURRENT APPLICATION NUMBER: US/10/281,479A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 60/391,478
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe
US-10-281-479A-28

  Query Match             94.1%;  Score 48;  DB 4;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 0.011;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||:||
Db          1 KASQDVGTAVA 11


RESULT 31
US-10-275-180A-28
; Sequence 28, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-275-180A-28

  Query Match             94.1%;  Score 48;  DB 4;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 0.011;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||:||
Db          1 KASQDVGTAVA 11


RESULT 32
US-10-286-132A-28
; Sequence 28, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
;  APPLICANT: Zhou, Tong
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
;  TITLE OF INVENTION:  APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U7
;  CURRENT APPLICATION NUMBER: US/10/286,132A
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: US 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthet
US-10-286-132A-28

  Query Match             94.1%;  Score 48;  DB 4;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 0.011;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||:||
Db          1 KASQDVGTAVA 11


RESULT 33
US-10-297-371A-10
; Sequence 10, Application US/10297371A
; Publication No. US20040131607A1
; GENERAL INFORMATION:
;  APPLICANT: Carroll, Michael C.
;  APPLICANT:  Moore, Jr., Francis D.
;  APPLICANT:  Hechtman, Herbert B.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
;  TITLE OF INVENTION:  IMMUNOGLOBULIN-MEDIATED REPERFUSION INJURY
;  FILE REFERENCE: 10861-024US1
;  CURRENT APPLICATION NUMBER: US/10/297,371A
;  CURRENT FILING DATE:  2004-01-02
;  PRIOR APPLICATION NUMBER: PCT/US01/18510
;  PRIOR FILING DATE: 2001-06-08
;  PRIOR APPLICATION NUMBER: US 60/210,272
;  PRIOR FILING DATE: 2000-06-08
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-297-371A-10

  Query Match             94.1%;  Score 48;  DB 4;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 0.011;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 KASQDVGTSVA 11
              ||||||||:||
Db          1 KASQDVGTAVA 11


RESULT 34
US-09-215-163-21
; Sequence 21, Application US/09215163
; Publication No. US20030170248A1
; GENERAL INFORMATION:
;  APPLICANT: STINSON, Jeffrey R.
;  APPLICANT: WONG, Hing
;  APPLICANT: O'BRIEN, ALISON
;  APPLICANT: SCHMITT, Clare K.
;  APPLICANT: MELTON-CELSA, Angela
;  TITLE OF INVENTION: HUMANIZED MONOCLONAL ANTIBODIES THAT PROTECT AGAINST
;  TITLE OF INVENTION: SHIGA TOXIN INDUCED DISEASE
;  FILE REFERENCE: 04995.0032-00000
;  CURRENT APPLICATION NUMBER: US/09/215,163
;  CURRENT FILING DATE: 1998-12-18
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: Shigella dysenteriae
US-09-215-163-21

  Query Match             94.1%;  Score 48;  DB 3;  Length 108;
  Best Local Similarity   90.9%;  Pred. No. 0.14;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||:||
Db         24 KASQDVGTAVA 34


RESULT 35
US-10-297-371A-8
; Sequence 8, Application US/10297371A
; Publication No. US20040131607A1
; GENERAL INFORMATION:
;  APPLICANT: Carroll, Michael C.
;  APPLICANT:  Moore, Jr., Francis D.
;  APPLICANT:  Hechtman, Herbert B.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
;  TITLE OF INVENTION:  IMMUNOGLOBULIN-MEDIATED REPERFUSION INJURY
;  FILE REFERENCE: 10861-024US1
;  CURRENT APPLICATION NUMBER: US/10/297,371A
;  CURRENT FILING DATE:  2004-01-02
;  PRIOR APPLICATION NUMBER: PCT/US01/18510
;  PRIOR FILING DATE: 2001-06-08
;  PRIOR APPLICATION NUMBER: US 60/210,272
;  PRIOR FILING DATE: 2000-06-08
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: VARIANT
;   LOCATION: 109
;   OTHER INFORMATION: Xaa = Unknown amino acid residue
US-10-297-371A-8

  Query Match             94.1%;  Score 48;  DB 4;  Length 115;
  Best Local Similarity   90.9%;  Pred. No. 0.15;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||:||
Db         23 KASQDVGTAVA 33


RESULT 36
US-10-281-479A-72
; Sequence 72, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  Oshumi, Jun
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERA
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 21085.0029U6
;  CURRENT APPLICATION NUMBER: US/10/281,479A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 60/391,478
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 72
;   LENGTH: 212
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthet
US-10-281-479A-72

  Query Match             94.1%;  Score 48;  DB 4;  Length 212;
  Best Local Similarity   90.9%;  Pred. No. 0.29;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||||:||
Db         24 KASQDVGTAVA 34


RESULT 37
US-10-275-180A-72
; Sequence 72, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSI
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 72
;   LENGTH: 212
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
```

US-10-275-180A-72

Query Match 94.1%; Score 48; DB 4; Length 212;
Best Local Similarity 90.9%; Pred. No. 0.29;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 KASQDVGTSVA 11
              |||||||||:||
Db         24 KASQDVGTAVA 34
```

RESULT 38
US-10-286-132A-72
; Sequence 72, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Tong
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
; FILE REFERENCE: 21085.0029U7
; CURRENT APPLICATION NUMBER: US/10/286,132A
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 72
; LENGTH: 212
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-72

Query Match 94.1%; Score 48; DB 4; Length 212;
Best Local Similarity 90.9%; Pred. No. 0.29;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 KASQDVGTSVA 11
              |||||||||:||
Db         24 KASQDVGTAVA 34
```

RESULT 39
US-10-281-479A-46
; Sequence 46, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THER
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 21085.0029U6
; CURRENT APPLICATION NUMBER: US/10/281,479A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
; LENGTH: 213
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthet
US-10-281-479A-46

Query Match 94.1%; Score 48; DB 4; Length 213;
Best Local Similarity 90.9%; Pred. No. 0.29;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 KASQDVGTSVA 11
              |||||||||:||
Db         24 KASQDVGTAVA 34
```

RESULT 40
US-10-281-479A-73
; Sequence 73, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERA
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 21085.0029U6
; CURRENT APPLICATION NUMBER: US/10/281,479A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 213
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthet
US-10-281-479A-73

Query Match 94.1%; Score 48; DB 4; Length 213;
Best Local Similarity 90.9%; Pred. No. 0.29;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 KASQDVGTSVA 11
              |||||||||:||
Db         24 KASQDVGTAVA 34
```

RESULT 41
US-10-281-479A-74
; Sequence 74, Application US/10281479A

; Publication No. US20030133932A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THER
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 21085.0029U6
; CURRENT APPLICATION NUMBER: US/10/281,479A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
; LENGTH: 213
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe
US-10-281-479A-74

Query Match 94.1%; Score 48; DB 4; Length 213;
Best Local Similarity 90.9%; Pred. No. 0.29;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||:||
Db 24 KASQDVGTAVA 34

RESULT 42
US-10-281-479A-75
; Sequence 75, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THER
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 21085.0029U6
; CURRENT APPLICATION NUMBER: US/10/281,479A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 75
; LENGTH: 213
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthet
US-10-281-479A-75

Query Match 94.1%; Score 48; DB 4; Length 213;
Best Local Similarity 90.9%; Pred. No. 0.29;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||:||
Db 24 KASQDVGTAVA 34

RESULT 43
US-10-281-479A-76
; Sequence 76, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; APPLICANT: Oshumi, Jun
; APPLICANT: LoBuglio, Albert S.
; APPLICANT: Buchsbaum, Donald J.
; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERA
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 21085.0029U6
; CURRENT APPLICATION NUMBER: US/10/281,479A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: 60/391,478
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 76
; LENGTH: 213
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthet
US-10-281-479A-76

Query Match 94.1%; Score 48; DB 4; Length 213;
Best Local Similarity 90.9%; Pred. No. 0.29;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||||||:||
Db 24 KASQDVGTAVA 34

RESULT 44
US-10-275-180A-46
; Sequence 46, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
; APPLICANT: The UAB Research Foundation
; APPLICANT: Zhou, Tong
; APPLICANT: Ichikawa, Kimihisa
; APPLICANT: Kimberly, Robert P.
; APPLICANT: Koopman, William J.
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSI

```
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-275-180A-46

  Query Match             94.1%;  Score 48;  DB 4;  Length 213;
  Best Local Similarity   90.9%;  Pred. No. 0.29;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||:||
Db         24 KASQDVGTAVA 34


RESULT 45
US-10-275-180A-73
; Sequence 73, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-275-180A-73

  Query Match             94.1%;  Score 48;  DB 4;  Length 213;
  Best Local Similarity   90.9%;  Pred. No. 0.29;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||:||
Db         24 KASQDVGTAVA 34


RESULT 46
US-10-275-180A-74
; Sequence 74, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-275-180A-74

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  Best Local Similarity   90.9%;  Pred. No. 0.29;
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Qy          1 KASQDVGTSVA 11
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Db         24 KASQDVGTAVA 34


RESULT 47
US-10-275-180A-75
; Sequence 75, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSI
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 75
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-275-180A-75

  Query Match             94.1%;  Score 48;  DB 4;  Length 213;
  Best Local Similarity   90.9%;  Pred. No. 0.29;
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Qy          1 KASQDVGTSVA 11
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Db         24 KASQDVGTAVA 34


RESULT 48
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; Sequence 76, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSI
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-275-180A-76

  Query Match             94.1%;  Score 48;  DB 4;  Length 213;
  Best Local Similarity   90.9%;  Pred. No. 0.29;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
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Db         24 KASQDVGTAVA 34


RESULT 49
US-10-286-132A-46
; Sequence 46, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
;  APPLICANT: Zhou, Tong
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
;  TITLE OF INVENTION:  APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U7
;  CURRENT APPLICATION NUMBER: US/10/286,132A
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: US 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
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;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
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US-10-286-132A-46

  Query Match             94.1%;  Score 48;  DB 4;  Length 213;
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  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||:||
Db         24 KASQDVGTAVA 34


RESULT 50
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; Sequence 73, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
;  APPLICANT: Zhou, Tong
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
;  TITLE OF INVENTION:  APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U7
;  CURRENT APPLICATION NUMBER: US/10/286,132A
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: US 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
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;   TYPE: PRT
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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthet
US-10-286-132A-73

  Query Match             94.1%;  Score 48;  DB 4;  Length 213;
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  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
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Db         24 KASQDVGTAVA 34


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OM protein - protein search, using sw model

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Title: US-10-755-382-20
Perfect score: 51
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	48	94.1	108	7	US-11-097-812-52	Sequence 52, Appl
5	48	94.1	109	7	US-11-097-812-113	Sequence 113, App
6	48	94.1	115	7	US-11-097-812-38	Sequence 38, Appl
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8	43	84.3	11	7	US-11-173-071-8	Sequence 8, Appli
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180	33	64.7	107	7	US-11-004-590-323	Sequence 323, App
181	33	64.7	107	7	US-11-004-590-324	Sequence 324, App
182	33	64.7	107	7	US-11-004-590-325	Sequence 325, App
183	33	64.7	107	7	US-11-004-590-326	Sequence 326, App
184	33	64.7	107	7	US-11-004-590-327	Sequence 327, App
185	33	64.7	107	7	US-11-004-590-328	Sequence 328, App
186	33	64.7	107	7	US-11-004-590-329	Sequence 329, App
187	33	64.7	107	7	US-11-004-590-330	Sequence 330, App
188	33	64.7	107	7	US-11-004-590-379	Sequence 379, App
189	33	64.7	107	7	US-11-004-590-380	Sequence 380, App
190	33	64.7	107	7	US-11-004-590-381	Sequence 381, App
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194	33	64.7	519	7	US-11-096-568A-25369	Sequence 25369, A
195	33	64.7	571	7	US-11-096-568A-24553	Sequence 24553, A
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199	32	62.7	140	6	US-10-510-386-222	Sequence 222, App
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202	32	62.7	1124	7	US-11-087-099-4855	Sequence 4855, Ap
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207	31	60.8	145	7	US-11-126-798-58	Sequence 58, Appl
208	31	60.8	265	7	US-11-096-568A-2234	Sequence 2234, Ap
209	31	60.8	270	7	US-11-096-568A-2233	Sequence 2233, Ap
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213	30	58.8	95	7	US-11-054-669-91	Sequence 91, Appl
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216	30	58.8	95	7	US-11-084-554-113	Sequence 113, App
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220	30	58.8	95	7	US-11-004-590-97	Sequence 97, Appl
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222	30	58.8	95	7	US-11-136-250-113	Sequence 113, App
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229	30	58.8	107	7	US-11-179-359-3	Sequence 3, Appli
230	30	58.8	107	7	US-11-181-030-3	Sequence 3, Appli
231	30	58.8	107	7	US-11-182-033-3	Sequence 3, Appli
232	30	58.8	107	7	US-11-195-589-3	Sequence 3, Appli
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234	30	58.8	108	6	US-10-925-366A-174	Sequence 174, App
235	30	58.8	108	6	US-10-925-366A-188	Sequence 188, App
236	30	58.8	108	6	US-10-925-366A-190	Sequence 190, App
237	30	58.8	108	6	US-10-925-366A-205	Sequence 205, App
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239	30	58.8	108	7	US-11-005-726-6	Sequence 6, Appli
240	30	58.8	108	7	US-11-005-726-7	Sequence 7, Appli
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263	30	58.8	518	7	US-11-096-568A-852	Sequence 852, App
264	30	58.8	539	7	US-11-203-251A-79	Sequence 79, Appl
265	30	58.8	592	6	US-10-016-686-4	Sequence 4, Appli
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267	30	58.8	983	7	US-11-113-424-59	Sequence 59, Appl
268	30	58.8	983	7	US-11-203-251A-78	Sequence 78, Appl
269	30	58.8	1571	7	US-11-134-587B-12	Sequence 12, Appl
270	30	58.8	1571	7	US-11-134-587B-13	Sequence 13, Appl
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272	30	58.8	1910	7	US-11-134-587B-2	Sequence 2, Appli
273	30	58.8	1910	7	US-11-134-587B-3	Sequence 3, Appli
274	30	58.8	1978	7	US-11-212-443-60	Sequence 60, Appl
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277	29	56.9	11	7	US-11-126-978-8	Sequence 8, Appli
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281	29	56.9	107	7	US-11-108-135-26	Sequence 26, Appl
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283	29	56.9	107	7	US-11-126-978-18	Sequence 18, Appl
284	29	56.9	107	7	US-11-126-978-20	Sequence 20, Appl
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286	29	56.9	107	7	US-11-126-978-26	Sequence 26, Appl
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313	29	56.9	574	6	US-10-966-483-31	Sequence 31, Appl
314	29	56.9	574	7	US-11-021-441-15	Sequence 15, Appl
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316	29	56.9	581	6	US-10-966-483-29	Sequence 29, Appl
317	29	56.9	581	7	US-11-021-441-11	Sequence 11, Appl
318	29	56.9	581	7	US-11-021-441-13	Sequence 13, Appl
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322	29	56.9	976	7	US-11-233-796-2	Sequence 2, Appli
323	29	56.9	976	7	US-11-072-175-138	Sequence 138, App
324	29	56.9	976	7	US-11-203-251A-77	Sequence 77, Appl
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326	29	56.9	986	7	US-11-203-251A-80	Sequence 80, Appl
327	29	56.9	998	7	US-11-203-251A-83	Sequence 83, Appl
328	29	56.9	1005	7	US-11-113-424-63	Sequence 63, Appl
329	29	56.9	1015	7	US-11-203-251A-82	Sequence 82, Appl
330	29	56.9	1035	6	US-10-966-483-20	Sequence 20, Appl
331	29	56.9	1035	7	US-11-021-441-4	Sequence 4, Appli
332	29	56.9	1037	7	US-11-203-251A-81	Sequence 81, Appl
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337	28	54.9	19	7	US-11-188-187A-53	Sequence 53, Appl
338	28	54.9	20	7	US-11-188-187A-17	Sequence 17, Appl
339	28	54.9	26	6	US-10-986-501-284	Sequence 284, App
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342	28	54.9	79	6	US-10-986-501-281	Sequence 281, App
343	28	54.9	105	7	US-11-049-536-224	Sequence 224, App
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345	28	54.9	106	7	US-11-095-822-4	Sequence 4, Appli
346	28	54.9	106	7	US-11-169-171-4	Sequence 4, Appli
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351	28	54.9	108	6	US-10-925-366A-181	Sequence 181, App
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353	28	54.9	111	6	US-10-507-662-38	Sequence 38, Appl
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359	28	54.9	128	7	US-11-096-074-24	Sequence 24, Appl
360	28	54.9	128	7	US-11-095-822-20	Sequence 20, Appl
361	28	54.9	128	7	US-11-095-822-22	Sequence 22, Appl
362	28	54.9	128	7	US-11-095-822-24	Sequence 24, Appl
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367	28	54.9	223	6	US-10-793-626-2824	Sequence 2824, Ap
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369	28	54.9	238	7	US-11-096-568A-24174	Sequence 24174, A
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371	28	54.9	241	7	US-11-190-364-14	Sequence 14, Appl
372	28	54.9	241	7	US-11-147-780-14	Sequence 14, Appl
373	28	54.9	247	7	US-11-087-099-11990	Sequence 11990, A
374	28	54.9	249	7	US-11-087-099-4987	Sequence 4987, Ap
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376	28	54.9	265	7	US-11-096-568A-4715	Sequence 4715, Ap
377	28	54.9	268	7	US-11-096-568A-1677	Sequence 1677, Ap
378	28	54.9	269	7	US-11-096-568A-20278	Sequence 20278, A
379	28	54.9	278	7	US-11-195-739-9	Sequence 9, Appli
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385	28	54.9	309	7	US-11-096-568A-20277	Sequence 20277, A
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388	28	54.9	329	7	US-11-087-099-10312	Sequence 10312, A
389	28	54.9	335	7	US-11-096-568A-23112	Sequence 23112, A
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391	28	54.9	339	7	US-11-096-568A-10798	Sequence 10798, A
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397	28	54.9	377	7	US-11-087-099-2447	Sequence 2447, Ap
398	28	54.9	377	7	US-11-087-099-6533	Sequence 6533, Ap
399	28	54.9	379	7	US-11-087-099-872	Sequence 872, App
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417	28	54.9	547	7	US-11-072-512-3096	Sequence 3096, Ap
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419	28	54.9	629	7	US-11-232-406A-24	Sequence 24, Appl
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431	28	54.9	3841	7	US-11-124-367A-272	Sequence 272, App
432	27.5	53.9	802	7	US-11-087-099-4882	Sequence 4882, Ap
433	27.5	53.9	823	7	US-11-087-099-1971	Sequence 1971, Ap
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439	27	52.9	95	7	US-11-084-554-119	Sequence 119, App
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442	27	52.9	95	7	US-11-004-590-95	Sequence 95, Appl
443	27	52.9	95	7	US-11-136-250-119	Sequence 119, App
444	27	52.9	102	7	US-11-049-536-26	Sequence 26, Appl
445	27	52.9	106	7	US-11-149-943-54	Sequence 54, Appl
446	27	52.9	107	7	US-11-105-268-25	Sequence 25, Appl
447	27	52.9	108	6	US-10-925-366A-186	Sequence 186, App
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454	27	52.9	108	7	US-11-061-848-15	Sequence 15, Appl
455	27	52.9	108	7	US-11-049-536-244	Sequence 244, App
456	27	52.9	116	7	US-11-072-512-2329	Sequence 2329, Ap
457	27	52.9	145	6	US-10-993-143-21	Sequence 21, Appl
458	27	52.9	161	6	US-10-965-694-12	Sequence 12, Appl
459	27	52.9	161	6	US-10-965-694-17	Sequence 17, Appl
460	27	52.9	162	6	US-10-467-657-1718	Sequence 1718, Ap
461	27	52.9	163	6	US-10-821-234-1356	Sequence 1356, Ap
462	27	52.9	163	6	US-10-965-694-1	Sequence 1, Appli
463	27	52.9	163	7	US-11-240-769-87	Sequence 87, Appl
464	27	52.9	163	7	US-11-240-769-100	Sequence 100, App
465	27	52.9	171	7	US-11-052-554A-59	Sequence 59, Appl
466	27	52.9	171	7	US-11-052-554A-201	Sequence 201, App
467	27	52.9	174	7	US-11-113-424-185	Sequence 185, App
468	27	52.9	196	7	US-11-096-568A-29129	Sequence 29129, A
469	27	52.9	214	7	US-11-102-621-129	Sequence 129, App
470	27	52.9	237	7	US-11-108-172-1062	Sequence 1062, Ap
471	27	52.9	238	7	US-11-087-099-3505	Sequence 3505, Ap
472	27	52.9	238	7	US-11-087-099-4326	Sequence 4326, Ap
473	27	52.9	238	7	US-11-087-099-5870	Sequence 5870, Ap
474	27	52.9	238	7	US-11-087-099-12125	Sequence 12125, A
475	27	52.9	243	7	US-11-108-172-1122	Sequence 1122, Ap
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477	27	52.9	246	7	US-11-087-099-9604	Sequence 9604, Ap
478	27	52.9	246	7	US-11-087-099-10127	Sequence 10127, A
479	27	52.9	248	7	US-11-054-515-1104	Sequence 1104, Ap
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481	27	52.9	250	6	US-10-527-500-33	Sequence 33, Appl
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484	27	52.9	265	7	US-11-098-686-11404	Sequence 11404, A
485	27	52.9	269	7	US-11-096-568A-29128	Sequence 29128, A
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487	27	52.9	280	7	US-11-087-099-1796	Sequence 1796, Ap
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494	27	52.9	325	7	US-11-102-240-64	Sequence 64, Appl
495	27	52.9	325	7	US-11-103-195-64	Sequence 64, Appl
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497	27	52.9	338	7	US-11-096-568A-24090	Sequence 24090, A
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504	27	52.9	358	7	US-11-087-099-7154	Sequence 7154, Ap
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513	27	52.9	409	7	US-11-096-568A-6083	Sequence 6083, Ap
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517	27	52.9	436	7	US-11-096-568A-3234	Sequence 3234, Ap
518	27	52.9	436	7	US-11-096-568A-7059	Sequence 7059, Ap
519	27	52.9	446	7	US-11-108-172-1121	Sequence 1121, Ap
520	27	52.9	446	7	US-11-096-568A-17840	Sequence 17840, A
521	27	52.9	446	7	US-11-096-568A-32831	Sequence 32831, A
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524	27	52.9	458	7	US-11-087-099-6039	Sequence 6039, Ap
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533	27	52.9	521	7	US-11-096-568A-29901	Sequence 29901, A
534	27	52.9	524	6	US-10-878-556A-152	Sequence 152, App
535	27	52.9	539	7	US-11-096-568A-29900	Sequence 29900, A
536	27	52.9	543	7	US-11-055-822-494	Sequence 494, App

537	27	52.9	543	7	US-11-055-822-874	Sequence 874, App
538	27	52.9	550	7	US-11-072-512-3495	Sequence 3495, Ap
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543	27	52.9	625	6	US-10-973-115B-70	Sequence 70, Appl
544	27	52.9	627	7	US-11-096-568A-29899	Sequence 29899, A
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547	27	52.9	638	7	US-11-077-619-28	Sequence 28, Appl
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551	27	52.9	679	7	US-11-096-568A-2506	Sequence 2506, Ap
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554	27	52.9	735	7	US-11-087-099-4908	Sequence 4908, Ap
555	27	52.9	753	7	US-11-096-568A-2505	Sequence 2505, Ap
556	27	52.9	763	7	US-11-087-099-8573	Sequence 8573, Ap
557	27	52.9	931	6	US-10-330-773-370	Sequence 370, App
558	27	52.9	1029	6	US-10-821-234-908	Sequence 908, App
559	27	52.9	1033	6	US-10-330-773-367	Sequence 367, App
560	27	52.9	1044	7	US-11-051-720-1563	Sequence 1563, Ap
561	27	52.9	1049	7	US-11-051-720-1565	Sequence 1565, Ap
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563	27	52.9	1302	7	US-11-210-471-2	Sequence 2, Appli
564	27	52.9	1347	7	US-11-087-099-5370	Sequence 5370, Ap
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566	27	52.9	1493	7	US-11-004-057-4	Sequence 4, Appli
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573	27	52.9	3116	6	US-10-995-561-826	Sequence 826, App
574	27	52.9	8746	7	US-11-098-686-10232	Sequence 10232, A
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576	26	51.0	16	7	US-11-188-187A-56	Sequence 56, Appl
577	26	51.0	43	6	US-10-957-887B-221	Sequence 221, App
578	26	51.0	48	6	US-10-957-887B-36	Sequence 36, Appl
579	26	51.0	53	7	US-11-240-769-88	Sequence 88, Appl
580	26	51.0	61	5	US-09-978-360A-447	Sequence 447, App
581	26	51.0	67	7	US-11-096-568A-1045	Sequence 1045, Ap
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583	26	51.0	95	7	US-11-054-669-84	Sequence 84, Appl
584	26	51.0	95	7	US-11-054-669-85	Sequence 85, Appl
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586	26	51.0	95	7	US-11-084-554-130	Sequence 130, App
587	26	51.0	95	7	US-11-061-848-50	Sequence 50, Appl
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589	26	51.0	95	7	US-11-061-848-67	Sequence 67, Appl
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591	26	51.0	95	7	US-11-004-590-91	Sequence 91, Appl
592	26	51.0	95	7	US-11-136-250-127	Sequence 127, App
593	26	51.0	95	7	US-11-136-250-130	Sequence 130, App
594	26	51.0	96	7	US-11-240-769-172	Sequence 172, App
595	26	51.0	104	7	US-11-049-536-384	Sequence 384, App
596	26	51.0	105	7	US-11-155-775-40	Sequence 40, Appl
597	26	51.0	107	6	US-10-982-440-62	Sequence 62, Appl
598	26	51.0	107	7	US-11-049-536-632	Sequence 632, App
599	26	51.0	108	6	US-10-925-366A-175	Sequence 175, App
600	26	51.0	108	7	US-11-049-536-268	Sequence 268, App
601	26	51.0	108	7	US-11-049-536-300	Sequence 300, App
602	26	51.0	108	7	US-11-049-536-664	Sequence 664, App
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607	26	51.0	120	6	US-10-994-820A-15	Sequence 15, Appl
608	26	51.0	135	7	US-11-194-246-297	Sequence 297, App
609	26	51.0	137	7	US-11-072-512-2583	Sequence 2583, Ap
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613	26	51.0	182	5	US-09-995-493-54	Sequence 54, Appl
614	26	51.0	213	6	US-10-793-626-1096	Sequence 1096, Ap
615	26	51.0	213	7	US-11-158-505-34	Sequence 34, Appl
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622	26	51.0	236	7	US-11-096-568A-33848	Sequence 33848, A
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628	26	51.0	247	7	US-11-087-099-4052	Sequence 4052, Ap
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635	26	51.0	254	7	US-11-004-399-620	Sequence 620, App
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638	26	51.0	261	7	US-11-096-568A-3035	Sequence 3035, Ap
639	26	51.0	261	7	US-11-096-568A-3037	Sequence 3037, Ap
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641	26	51.0	264	7	US-11-055-822-596	Sequence 596, App
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645	26	51.0	287	7	US-11-096-568A-5022	Sequence 5022, Ap
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648	26	51.0	296	7	US-11-074-176-166	Sequence 166, App
649	26	51.0	302	6	US-10-467-657-80	Sequence 80, Appl
650	26	51.0	302	6	US-10-467-657-4818	Sequence 4818, Ap
651	26	51.0	308	6	US-10-467-657-8054	Sequence 8054, Ap
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653	26	51.0	314	7	US-11-087-099-2161	Sequence 2161, Ap
654	26	51.0	317	6	US-10-329-258-29	Sequence 29, Appl
655	26	51.0	317	7	US-11-072-512-3036	Sequence 3036, Ap
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662	26	51.0	336	7	US-11-087-099-6211	Sequence 6211, Ap
663	26	51.0	336	7	US-11-096-568A-5021	Sequence 5021, Ap
664	26	51.0	343	7	US-11-087-099-1522	Sequence 1522, Ap
665	26	51.0	344	6	US-10-454-437-148	Sequence 148, App
666	26	51.0	350	7	US-11-103-957-19	Sequence 19, Appl
667	26	51.0	358	7	US-11-087-099-641	Sequence 641, App
668	26	51.0	358	7	US-11-096-568A-3632	Sequence 3632, Ap
669	26	51.0	360	7	US-11-064-246-7	Sequence 7, Appli
670	26	51.0	372	7	US-11-096-568A-5020	Sequence 5020, Ap
671	26	51.0	390	6	US-10-131-826A-338	Sequence 338, App
672	26	51.0	390	6	US-10-973-115B-338	Sequence 338, App
673	26	51.0	392	7	US-11-084-458-2	Sequence 2, Appli
674	26	51.0	399	7	US-11-065-943-53	Sequence 53, Appl
675	26	51.0	405	7	US-11-096-568A-3631	Sequence 3631, Ap
676	26	51.0	407	7	US-11-087-099-3407	Sequence 3407, Ap
677	26	51.0	413	6	US-10-330-773-215	Sequence 215, App
678	26	51.0	415	7	US-11-096-568A-34386	Sequence 34386, A
679	26	51.0	416	7	US-11-096-568A-34385	Sequence 34385, A
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686	26	51.0	449	6	US-10-641-678-38	Sequence 38, Appl
687	26	51.0	458	7	US-11-087-099-11080	Sequence 11080, A
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689	26	51.0	466	7	US-11-087-099-2102	Sequence 2102, Ap
690	26	51.0	466	7	US-11-087-099-5346	Sequence 5346, Ap
691	26	51.0	466	7	US-11-087-099-7729	Sequence 7729, Ap
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694	26	51.0	466	7	US-11-087-099-12077	Sequence 12077, A
695	26	51.0	467	7	US-11-087-099-3539	Sequence 3539, Ap
696	26	51.0	473	7	US-11-075-185-12	Sequence 12, Appl
697	26	51.0	476	7	US-11-055-822-942	Sequence 942, App
698	26	51.0	476	7	US-11-055-822-962	Sequence 962, App
699	26	51.0	478	7	US-11-096-568A-30175	Sequence 30175, A
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702	26	51.0	488	6	US-10-485-517-307	Sequence 307, App
703	26	51.0	496	6	US-10-793-626-2896	Sequence 2896, Ap
704	26	51.0	496	7	US-11-096-568A-19471	Sequence 19471, A
705	26	51.0	506	6	US-10-641-678-69	Sequence 69, Appl
706	26	51.0	506	7	US-11-096-568A-19470	Sequence 19470, A
707	26	51.0	514	7	US-11-096-568A-30174	Sequence 30174, A
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712	26	51.0	594	6	US-10-467-657-3952	Sequence 3952, Ap
713	26	51.0	600	6	US-10-131-826A-462	Sequence 462, App
714	26	51.0	600	6	US-10-973-115B-462	Sequence 462, App
715	26	51.0	602	7	US-11-087-099-10340	Sequence 10340, A
716	26	51.0	609	7	US-11-087-099-8265	Sequence 8265, Ap
717	26	51.0	611	7	US-11-096-568A-1848	Sequence 1848, Ap
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724	26	51.0	666	7	US-11-087-099-8103	Sequence 8103, Ap
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726	26	51.0	690	7	US-11-212-443-171	Sequence 171, App
727	26	51.0	694	7	US-11-087-099-462	Sequence 462, App
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729	26	51.0	702	7	US-11-072-512-2154	Sequence 2154, Ap
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731	26	51.0	710	7	US-11-212-443-30	Sequence 30, Appl
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733	26	51.0	779	7	US-11-128-420-12	Sequence 12, Appl
734	26	51.0	817	6	US-10-793-626-50	Sequence 50, Appl
735	26	51.0	817	6	US-10-793-626-1528	Sequence 1528, Ap
736	26	51.0	823	6	US-10-467-657-2526	Sequence 2526, Ap
737	26	51.0	862	7	US-11-096-568A-28539	Sequence 28539, A
738	26	51.0	897	7	US-11-137-465-35	Sequence 35, Appl
739	26	51.0	914	6	US-10-501-035-373	Sequence 373, App
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741	26	51.0	955	7	US-11-096-568A-28538	Sequence 28538, A
742	26	51.0	967	7	US-11-171-701-4	Sequence 4, Appli
743	26	51.0	971	7	US-11-052-554A-3	Sequence 3, Appli
744	26	51.0	993	7	US-11-137-465-36	Sequence 36, Appl
745	26	51.0	1005	7	US-11-203-251A-84	Sequence 84, Appl
746	26	51.0	1142	7	US-11-087-099-6734	Sequence 6734, Ap
747	26	51.0	1166	7	US-11-072-512-2949	Sequence 2949, Ap
748	26	51.0	1388	7	US-11-098-686-11149	Sequence 11149, A
749	26	51.0	1770	7	US-11-103-957-21	Sequence 21, Appl
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754	26	51.0	2910	6	US-10-330-773-39	Sequence 39, Appl
755	26	51.0	3674	7	US-11-000-463-454	Sequence 454, App
756	26	51.0	8695	7	US-11-205-109-15	Sequence 15, Appl
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758	25	49.0	20	6	US-10-939-890-178	Sequence 178, App
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766	25	49.0	43	6	US-10-957-887B-232	Sequence 232, App
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768	25	49.0	97	7	US-11-096-568A-787	Sequence 787, App
769	25	49.0	100	6	US-10-793-626-2550	Sequence 2550, Ap
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775	25	49.0	106	7	US-11-107-028-9	Sequence 9, Appli
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778	25	49.0	107	7	US-11-105-268-28	Sequence 28, Appl
779	25	49.0	107	7	US-11-105-268-32	Sequence 32, Appl
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784	25	49.0	108	6	US-10-925-366A-316	Sequence 316, App
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797	25	49.0	127	6	US-10-714-887-96	Sequence 96, Appl
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805	25	49.0	154	7	US-11-096-568A-19693	Sequence 19693, A
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809	25	49.0	170	7	US-11-232-406A-26	Sequence 26, Appl
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821	25	49.0	202	7	US-11-166-412-143	Sequence 143, App
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886	25	49.0	310	6	US-10-994-820A-10	Sequence 10, Appl
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908	25	49.0	331	7	US-11-167-856-6	Sequence 6, Appli
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914	25	49.0	338	7	US-11-087-099-1223	Sequence 1223, Ap
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936	25	49.0	358	7	US-11-174-816-65	Sequence 65, Appl
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939	25	49.0	358	7	US-11-174-816-68	Sequence 68, Appl
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943	25	49.0	358	7	US-11-174-819-22	Sequence 22, Appl
944	25	49.0	358	7	US-11-174-819-24	Sequence 24, Appl
945	25	49.0	358	7	US-11-174-819-26	Sequence 26, Appl
946	25	49.0	358	7	US-11-174-819-83	Sequence 83, Appl
947	25	49.0	358	7	US-11-174-819-84	Sequence 84, Appl
948	25	49.0	358	7	US-11-174-819-85	Sequence 85, Appl
949	25	49.0	358	7	US-11-174-819-86	Sequence 86, Appl
950	25	49.0	358	7	US-11-174-819-87	Sequence 87, Appl
951	25	49.0	358	7	US-11-174-819-88	Sequence 88, Appl
952	25	49.0	358	7	US-11-174-819-89	Sequence 89, Appl
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954	25	49.0	360	7	US-11-096-568A-25913	Sequence 25913, A
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957	25	49.0	361	7	US-11-096-568A-26213	Sequence 26213, A
958	25	49.0	362	7	US-11-174-816-70	Sequence 70, Appl
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964	25	49.0	374	7	US-11-087-099-9412	Sequence 9412, Ap
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972	25	49.0	385	7	US-11-087-099-1453	Sequence 1453, Ap
973	25	49.0	385	7	US-11-116-881A-474	Sequence 474, App
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986	25	49.0	398	7	US-11-087-099-366	Sequence 366, App
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995	25	49.0	405	7	US-11-087-099-2111	Sequence 2111, Ap
996	25	49.0	406	7	US-11-167-856-14	Sequence 14, Appl
997	25	49.0	406	7	US-11-087-099-316	Sequence 316, App
998	25	49.0	406	7	US-11-087-099-11832	Sequence 11832, A
999	25	49.0	406	7	US-11-087-099-12148	Sequence 12148, A
1000	25	49.0	407	7	US-11-096-568A-20442	Sequence 20442, A

ALIGNMENTS

```
RESULT 1
US-11-097-812-53
; Sequence 53, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
;   LENGTH: 105
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-53

  Query Match             94.1%;  Score 48;  DB 7;  Length 105;
  Best Local Similarity   90.9%;  Pred. No. 0.0089;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||||:||
Db         24 KASQDVGTAVA 34


RESULT 2
US-11-097-812-45
; Sequence 45, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-45

  Query Match             94.1%;  Score 48;  DB 7;  Length 108;
  Best Local Similarity   90.9%;  Pred. No. 0.0092;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||||:||
Db         23 KASQDVGTAVA 33


RESULT 3
US-11-097-812-50
; Sequence 50, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-50

  Query Match             94.1%;  Score 48;  DB 7;  Length 108;
  Best Local Similarity   90.9%;  Pred. No. 0.0092;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 KASQDVGTSVA 11
              |||||||||:||
Db         23 KASQDVGTAVA 33


RESULT 4
US-11-097-812-52
; Sequence 52, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-52

  Query Match             94.1%;  Score 48;  DB 7;  Length 108;
  Best Local Similarity   90.9%;  Pred. No. 0.0092;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||||:||
Db         24 KASQDVGTAVA 34


RESULT 5
US-11-097-812-113
; Sequence 113, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 113
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: mouse
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (6)..(6)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-097-812-113

  Query Match             94.1%;  Score 48;  DB 7;  Length 109;
  Best Local Similarity   90.9%;  Pred. No. 0.0093;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||||:||
Db         24 KASQDVGTAVA 34


RESULT 6
US-11-097-812-38
; Sequence 38, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-38

  Query Match             94.1%;  Score 48;  DB 7;  Length 115;
  Best Local Similarity   90.9%;  Pred. No. 0.0099;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||||||:||
Db         24 KASQDVGTAVA 34


RESULT 7
US-10-839-799-118
; Sequence 118, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
```

```
;           ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/839,799
;           FILING DATE: 06-May-2004
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/08/646,265
;           FILING DATE: 09-SEP-1996
;           APPLICATION NUMBER: WO PCT/JP94/01763
;           FILING DATE: 19-OCT-1994
;           APPLICATION NUMBER: JP 5-291078
;           FILING DATE: 19-NOV-1993
;       ATTORNEY/AGENT INFORMATION:
;           NAME: WEGNER, Harold C.
;           REGISTRATION NUMBER: 25,258
;           REFERENCE/DOCKET NUMBER: 53466/184
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 118:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 11 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 118:
US-10-839-799-118

  Query Match             84.3%;  Score 43;  DB 6;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 0.0076;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db          1 KASQNVGTNVA 11


RESULT 8
US-11-173-071-8
; Sequence 8, Application US/11173071
; Publication No. US20050244409A1
; GENERAL INFORMATION:
;  APPLICANT: ERICKSON-MILLER, CONNIE
;  APPLICANT:  HOLMES, STEPHEN D.
;  APPLICANT:  TAYLOR, ALEXANDER H.
;  APPLICANT:  YOUNG, PETER R.
;  TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR ANTIBODIES
;  FILE REFERENCE: P50911
;  CURRENT APPLICATION NUMBER: US/11/173,071
;  CURRENT FILING DATE:  2005-07-01
;  PRIOR APPLICATION NUMBER: US/09/958,620
;  PRIOR FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: PCT/US00/10284
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/129,263
;  PRIOR FILING DATE: 1999-04-14
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-173-071-8

  Query Match             84.3%;  Score 43;  DB 7;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 0.0076;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db          1 KASQNVGTNVA 11


RESULT 9
US-10-839-799-130
; Sequence 130, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;       APPLICANT: OHTOMO, Toshihiko
;                  SATO, Koh
;                  TSUCHIYA, Masayuki
;       TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                           MEDULLOBLASTOMA CELLS
;       NUMBER OF SEQUENCES: 132
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Foley & Lardner
;           STREET: 3000 K Street, N.W., Suite 500
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/839,799
;           FILING DATE: 06-May-2004
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/08/646,265
;           FILING DATE: 09-SEP-1996
;           APPLICATION NUMBER: WO PCT/JP94/01763
;           FILING DATE: 19-OCT-1994
;           APPLICATION NUMBER: JP 5-291078
;           FILING DATE: 19-NOV-1993
;       ATTORNEY/AGENT INFORMATION:
;           NAME: WEGNER, Harold C.
;           REGISTRATION NUMBER: 25,258
;           REFERENCE/DOCKET NUMBER: 53466/184
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 130:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 107 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 130:
US-10-839-799-130

  Query Match             84.3%;  Score 43;  DB 6;  Length 107;
  Best Local Similarity   81.8%;  Pred. No. 0.094;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 10
US-10-839-799-131
; Sequence 131, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;       APPLICANT: OHTOMO, Toshihiko
;                  SATO, Koh
```

```
;                 TSUCHIYA, Masayuki
;       TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                           MEDULLOBLASTOMA CELLS
;       NUMBER OF SEQUENCES: 132
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/839,799
;            FILING DATE: 06-May-2004
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/646,265
;            FILING DATE: 09-SEP-1996
;            APPLICATION NUMBER: WO PCT/JP94/01763
;            FILING DATE: 19-OCT-1994
;            APPLICATION NUMBER: JP 5-291078
;            FILING DATE: 19-NOV-1993
;       ATTORNEY/AGENT INFORMATION:
;            NAME: WEGNER, Harold C.
;            REGISTRATION NUMBER: 25,258
;            REFERENCE/DOCKET NUMBER: 53466/184
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 131:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 107 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-10-839-799-131

  Query Match             84.3%;  Score 43;  DB 6;  Length 107;
  Best Local Similarity   81.8%;  Pred. No. 0.094;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 11
US-11-173-071-16
; Sequence 16, Application US/11173071
; Publication No. US20050244409A1
; GENERAL INFORMATION:
;  APPLICANT: ERICKSON-MILLER, CONNIE
;  APPLICANT:  HOLMES, STEPHEN D.
;  APPLICANT:  TAYLOR, ALEXANDER H.
;  APPLICANT:  YOUNG, PETER R.
;  TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR ANTIBODIES
;  FILE REFERENCE: P50911
;  CURRENT APPLICATION NUMBER: US/11/173,071
;  CURRENT FILING DATE:  2005-07-01
;  PRIOR APPLICATION NUMBER: US/09/958,620
;  PRIOR FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: PCT/US00/10284
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/129,263
;  PRIOR FILING DATE: 1999-04-14
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: light chain variable region 3G9HZLC1-0
US-11-173-071-16

  Query Match             84.3%;  Score 43;  DB 7;  Length 108;
  Best Local Similarity   81.8%;  Pred. No. 0.095;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         30 KASQNVGTNVA 40


RESULT 12
US-11-173-071-18
; Sequence 18, Application US/11173071
; Publication No. US20050244409A1
; GENERAL INFORMATION:
;  APPLICANT: ERICKSON-MILLER, CONNIE
;  APPLICANT:  HOLMES, STEPHEN D.
;  APPLICANT:  TAYLOR, ALEXANDER H.
;  APPLICANT:  YOUNG, PETER R.
;  TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR ANTIBODIES
;  FILE REFERENCE: P50911
;  CURRENT APPLICATION NUMBER: US/11/173,071
;  CURRENT FILING DATE:  2005-07-01
;  PRIOR APPLICATION NUMBER: US/09/958,620
;  PRIOR FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: PCT/US00/10284
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/129,263
;  PRIOR FILING DATE: 1999-04-14
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-173-071-18

  Query Match             84.3%;  Score 43;  DB 7;  Length 108;
  Best Local Similarity   81.8%;  Pred. No. 0.095;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         30 KASQNVGTNVA 40


RESULT 13
US-11-173-071-20
; Sequence 20, Application US/11173071
; Publication No. US20050244409A1
; GENERAL INFORMATION:
;  APPLICANT: ERICKSON-MILLER, CONNIE
;  APPLICANT:  HOLMES, STEPHEN D.
;  APPLICANT:  TAYLOR, ALEXANDER H.
;  APPLICANT:  YOUNG, PETER R.
;  TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR ANTIBODIES
;  FILE REFERENCE: P50911
;  CURRENT APPLICATION NUMBER: US/11/173,071
;  CURRENT FILING DATE:  2005-07-01
;  PRIOR APPLICATION NUMBER: US/09/958,620
;  PRIOR FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: PCT/US00/10284
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/129,263
;  PRIOR FILING DATE: 1999-04-14
```

; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-173-071-20

Query Match 84.3%; Score 43; DB 7; Length 108;
Best Local Similarity 81.8%; Pred. No. 0.095;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||:|||:||
Db 30 KASQNVGTNVA 40

RESULT 14
US-11-173-071-22
; Sequence 22, Application US/11173071
; Publication No. US20050244409A1
; GENERAL INFORMATION:
; APPLICANT: ERICKSON-MILLER, CONNIE
; APPLICANT: HOLMES, STEPHEN D.
; APPLICANT: TAYLOR, ALEXANDER H.
; APPLICANT: YOUNG, PETER R.
; TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR ANTIBODIES
; FILE REFERENCE: P50911
; CURRENT APPLICATION NUMBER: US/11/173,071
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US/09/958,620
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: PCT/US00/10284
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,263
; PRIOR FILING DATE: 1999-04-14
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-173-071-22

Query Match 84.3%; Score 43; DB 7; Length 108;
Best Local Similarity 81.8%; Pred. No. 0.095;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||:|||:||
Db 30 KASQNVGTNVA 40

RESULT 15
US-11-097-812-51
; Sequence 51, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 108
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-51

Query Match 84.3%; Score 43; DB 7; Length 108;
Best Local Similarity 81.8%; Pred. No. 0.095;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||:|||:||
Db 24 KASQNVGTAVA 34

RESULT 16
US-11-097-812-42
; Sequence 42, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 109
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-42

Query Match 84.3%; Score 43; DB 7; Length 109;
Best Local Similarity 81.8%; Pred. No. 0.096;
Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KASQDVGTSVA 11
||||:|||:||
Db 24 KASQNVGTAVA 34

RESULT 17
US-11-097-812-43
; Sequence 43, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01

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;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-43

  Query Match             84.3%;  Score 43;  DB 7;  Length 109;
  Best Local Similarity   81.8%;  Pred. No. 0.096;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTAVA 34


RESULT 18
US-11-097-812-48
; Sequence 48, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-48

  Query Match             84.3%;  Score 43;  DB 7;  Length 109;
  Best Local Similarity   81.8%;  Pred. No. 0.096;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTAVA 34


RESULT 19
US-11-097-812-54
; Sequence 54, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-54

  Query Match             84.3%;  Score 43;  DB 7;  Length 109;
  Best Local Similarity   81.8%;  Pred. No. 0.096;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTAVA 34


RESULT 20
US-11-195-095-2
; Sequence 2, Application US/11195095
; Publication No. US20060040323A1
; GENERAL INFORMATION:
;  APPLICANT: Arepally, Gowthami
;  APPLICANT:  Kisiel, Walter
;  APPLICANT:  Kamei, Keiko
;  APPLICANT:  Kamei, Shintaro
;  TITLE OF INVENTION: Compositions and Methods Useful for the Diagnosis and Treatment o
;  TITLE OF INVENTION:  Heparin Induced Thrombocytopenia/Thrombosis
;  FILE REFERENCE: 10312-2U1
;  CURRENT APPLICATION NUMBER: US/11/195,095
;  CURRENT FILING DATE:  2005-08-02
;  PRIOR APPLICATION NUMBER: US/09/615,872
;  PRIOR FILING DATE: 2000-07-13
;  PRIOR APPLICATION NUMBER: US 60/143,536
;  PRIOR FILING DATE: 1999-07-13
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-195-095-2

  Query Match             84.3%;  Score 43;  DB 7;  Length 110;
  Best Local Similarity   81.8%;  Pred. No. 0.097;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         27 KASQNVGTNVA 37


RESULT 21
US-11-173-071-4
; Sequence 4, Application US/11173071
; Publication No. US20050244409A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: ERICKSON-MILLER, CONNIE
;  APPLICANT:  HOLMES, STEPHEN D.
;  APPLICANT:  TAYLOR, ALEXANDER H.
;  APPLICANT:  YOUNG, PETER R.
;  TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR ANTIBODIES
;  FILE REFERENCE: P50911
;  CURRENT APPLICATION NUMBER: US/11/173,071
;  CURRENT FILING DATE:  2005-07-01
;  PRIOR APPLICATION NUMBER: US/09/958,620
;  PRIOR FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: PCT/US00/10284
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/129,263
;  PRIOR FILING DATE: 1999-04-14
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 112
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: 3G9 light chain variable region
US-11-173-071-4

  Query Match             84.3%;  Score 43;  DB 7;  Length 112;
  Best Local Similarity   81.8%;  Pred. No. 0.099;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         24 KASQNVGTNVA 34


RESULT 22
US-10-839-799-43
; Sequence 43, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 43:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 126 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-10-839-799-43

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 23
US-10-839-799-47
; Sequence 47, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 47:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 126 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-10-839-799-47

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
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  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 24
US-10-839-799-51
; Sequence 51, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 51:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 126 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-10-839-799-51

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 25
US-10-839-799-53
; Sequence 53, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 53:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 126 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-839-799-53

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 26
US-10-839-799-57
; Sequence 57, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
```

```
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/839,799
;              FILING DATE: 06-May-2004
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/08/646,265
;              FILING DATE: 09-SEP-1996
;              APPLICATION NUMBER: WO PCT/JP94/01763
;              FILING DATE: 19-OCT-1994
;              APPLICATION NUMBER: JP 5-291078
;              FILING DATE: 19-NOV-1993
;         ATTORNEY/AGENT INFORMATION:
;              NAME: WEGNER, Harold C.
;              REGISTRATION NUMBER: 25,258
;              REFERENCE/DOCKET NUMBER: 53466/184
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (202)672-5300
;              TELEFAX: (202)672-5399
;              TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 57:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 126 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-839-799-57

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 27
US-10-839-799-59
; Sequence 59, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;         APPLICANT: OHTOMO, Toshihiko
;                    SATO, Koh
;                    TSUCHIYA, Masayuki
;         TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                             MEDULLOBLASTOMA CELLS
;         NUMBER OF SEQUENCES: 132
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Foley & Lardner
;              STREET: 3000 K Street, N.W., Suite 500
;              CITY: Washington
;              STATE: D.C.
;              COUNTRY: USA
;              ZIP: 20007-5109
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/839,799
;              FILING DATE: 06-May-2004
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/08/646,265
;              FILING DATE: 09-SEP-1996
;              APPLICATION NUMBER: WO PCT/JP94/01763
;              FILING DATE: 19-OCT-1994
;              APPLICATION NUMBER: JP 5-291078
;              FILING DATE: 19-NOV-1993
;         ATTORNEY/AGENT INFORMATION:
;              NAME: WEGNER, Harold C.
;              REGISTRATION NUMBER: 25,258
;              REFERENCE/DOCKET NUMBER: 53466/184
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (202)672-5300
;              TELEFAX: (202)672-5399
;              TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 59:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 126 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-10-839-799-59

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 28
US-10-839-799-63
; Sequence 63, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;         APPLICANT: OHTOMO, Toshihiko
;                    SATO, Koh
;                    TSUCHIYA, Masayuki
;         TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                             MEDULLOBLASTOMA CELLS
;         NUMBER OF SEQUENCES: 132
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Foley & Lardner
;              STREET: 3000 K Street, N.W., Suite 500
;              CITY: Washington
;              STATE: D.C.
;              COUNTRY: USA
;              ZIP: 20007-5109
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/10/839,799
;              FILING DATE: 06-May-2004
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/08/646,265
;              FILING DATE: 09-SEP-1996
;              APPLICATION NUMBER: WO PCT/JP94/01763
;              FILING DATE: 19-OCT-1994
;              APPLICATION NUMBER: JP 5-291078
;              FILING DATE: 19-NOV-1993
;         ATTORNEY/AGENT INFORMATION:
;              NAME: WEGNER, Harold C.
;              REGISTRATION NUMBER: 25,258
;              REFERENCE/DOCKET NUMBER: 53466/184
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (202)672-5300
;              TELEFAX: (202)672-5399
;              TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 63:
;         SEQUENCE CHARACTERISTICS:
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;             LENGTH: 126 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-839-799-63

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 29
US-10-839-799-65
; Sequence 65, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 65:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 126 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-10-839-799-65

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 30
US-10-839-799-69
; Sequence 69, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 69:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 126 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-10-839-799-69

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 31
US-10-839-799-73
; Sequence 73, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
```

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;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 73:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 126 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 73:
US-10-839-799-73

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 32
US-10-839-799-75
; Sequence 75, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 75:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 126 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-10-839-799-75

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 33
US-10-839-799-77
; Sequence 77, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
```

```
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 77:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 126 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 77:
US-10-839-799-77

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 34
US-10-839-799-81
; Sequence 81, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 81:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 126 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 81:
US-10-839-799-81

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 35
US-10-839-799-85
; Sequence 85, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 85:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 126 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-10-839-799-85

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 36
US-10-839-799-87
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; Sequence 87, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 87:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 126 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 87:
US-10-839-799-87

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 37
US-10-839-799-91
; Sequence 91, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 91:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 126 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 91:
US-10-839-799-91

  Query Match             84.3%;  Score 43;  DB 6;  Length 126;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         43 KASQNVGTNVA 53


RESULT 38
US-10-839-799-27
; Sequence 27, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
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;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;       ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 27:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 127 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-839-799-27

  Query Match             84.3%;  Score 43;  DB 6;  Length 127;
  Best Local Similarity   81.8%;  Pred. No. 0.11;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         44 KASQNVGTNVA 54


RESULT 39
US-10-504-389A-47
; Sequence 47, Application US/10504389A
; Publication No. US20060045876A1
; GENERAL INFORMATION:
;  APPLICANT: Renner, Christoph
;  APPLICANT:  Scott, Andrew
;  TITLE OF INVENTION: FUSION PROTEINS OF HUMANIZED G250 SPECIFIC
;  TITLE OF INVENTION:  ANTIBODIES AND USES THEREOF
;  FILE REFERENCE: LUD 5821
;  CURRENT APPLICATION NUMBER: US/10/504,389A
;  CURRENT FILING DATE:  2004-08-10
;  PRIOR APPLICATION NUMBER: PCT/US03/04243
;  PRIOR FILING DATE: 2002-02-12
;  NUMBER OF SEQ ID NOS: 56
; SEQ ID NO 47
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Mus musculus
;   FEATURE:
;   OTHER INFORMATION: amino acid sequence for murine light chain variable region
US-10-504-389A-47

  Query Match             84.3%;  Score 43;  DB 6;  Length 129;
  Best Local Similarity   81.8%;  Pred. No. 0.12;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db         45 KASQNVGTNVA 55


RESULT 40
US-10-839-799-109
; Sequence 109, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;       APPLICANT: OHTOMO, Toshihiko
;                  SATO, Koh
;                  TSUCHIYA, Masayuki
;       TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                           MEDULLOBLASTOMA CELLS
;       NUMBER OF SEQUENCES: 132
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/839,799
;            FILING DATE: 06-May-2004
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/646,265
;            FILING DATE: 09-SEP-1996
;            APPLICATION NUMBER: WO PCT/JP94/01763
;            FILING DATE: 19-OCT-1994
;            APPLICATION NUMBER: JP 5-291078
;            FILING DATE: 19-NOV-1993
;       ATTORNEY/AGENT INFORMATION:
;            NAME: WEGNER, Harold C.
;            REGISTRATION NUMBER: 25,258
;            REFERENCE/DOCKET NUMBER: 53466/184
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 109:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 269 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-10-839-799-109

  Query Match             84.3%;  Score 43;  DB 6;  Length 269;
  Best Local Similarity   81.8%;  Pred. No. 0.26;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||:|||:||
Db        178 KASQNVGTNVA 188


RESULT 41
US-10-982-357-18
; Sequence 18, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-18

  Query Match             82.4%;  Score 42;  DB 6;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 0.012;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 KASQDVGTSVA 11
              ||||||| :||
Db          1 KASQDVGIAVA 11


RESULT 42
US-10-982-357-35
; Sequence 35, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-35

  Query Match             82.4%;  Score 42;  DB 6;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 0.012;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||| :||
Db          1 KASQDVGIAVA 11


RESULT 43
US-10-982-357-56
; Sequence 56, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-56

  Query Match             82.4%;  Score 42;  DB 6;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 0.012;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||| |:||
Db          1 KASQDVSTAVA 11


RESULT 44
US-10-982-357-72
; Sequence 72, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-72

  Query Match             82.4%;  Score 42;  DB 6;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 0.012;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||| |:||
Db          1 KASQDVSTAVA 11


RESULT 45
US-11-226-325-5
; Sequence 5, Application US/11226325
; Publication No. US20060008456A1
; GENERAL INFORMATION:
;  APPLICANT: TSUCHIYA, MASAYUKI
;  TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
;  FILE REFERENCE: 053466/0274
;  CURRENT APPLICATION NUMBER: US/11/226,325
;  CURRENT FILING DATE:  2005-09-15
;  PRIOR APPLICATION NUMBER: US/09/509,098
;  PRIOR FILING DATE: 2000-03-22
;  PRIOR APPLICATION NUMBER: PCT/JP98/04469
;  PRIOR FILING DATE: 1998-10-02
;  PRIOR APPLICATION NUMBER: JP 9-271726
;  PRIOR FILING DATE: 1997-10-03
;  NUMBER OF SEQ ID NOS: 203
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: CDR (1) of L
;   OTHER INFORMATION: chain V region of anti-HM1.24 antibody
US-11-226-325-5

  Query Match             82.4%;  Score 42;  DB 7;  Length 11;
  Best Local Similarity   81.8%;  Pred. No. 0.012;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||| |:||
Db          1 KASQDVNTAVA 11


RESULT 46
US-11-226-325-133
; Sequence 133, Application US/11226325
; Publication No. US20060008456A1
; GENERAL INFORMATION:
;  APPLICANT: TSUCHIYA, MASAYUKI
;  TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
;  FILE REFERENCE: 053466/0274
;  CURRENT APPLICATION NUMBER: US/11/226,325
;  CURRENT FILING DATE:  2005-09-15
;  PRIOR APPLICATION NUMBER: US/09/509,098
;  PRIOR FILING DATE: 2000-03-22
;  PRIOR APPLICATION NUMBER: PCT/JP98/04469
;  PRIOR FILING DATE: 1998-10-02
;  PRIOR APPLICATION NUMBER: JP 9-271726
;  PRIOR FILING DATE: 1997-10-03
;  NUMBER OF SEQ ID NOS: 203
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
;   LENGTH: 106
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Amino acid
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;   OTHER INFORMATION: sequence of the L chain V region of RVLa
US-11-226-325-133

  Query Match             82.4%;  Score 42;  DB 7;  Length 106;
  Best Local Similarity   81.8%;  Pred. No. 0.15;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              |||||| |:||
Db         24 KASQDVNTAVA 34


RESULT 47
US-10-982-357-6
; Sequence 6, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-6

  Query Match             82.4%;  Score 42;  DB 6;  Length 107;
  Best Local Similarity   81.8%;  Pred. No. 0.15;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||| :||
Db         24 KASQDVGIAVA 34


RESULT 48
US-10-982-357-42
; Sequence 42, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-42

  Query Match             82.4%;  Score 42;  DB 6;  Length 107;
  Best Local Similarity   81.8%;  Pred. No. 0.15;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||| :||
Db         24 KASQDVGIAVA 34


RESULT 49
US-10-982-357-44
; Sequence 44, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-982-357-44

  Query Match             82.4%;  Score 42;  DB 6;  Length 107;
  Best Local Similarity   81.8%;  Pred. No. 0.15;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||| :||
Db         24 KASQDVGIAVA 34


RESULT 50
US-10-982-357-48
; Sequence 48, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-48

  Query Match             82.4%;  Score 42;  DB 6;  Length 107;
  Best Local Similarity   81.8%;  Pred. No. 0.15;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 KASQDVGTSVA 11
              ||||||| :||
Db         24 KASQDVGIAVA 34


Search completed: March 23, 2006, 02:52:52
Job time : 16.3425 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:40:10 ; Search time 60.8904 Seconds
(without alignments)
50.511 Million cell updates/sec

Title: US-10-755-382-21
Perfect score: 43
Sequence: 1 WTSTRHT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	100.0	7	2	AAR97314	Aar97314 Humanised
2	43	100.0	7	4	AAB86085	Aab86085 H. pylori
3	43	100.0	7	4	AAB86053	Aab86053 H. pylori
4	43	100.0	7	8	ADM95103	Adm95103 Murine MN
5	43	100.0	7	8	ADM98312	Adm98312 Humanised
6	43	100.0	106	2	AAR97337	Aar97337 Humanised
7	43	100.0	106	2	AAR97335	Aar97335 Murine NE
8	43	100.0	106	4	AAB86108	Aab86108 H. pylori
9	43	100.0	106	4	AAB86070	Aab86070 H. pylori
10	43	100.0	106	8	ADM95097	Adm95097 Murine MN
11	43	100.0	106	8	ADM95100	Adm95100 Humanised
12	43	100.0	106	8	ADM98320	Adm98320 Murine MN
13	43	100.0	106	8	ADM98322	Adm98322 Humanised
14	43	100.0	108	7	ADD05266	Add05266 Female mo
15	43	100.0	108	8	ADM80357	Adm80357 Murine ho
16	43	100.0	115	6	ABR42756	Abr42756 Anti-CEA
17	43	100.0	232	6	ABG76490	Abg76490 Light cha
18	43	100.0	232	7	ADE64204	Ade64204 MN14LC pr
19	43	100.0	232	7	ADF60817	Adf60817 hMN-14 li
20	43	100.0	250	2	AAW02278	Aaw02278 741F8 ant
21	43	100.0	250	2	AAW29261	Aaw29261 Anti-c-er
22	43	100.0	250	2	AAW22400	Aaw22400 Single ch
23	43	100.0	250	2	AAW47012	Aaw47012 Single ch
24	43	100.0	250	2	AAW53168	Aaw53168 741F8 ant
25	43	100.0	250	2	AAW80422	Aaw80422 Anti-c-er
26	43	100.0	250	7	ABW00714	Abw00714 741F8 sFv
27	43	100.0	250	9	ADY60804	Ady60804 741F8 sFv
28	43	100.0	256	6	ABR42757	Abr42757 Anti-CEA
29	43	100.0	257	6	ABR42758	Abr42758 Anti-CEA
30	43	100.0	261	6	ABR42289	Abr42289 Diabody 6
31	43	100.0	261	6	ABR42754	Abr42754 Anti-CEA
32	43	100.0	261	6	ABR83645	Abr83645 hMN14-scF
33	43	100.0	262	6	ABR42295	Abr42295 Bispecifi
34	43	100.0	262	6	ABR42293	Abr42293 Bispecifi
35	43	100.0	262	6	ABR42298	Abr42298 Bispecifi
36	43	100.0	262	6	ABR42290	Abr42290 Diabody h
37	43	100.0	262	6	ABR42291	Abr42291 Bispecifi
38	43	100.0	358	8	ADU26571	Adu26571 Chimeric
39	43	100.0	363	8	ADU26561	Adu26561 Chimeric
40	43	100.0	364	8	ADU26570	Adu26570 Chimeric
41	43	100.0	370	8	ADU26560	Adu26560 Chimeric
42	43	100.0	391	6	ABR83649	Abr83649 TS1 VL ch
43	43	100.0	443	6	ABG76488	Abg76488 Humanised
44	43	100.0	443	6	ABG74240	Abg74240 Chimaeric
45	43	100.0	667	2	AAR39573	Aar39573 Sequence
46	43	100.0	669	9	ADY97271	Ady97271 Exemplary
47	39	90.7	238	5	AAE27930	Aae27930 Human C5E
48	39	90.7	238	6	ABB82839	Abb82839 Antibody
49	39	90.7	239	6	ABU07879	Abu07879 Venezuela
50	39	90.7	240	6	ABU07882	Abu07882 Venezuela
51	39	90.7	240	6	ABU07880	Abu07880 Venezuela
52	39	90.7	240	6	ABU07883	Abu07883 Venezuela
53	39	90.7	240	6	ABU07881	Abu07881 Venezuela
54	39	90.7	257	6	ABU07877	Abu07877 Anti-Vene
55	39	90.7	296	8	ADS20752	Ads20752 SBP tagge
56	38	88.4	7	5	AAU72807	Aau72807 TRA-8 lig
57	38	88.4	7	5	ABB07361	Abb07361 22A5 IgM
58	38	88.4	7	6	ABO10688	Abo10688 Murine J5
59	38	88.4	7	6	AAO29875	Aao29875 Mouse ant
60	38	88.4	7	6	ABR44632	Abr44632 Murine J5
61	38	88.4	7	7	ADJ79793	Adj79793 TRA-8 lig
62	38	88.4	7	8	ADQ90756	Adq90756 Mouse com
63	38	88.4	7	8	ADU67884	Adu67884 Mouse ant
64	38	88.4	7	8	ADU87706	Adu87706 Mouse Luc
65	38	88.4	7	8	ADU87722	Adu87722 Anti-CS1
66	38	88.4	7	9	ADY52291	Ady52291 SP-3b1 li
67	38	88.4	7	9	ADZ45550	Adz45550 Murine fa
68	38	88.4	7	9	ADZ45503	Adz45503 Murine fa
69	38	88.4	7	9	AEC20791	Aec20791 M-CSF spe
70	38	88.4	8	8	ADT75086	Adt75086 Murine li
71	38	88.4	104	8	ADQ27999	Adq27999 Anti-DR5'
72	38	88.4	105	8	ADT75007	Adt75007 Light cha
73	38	88.4	106	2	AAW31647	Aaw31647 Monoclona
74	38	88.4	107	2	AAR25723	Aar25723 Humanised
75	38	88.4	107	2	AAR55121	Aar55121 Mouse ant
76	38	88.4	107	2	AAR55125	Aar55125 Mouse-hum
77	38	88.4	107	2	AAR60300	Aar60300 Anti HIV
78	38	88.4	107	2	AAR60304	Aar60304 Chimeric
79	38	88.4	107	2	AAW47087	Aaw47087 Mouse J59
80	38	88.4	107	2	AAY90375	Aay90375 J591 mono
81	38	88.4	107	2	AAB36226	Aab36226 Monoclona
82	38	88.4	107	4	AAB69665	Aab69665 Murine Fd
83	38	88.4	107	4	AAB69666	Aab69666 Humanised
84	38	88.4	107	6	ABO10705	Abo10705 Variable
85	38	88.4	107	6	ABO10703	Abo10703 Variable
86	38	88.4	107	6	ABR44614	Abr44614 Murine de
87	38	88.4	107	6	ABR44647	Abr44647 Murine J5
88	38	88.4	107	6	ABR44649	Abr44649 Murine J5
89	38	88.4	107	6	ABR44616	Abr44616 Murine de
90	38	88.4	107	8	ADO47713	Ado47713 Humanised
91	38	88.4	107	8	ADO47768	Ado47768 Mouse Fd1
92	38	88.4	107	8	ADO47712	Ado47712 Mouse Fd1
93	38	88.4	107	8	ADO47769	Ado47769 Humanised
94	38	88.4	107	8	ADQ90771	Adq90771 Mouse J59
95	38	88.4	107	8	ADU67901	Adu67901 Mouse ant
96	38	88.4	107	8	ADU67899	Adu67899 Mouse ant
97	38	88.4	107	8	ADU87730	Adu87730 Humanized

98	38	88.4	107	8	ADU87728	Adu87728 Light cha
99	38	88.4	107	8	ADU87734	Adu87734 VL region
100	38	88.4	107	8	ADU87693	Adu87693 Mouse Luc
101	38	88.4	107	8	ADU87736	Adu87736 Light cha
102	38	88.4	107	9	ADY52287	Ady52287 1H7 light
103	38	88.4	107	9	ADZ45501	Adz45501 Murine fa
104	38	88.4	108	2	AAY21817	Aay21817 Anti-STX1
105	38	88.4	108	8	ADG25826	Adg25826 Anti-CD30
106	38	88.4	108	8	ADT75004	Adt75004 Light cha
107	38	88.4	108	8	ADT74999	Adt74999 Light cha
108	38	88.4	108	9	AEB21883	Aeb21883 Human DC-
109	38	88.4	108	9	AEB21886	Aeb21886 Human DC-
110	38	88.4	109	8	ADG25817	Adg25817 Anti-CD30
111	38	88.4	109	8	ADI26471	Adi26471 Murine 14
112	38	88.4	109	8	ADQ27995	Adq27995 Anti-DR5
113	38	88.4	109	8	ADT75067	Adt75067 Light cha
114	38	88.4	115	5	ABB07359	Abb07359 22A5 IgM
115	38	88.4	116	9	AEA88778	Aea88778 Murine SA
116	38	88.4	116	9	AEA88779	Aea88779 Murine SA
117	38	88.4	127	8	ADU87781	Adu87781 Anti-CS1
118	38	88.4	212	5	AAU72815	Aau72815 DNA encod
119	38	88.4	212	6	AAO29883	Aao29883 LM1 fusio
120	38	88.4	212	7	ADJ79836	Adj79836 LM1-type
121	38	88.4	213	5	AAU72810	Aau72810 TRA-8 lig
122	38	88.4	213	5	AAU72819	Aau72819 DNA encod
123	38	88.4	213	5	AAU72818	Aau72818 DNA encod
124	38	88.4	213	5	AAU72817	Aau72817 DNA encod
125	38	88.4	213	5	AAU72816	Aau72816 DNA encod
126	38	88.4	213	6	AAO29886	Aao29886 LM5 fusio
127	38	88.4	213	6	AAO29878	Aao29878 LM2 fusio
128	38	88.4	213	6	AAO29884	Aao29884 LM3 fusio
129	38	88.4	213	6	AAO29887	Aao29887 LM6 fusio
130	38	88.4	213	6	AAO29885	Aao29885 LM4 fusio
131	38	88.4	213	7	ADJ79838	Adj79838 LM4-type
132	38	88.4	213	7	ADJ79837	Adj79837 LM3-type
133	38	88.4	213	7	ADJ79810	Adj79810 Humanized
134	38	88.4	213	7	ADJ79839	Adj79839 LM5-type
135	38	88.4	213	7	ADJ79840	Adj79840 LM6-type
136	38	88.4	214	9	AEC20772	Aec20772 M-CSF spe
137	38	88.4	223	1	AAP40031	Aap40031 Kappa ant
138	38	88.4	233	8	ADU68009	Adu68009 Mouse ant
139	38	88.4	234	5	AAU72802	Aau72802 TRA-8 lig
140	38	88.4	234	6	AAO29870	Aao29870 Mouse ant
141	38	88.4	234	7	ADJ79788	Adj79788 TRA-8 ant
142	38	88.4	245	9	ADY52285	Ady52285 Single ch
143	38	88.4	247	1	AAP80155	Aap80155 FRs and C
144	38	88.4	247	1	AAP80156	Aap80156 Biosynthe
145	37	86.0	75	4	AAM95560	Aam95560 Human rep
146	37	86.0	75	4	ABB96239	Abb96239 Human tes
147	36	83.7	228	2	AAR74631	Aar74631 Tomato TG
148	36	83.7	228	2	AAW73127	Aaw73127 Tomato et
149	36	83.7	461	8	ADO59779	Ado59779 B. subtil
150	35	81.4	72	4	AAU17898	Aau17898 Novel hum
151	35	81.4	72	7	ADG41278	Adg41278 Human res
152	35	81.4	72	7	ADI97052	Adi97052 Human res
153	35	81.4	19938	6	ABP76682	Abp76682 Streptomy
154	34	79.1	7	3	AAY79430	Aay79430 Tie2 rece
155	34	79.1	12	8	ADJ25673	Adj25673 Mouse aPC
156	34	79.1	107	3	AAY79425	Aay79425 Tie2 rece
157	34	79.1	113	8	ADJ25652	Adj25652 Mouse act
158	34	79.1	139	7	ABO75792	Abo75792 Pseudomon
159	34	79.1	184	7	ADC42709	Adc42709 Murine To
160	34	79.1	186	7	ADC42704	Adc42704 Murine To
161	34	79.1	186	7	ADC42713	Adc42713 Human Tol
162	34	79.1	193	8	ADY12691	Ady12691 Plant ful
163	34	79.1	246	4	AAB84938	Aab84938 Human FCT
164	34	79.1	260	8	ADL06126	Adl06126 M. catarr
165	34	79.1	268	3	AAG36834	Aag36834 Arabidops
166	34	79.1	269	3	AAG36833	Aag36833 Arabidops
167	34	79.1	362	3	AAG36832	Aag36832 Arabidops
168	34	79.1	375	8	ADM94296	Adm94296 Wheat Eth
169	34	79.1	488	6	ABR53346	Abr53346 Protein s
170	34	79.1	488	7	ADK63418	Adk63418 Disease t
171	34	79.1	496	4	AAU35121	Aau35121 Enterococ
172	34	79.1	501	7	ADH86808	Adh86808 Enterococ
173	34	79.1	670	8	ADU02590	Adu02590 Novel hum
174	34	79.1	795	8	ADU23197	Adu23197 Murine To
175	34	79.1	806	3	AAY88055	Aay88055 Murine To
176	34	79.1	806	8	ADU23194	Adu23194 Murine To
177	34	79.1	806	8	ADU23196	Adu23196 Murine To
178	34	79.1	806	8	ADU23195	Adu23195 Murine To
179	33	76.7	53	2	AAY20985	Aay20985 Human gli
180	33	76.7	68	4	AAU57138	Aau57138 Propionib
181	33	76.7	68	6	ABM53657	Abm53657 Propionib
182	33	76.7	72	8	ADU04135	Adu04135 Murine im
183	33	76.7	109	8	ADO32156	Ado32156 Mouse ant
184	33	76.7	142	7	ABO82700	Abo82700 Pseudomon
185	33	76.7	210	4	AAU29480	Aau29480 Human G p
186	33	76.7	210	5	ABG60768	Abg60768 Novel G p
187	33	76.7	268	4	AAG91918	Aag91918 C glutami
188	33	76.7	513	3	AAY52443	Aay52443 Mycobacte
189	33	76.7	1099	5	ABR38814	Abr38814 A. niger
190	33	76.7	1555	8	ADQ96156	Adq96156 T cell ac
191	33	76.7	1739	4	AAM42197	Aam42197 Human pol
192	33	76.7	1745	7	ADF76869	Adf76869 Novel hum
193	33	76.7	1745	8	ADO71781	Ado71781 BFLP0169
194	33	76.7	1752	8	ADO71766	Ado71766 BFLP0169
195	33	76.7	1753	8	ADO71777	Ado71777 BFLP0169
196	33	76.7	1753	8	ADO71767	Ado71767 BFLP0169
197	33	76.7	1753	8	ADO71775	Ado71775 BFLP0169
198	33	76.7	1753	8	ADO71768	Ado71768 BFLP0169
199	33	76.7	1753	8	ADO71771	Ado71771 BFLP0169
200	33	76.7	1753	8	ADO71780	Ado71780 BFLP0169
201	33	76.7	1753	8	ADO71772	Ado71772 BFLP0169
202	33	76.7	1753	8	ADO71764	Ado71764 BFLP0169
203	33	76.7	1753	8	ADO71765	Ado71765 BFLP0169
204	33	76.7	1753	8	ADO71773	Ado71773 BFLP0169
205	33	76.7	1753	8	ADO71778	Ado71778 BFLP0169
206	33	76.7	1753	8	ADO71769	Ado71769 BFLP0169
207	33	76.7	1753	8	ADO71774	Ado71774 BFLP0169
208	33	76.7	1753	8	ADO71779	Ado71779 BFLP0169
209	33	76.7	1753	8	ADO71763	Ado71763 Human BFL
210	33	76.7	1753	8	ADO71776	Ado71776 BFLP0169
211	33	76.7	1767	8	ADO71782	Ado71782 BFLP0169
212	33	76.7	1767	8	ABM81078	Abm81078 Tumour-as
213	33	76.7	1889	4	ABG09906	Abg09906 Novel hum
214	32	74.4	16	2	AAR58698	Aar58698 Rat MR22
215	32	74.4	19	8	ADU16719	Adu16719 M. tuberc
216	32	74.4	21	8	ADU16710	Adu16710 M. tuberc
217	32	74.4	88	4	ABG03821	Abg03821 Novel hum
218	32	74.4	91	7	ADC00913	Adc00913 Enterohae
219	32	74.4	102	2	AAW28155	Aaw28155 Amino aci
220	32	74.4	105	4	AAU23242	Aau23242 Novel hum
221	32	74.4	106	8	ADQ67647	Adq67647 Novel hum
222	32	74.4	116	4	AAU86835	Aau86835 Novel hum
223	32	74.4	116	7	ADB60169	Adb60169 Connectiv
224	32	74.4	119	2	AAY04847	Aay04847 Mycobacte
225	32	74.4	127	5	ABB83379	Abb83379 Human S4
226	32	74.4	129	4	AAU42814	Aau42814 Propionib
227	32	74.4	129	6	ABM39333	Abm39333 Propionib
228	32	74.4	159	8	ADY06205	Ady06205 Plant ful
229	32	74.4	162	2	AAY04849	Aay04849 Mycobacte
230	32	74.4	168	8	ADY23652	Ady23652 Plant ful
231	32	74.4	189	8	ADX90324	Adx90324 Plant ful
232	32	74.4	260	7	ABO72865	Abo72865 Pseudomon
233	32	74.4	268	4	AAG81194	Aag81194 Mycobacte
234	32	74.4	286	8	ADX76855	Adx76855 Plant ful
235	32	74.4	297	4	AAG92549	Aag92549 C glutami
236	32	74.4	314	7	ADC23909	Adc23909 Protein s
237	32	74.4	314	8	ADH36010	Adh36010 Chemical
238	32	74.4	314	8	ADG93711	Adg93711 Nitrilase
239	32	74.4	314	8	ADI62308	Adi62308 Nitrilase
240	32	74.4	314	8	ADI64429	Adi64429 Nitrilase
241	32	74.4	370	2	AAR57066	Aar57066 Murine se
242	32	74.4	370	2	AAR58686	Aar58686 Rat MR22
243	32	74.4	370	6	AAE31673	Aae31673 Mouse 5-H

244	32	74.4	370	7	ADE56994	Ade56994 Rat Prote
245	32	74.4	370	8	ADO29719	Ado29719 Mouse GPC
246	32	74.4	407	4	AAB67591	Aab67591 Amino aci
247	32	74.4	407	4	AAB67585	Aab67585 Amino aci
248	32	74.4	419	7	ABO62327	Abo62327 Klebsiell
249	32	74.4	430	6	ABU23429	Abu23429 Protein e
250	32	74.4	462	3	AAB07572	Aab07572 Protein e
251	32	74.4	545	4	ABG26079	Abg26079 Novel hum
252	32	74.4	572	4	AAU34516	Aau34516 E. coli c
253	32	74.4	572	5	ABB76486	Abb76486 Escherich
254	32	74.4	572	6	ABU28573	Abu28573 Protein e
255	32	74.4	611	4	AAB85681	Aab85681 Salmonell
256	32	74.4	626	6	ABR41653	Abr41653 Human DIT
257	32	74.4	751	4	ABG13333	Abg13333 Novel hum
258	32	74.4	785	4	ABG27221	Abg27221 Novel hum
259	32	74.4	818	4	ABB63426	Abb63426 Drosophil
260	32	74.4	919	4	ABG07234	Abg07234 Novel hum
261	32	74.4	995	8	ADM57327	Adm57327 Recombina
262	32	74.4	1005	4	ABG27940	Abg27940 Novel hum
263	32	74.4	1232	9	ABM95065	Abm95065 M. xanthu
264	32	74.4	1468	4	ABB65329	Abb65329 Drosophil
265	32	74.4	1809	6	ABU70355	Abu70355 pIAO-P/L
266	32	74.4	2356	6	ABJ25846	Abj25846 Aspergill
267	32	74.4	2616	4	ABB64889	Abb64889 Drosophil
268	32	74.4	2887	9	AEA63534	Aea63534 H. capsul
269	32	74.4	2959	9	AEA63532	Aea63532 A. nidula
270	32	74.4	3135	9	AEA63533	Aea63533 A. fumiga
271	32	74.4	3170	6	ABJ26446	Abj26446 Aspergill
272	31	72.1	17	2	AAW17555	Aaw17555 Beta-B2-c
273	31	72.1	23	4	ABB43019	Abb43019 Peptide #
274	31	72.1	23	4	AAM36849	Aam36849 Peptide #
275	31	72.1	23	4	AAM76742	Aam76742 Human bon
276	31	72.1	23	4	AAM63924	Aam63924 Human bra
277	31	72.1	23	4	ABG58427	Abg58427 Human liv
278	31	72.1	23	5	ABG45921	Abg45921 Human pep
279	31	72.1	30	6	ABO14381	Abo14381 Novel hum
280	31	72.1	30	8	ADG78793	Adg78793 Human sec
281	31	72.1	30	8	ADN61079	Adn61079 Human sec
282	31	72.1	33	4	ABG02643	Abg02643 Novel hum
283	31	72.1	55	4	AAU41536	Aau41536 Propionib
284	31	72.1	55	6	ABM38055	Abm38055 Propionib
285	31	72.1	66	5	ABP31920	Abp31920 Human ORF
286	31	72.1	93	7	ADF13923	Adf13923 Human end
287	31	72.1	94	4	AAM83114	Aam83114 Human imm
288	31	72.1	102	1	AAP90009	Aap90009 Mouse gam
289	31	72.1	108	4	AAO01701	Aao01701 Human pol
290	31	72.1	110	2	AAY29119	Aay29119 Amino aci
291	31	72.1	114	5	ABP31984	Abp31984 Human ORF
292	31	72.1	116	3	AAG47507	Aag47507 Arabidops
293	31	72.1	116	3	AAG10908	Aag10908 Arabidops
294	31	72.1	117	4	AAM81603	Aam81603 Human hae
295	31	72.1	117	4	AAM81855	Aam81855 Human hae
296	31	72.1	117	4	AAM81259	Aam81259 Human hae
297	31	72.1	117	4	AAM80807	Aam80807 Human hae
298	31	72.1	123	3	AAG47506	Aag47506 Arabidops
299	31	72.1	124	3	AAG10907	Aag10907 Arabidops
300	31	72.1	135	6	ABG74546	Abg74546 Human LDL
301	31	72.1	150	7	ADM05791	Adm05791 Human pro
302	31	72.1	151	6	ABO04847	Abo04847 Human epi
303	31	72.1	151	9	AEA17759	Aea17759 Hybridoma
304	31	72.1	159	8	ADK52406	Adk52406 Human ant
305	31	72.1	169	6	ABG74545	Abg74545 Human LDL
306	31	72.1	170	3	AAG13652	Aag13652 Arabidops
307	31	72.1	170	4	ABG07517	Abg07517 Novel hum
308	31	72.1	171	3	AAG13651	Aag13651 Arabidops
309	31	72.1	171	8	ADK52422	Adk52422 Human ant
310	31	72.1	172	3	AAG13650	Aag13650 Arabidops
311	31	72.1	193	4	AAU62014	Aau62014 Propionib
312	31	72.1	193	6	ABM58533	Abm58533 Propionib
313	31	72.1	203	6	ABG74548	Abg74548 Human LDL
314	31	72.1	204	7	ADE63507	Ade63507 Rat Prote
315	31	72.1	205	2	AAW17523	Aaw17523 Human bet
316	31	72.1	205	8	ADP22671	Adp22671 Golden ha
317	31	72.1	218	3	AAB07481	Aab07481 Amino aci
318	31	72.1	218	4	AAB76428	Aab76428 Murine Ig
319	31	72.1	218	4	AAB67208	Aab67208 Murine Ig
320	31	72.1	218	5	AAG78439	Aag78439 Native se
321	31	72.1	218	6	ABR42445	Abr42445 Mouse IgG
322	31	72.1	218	8	ADH75383	Adh75383 Mouse IgG
323	31	72.1	218	9	AEB86181	Aeb86181 Amino aci
324	31	72.1	223	2	AAR87020	Aar87020 BZLF2 pro
325	31	72.1	223	2	AAW47351	Aaw47351 Epstein-b
326	31	72.1	223	2	AAY23634	Aay23634 BZLF2 pro
327	31	72.1	229	8	ADX88887	Adx88887 Plant ful
328	31	72.1	255	6	ABG74550	Abg74550 Human LDL
329	31	72.1	260	4	AAU17465	Aau17465 Novel sig
330	31	72.1	260	7	ADB94173	Adb94173 Human nov
331	31	72.1	263	7	ABO68580	Abo68580 Pseudomon
332	31	72.1	270	5	AAU93043	Aau93043 Arabidops
333	31	72.1	270	7	ADD30558	Add30558 Plant yie
334	31	72.1	270	8	ADI41745	Adi41745 Plant tra
335	31	72.1	278	8	ABO84820	Abo84820 Human can
336	31	72.1	283	4	AAU52245	Aau52245 Propionib
337	31	72.1	283	6	ABM48764	Abm48764 Propionib
338	31	72.1	296	3	AAG50135	Aag50135 Arabidops
339	31	72.1	296	3	AAG05829	Aag05829 Arabidops
340	31	72.1	308	6	ABG74551	Abg74551 Human LDL
341	31	72.1	308	6	ABG74547	Abg74547 Human LDL
342	31	72.1	308	6	ABG74542	Abg74542 X. laevis
343	31	72.1	308	6	ABG74552	Abg74552 Human LDL
344	31	72.1	308	6	ABG74540	Abg74540 Human LDL
345	31	72.1	308	6	ABG74549	Abg74549 Human LDL
346	31	72.1	308	6	ABG74541	Abg74541 Murine LD
347	31	72.1	310	4	AAG67483	Aag67483 Amino aci
348	31	72.1	315	3	AAB41969	Aab41969 Human ORF
349	31	72.1	320	8	ABO84819	Abo84819 Murine ca
350	31	72.1	341	1	AAP83200	Aap83200 Sequence
351	31	72.1	346	3	AAY85692	Aay85692 Murine Sa
352	31	72.1	346	4	AAB49333	Aab49333 Murine SL
353	31	72.1	346	6	AAO16301	Aao16301 Human SAM
354	31	72.1	346	6	AAO16302	Aao16302 Human SAM
355	31	72.1	346	7	ADB79941	Adb79941 Human put
356	31	72.1	346	7	ABM85329	Abm85329 Human pro
357	31	72.1	346	8	ADQ20994	Adq20994 Human sof
358	31	72.1	353	9	AEB27312	Aeb27312 Pinus rad
359	31	72.1	394	4	AAE10147	Aae10147 Streptomy
360	31	72.1	403	4	AAB31685	Aab31685 Amino aci
361	31	72.1	409	8	ADX73820	Adx73820 Plant ful
362	31	72.1	418	4	AAG67481	Aag67481 Amino aci
363	31	72.1	418	8	ADX93943	Adx93943 Plant ful
364	31	72.1	441	7	ABO70124	Abo70124 Pseudomon
365	31	72.1	454	5	ABB93037	Abb93037 Herbicida
366	31	72.1	454	5	ABB76124	Abb76124 Recombina
367	31	72.1	455	2	AAW17830	Aaw17830 Thermophi
368	31	72.1	456	4	AAG67485	Aag67485 Amino aci
369	31	72.1	456	5	ABP69716	Abp69716 Human pol
370	31	72.1	462	5	ABB76126	Abb76126 Recombina
371	31	72.1	473	4	AAE10333	Aae10333 Human tra
372	31	72.1	478	5	ABG31730	Abg31730 Murine m1
373	31	72.1	522	9	AEC20775	Aec20775 M-CSF spe
374	31	72.1	571	7	ABO82211	Abo82211 Pseudomon
375	31	72.1	634	8	ADM94300	Adm94300 Corn Ethy
376	31	72.1	634	8	ADM94288	Adm94288 Corn Ethy
377	31	72.1	634	9	ADY86081	Ady86081 Z. mays e
378	31	72.1	634	9	ADY86076	Ady86076 Z. mays e
379	31	72.1	1144	2	AAR88122	Aar88122 Tobacco m
380	31	72.1	1144	2	AAR88123	Aar88123 Tobacco m
381	31	72.1	1144	5	AAO14439	Aao14439 Nicotiana
382	31	72.1	1207	5	AAE23872	Aae23872 C. elegan
383	31	72.1	1209	4	AAU02094	Aau02094 Bacillus
384	31	72.1	1221	4	AAU00420	Aau00420 B. thurin
385	31	72.1	1221	4	AAU00421	Aau00421 B. thurin
386	31	72.1	1227	2	AAY31990	Aay31990 Chimeric
387	31	72.1	1228	2	AAR50955	Aar50955 Bacillus
388	31	72.1	1228	4	AAB84628	Aab84628 Amino aci
389	31	72.1	1228	4	AAU02039	Aau02039 B. thurin

390	31	72.1	1228	9	ADY59858
391	31	72.1	3723	8	ADU47672
392	31	72.1	5674	8	ADU47676
393	31	72.1	6043	8	ADU47673
394	30	69.8	10	8	ADK02421
395	30	69.8	10	8	ADK07185
396	30	69.8	10	8	ADK02420
397	30	69.8	10	8	ADK07186
398	30	69.8	13	8	ADJ93384
399	30	69.8	32	8	ADQ39310
400	30	69.8	33	8	ADK01396
401	30	69.8	33	8	ADK02107
402	30	69.8	46	8	ADQ39302
403	30	69.8	46	8	ADQ39315
404	30	69.8	56	4	AAU49446
405	30	69.8	56	6	ABM45965
406	30	69.8	57	4	AAU54157
407	30	69.8	57	6	ABM50676
408	30	69.8	63	8	ADX66984
409	30	69.8	71	4	AAU60736
410	30	69.8	71	6	ABM57255
411	30	69.8	72	4	AAB63616
412	30	69.8	72	4	AAU49123
413	30	69.8	72	6	ABM45642
414	30	69.8	73	4	AAM20740
415	30	69.8	73	4	ABB42243
416	30	69.8	73	4	AAM36051
417	30	69.8	73	4	ABB25766
418	30	69.8	73	4	AAM75942
419	30	69.8	73	4	AAM63129
420	30	69.8	73	4	ABG57673
421	30	69.8	73	5	ABG45368
422	30	69.8	77	4	AAU41116
423	30	69.8	77	6	ABM37635
424	30	69.8	79	4	AAO06884
425	30	69.8	80	5	ABP09845
426	30	69.8	86	2	AAY11655
427	30	69.8	91	8	ADQ39313
428	30	69.8	92	2	AAY59942
429	30	69.8	93	4	AAO03228
430	30	69.8	94	3	AAG22673
431	30	69.8	99	4	AAU00391
432	30	69.8	99	5	ABP32275
433	30	69.8	99	8	ADH89008
434	30	69.8	103	4	AAU32990
435	30	69.8	104	4	AAM23811
436	30	69.8	107	4	AAU29953
437	30	69.8	116	8	ADX95008
438	30	69.8	120	7	ABM89852
439	30	69.8	124	4	AAM24229
440	30	69.8	127	3	AAG14104
441	30	69.8	132	6	AAO30178
442	30	69.8	137	4	AAU50475
443	30	69.8	137	6	ABM46994
444	30	69.8	141	8	ADX95466
445	30	69.8	141	8	ADX80178
446	30	69.8	143	7	ABO82815
447	30	69.8	144	8	ADY24094
448	30	69.8	146	4	ABG29314
449	30	69.8	146	4	ABG18275
450	30	69.8	148	2	AAY74165
451	30	69.8	148	7	ABO68730
452	30	69.8	160	4	AAB63513
453	30	69.8	170	7	ADD69578
454	30	69.8	171	8	ADX65744
455	30	69.8	174	9	ADY39463
456	30	69.8	179	8	ADU02644
457	30	69.8	181	8	ADP30214
458	30	69.8	193	7	ABO80174
459	30	69.8	197	2	AAW61625
460	30	69.8	197	2	AAW88494
461	30	69.8	197	2	AAW84273
462	30	69.8	197	7	ADD10280

Ady59858	Bacillus
Adu47672	S. cyaneo
Adu47676	S. cyaneo
Adu47673	S. cyaneo
Adk02421	Hepatitis
Adk07185	Hepatitis
Adk02420	Hepatitis
Adk07186	Hepatitis
Adj93384	Human BGS
Adq39310	Human myo
Adk01396	Hepatitis
Adk02107	Hepatitis
Adq39302	Human myo
Adq39315	Human myo
Aau49446	Propionib
Abm45965	Propionib
Aau54157	Propionib
Abm50676	Propionib
Adx66984	Plant ful
Aau60736	Propionib
Abm57255	Propionib
Aab63616	Human gas
Aau49123	Propionib
Abm45642	Propionib
Aam20740	Peptide #
Abb42243	Peptide #
Aam36051	Peptide #
Abb25766	Protein #
Aam75942	Human bon
Aam63129	Human bra
Abg57673	Human liv
Abg45368	Human pep
Aau41116	Propionib
Abm37635	Propionib
Aao06884	Human pol
Abp09845	Human ORF
Aay11655	Human 5'
Adq39313	Human myo
Aay59942	Human end
Aao03228	Human pol
Aag22673	Zea mays
Aau00391	Human sec
Abp32275	Human ORF
Adh89008	Human POL
Aau32990	Novel hum
Aam23811	Human EST
Aau29953	Novel hum
Adx95008	Plant ful
Abm89852	Rice abio
Aam24229	Human EST
Aag14104	Arabidops
Aao30178	Human tra
Aau50475	Propionib
Abm46994	Propionib
Adx95466	Plant ful
Adx80178	Plant ful
Abo82815	Pseudomon
Ady24094	Plant ful
Abg29314	Novel hum
Abg18275	Novel hum
Aay74165	Human pro
Abo68730	Pseudomon
Aab63513	Human gas
Add69578	Human REM
Adx65744	Plant ful
Ady39463	Thale cre
Adu02644	Novel hum
Adp30214	Human sec
Abo80174	Pseudomon
Aaw61625	Clone HGB
Aaw88494	Human sto
Aaw84273	A tumour
Add10280	Human tum

463	30	69.8	197	7	ABW01507
464	30	69.8	197	7	ABW01520
465	30	69.8	197	8	ADN41032
466	30	69.8	197	9	AEB98451
467	30	69.8	197	9	AEB98438
468	30	69.8	198	2	AAY02732
469	30	69.8	198	7	ADA07411
470	30	69.8	209	6	ABU11993
471	30	69.8	210	6	ABP78141
472	30	69.8	215	6	ADA54191
473	30	69.8	224	6	ABM67706
474	30	69.8	227	7	ABO63675
475	30	69.8	228	7	ADI21607
476	30	69.8	232	4	ABG03306
477	30	69.8	235	4	AAU57493
478	30	69.8	235	6	ABM54012
479	30	69.8	240	4	AAU30502
480	30	69.8	242	8	ADJ93360
481	30	69.8	245	6	AAE33558
482	30	69.8	245	8	ADQ39309
483	30	69.8	245	8	ADX75898
484	30	69.8	282	7	ABO84083
485	30	69.8	286	7	ADF06697
486	30	69.8	293	8	ADJ93366
487	30	69.8	317	8	ADY23697
488	30	69.8	333	7	ABO68367
489	30	69.8	339	8	ADH41829
490	30	69.8	356	2	AAR37715
491	30	69.8	359	4	AAU54823
492	30	69.8	359	6	ABM51342
493	30	69.8	360	7	ABO81188
494	30	69.8	362	3	AAY77912
495	30	69.8	369	8	ADM48231
496	30	69.8	372	4	ABG29671
497	30	69.8	402	8	ADY07293
498	30	69.8	416	8	ADS23729
499	30	69.8	417	8	ADX93395
500	30	69.8	419	2	AAW27464
501	30	69.8	439	7	ABO71604
502	30	69.8	451	8	ADS78307
503	30	69.8	458	8	ADH22508
504	30	69.8	466	8	ADH22527
505	30	69.8	470	7	ABO71754
506	30	69.8	474	4	AAU33893
507	30	69.8	474	4	AAU37063
508	30	69.8	474	6	ABU16397
509	30	69.8	474	6	ABM72695
510	30	69.8	478	8	ADJ49696
511	30	69.8	490	8	ADY09603
512	30	69.8	501	2	AAW06826
513	30	69.8	506	1	AAP91491
514	30	69.8	513	4	ABG16438
515	30	69.8	537	4	AAU30254
516	30	69.8	541	8	ADJ93365
517	30	69.8	541	8	ADJ93358
518	30	69.8	555	6	ABB99660
519	30	69.8	559	8	ABM84024
520	30	69.8	561	8	ADU24099
521	30	69.8	567	7	ADF07230
522	30	69.8	595	2	AAY34656
523	30	69.8	598	6	ABU26962
524	30	69.8	606	5	ABP52121
525	30	69.8	620	7	ADE10036
526	30	69.8	638	4	AAB74496
527	30	69.8	645	8	ADG32062
528	30	69.8	653	4	AAU02023
529	30	69.8	675	1	AAP81136
530	30	69.8	688	7	ADF89799
531	30	69.8	700	2	AAR70235
532	30	69.8	700	2	AAW22481
533	30	69.8	700	3	AAY77903
534	30	69.8	706	2	AAY28503
535	30	69.8	706	4	AAB93013

Abw01507	Human rec
Abw01520	Protein #
Adn41032	Novel hum
Aeb98451	Human tra
Aeb98438	Human HGB
Aay02732	Human sec
Ada07411	Human sec
Abu11993	M. echino
Abp78141	N. gonorr
Ada54191	Human pro
Abm67706	Photorhab
Abo63675	Klebsiell
Adi21607	Novel hum
Abg03306	Novel hum
Aau57493	Propionib
Abm54012	Propionib
Aau30502	Novel hum
Adj93360	Human BGS
Aae33558	Human pla
Adq39309	Human myo
Adx75898	Plant ful
Abo84083	Pseudomon
Adf06697	Bacterial
Adj93366	Human BGS
Ady23697	Plant ful
Abo68367	Pseudomon
Adh41829	Novel hum
Aar37715	Carminomy
Aau54823	Propionib
Abm51342	Propionib
Abo81188	Pseudomon
Aay77912	Plasmodiu
Adm48231	Polypepti
Abg29671	Novel hum
Ady07293	Plant ful
Ads23729	Bacterial
Adx93395	Plant ful
Aaw27464	B. cepaci
Abo71604	Pseudomon
Ads78307	Aminotran
Adh22508	Human tra
Adh22527	Human tra
Abo71754	Pseudomon
Aau33893	Staphyloc
Aau37063	Staphyloc
Abu16397	Protein e
Abm72695	Staphyloc
Adj49696	Oil-assoc
Ady09603	Plant ful
Aaw06826	Marek's d
Aap91491	Glycoprot
Abg16438	Novel hum
Aau30254	Novel hum
Adj93365	Human tub
Adj93358	Human BGS
Abb99660	Amino aci
Abm84024	Human dia
Adu24099	Human asp
Adf07230	Bacterial
Aay34656	Chlamydia
Abu26962	Protein e
Abp52121	Homo sapi
Ade10036	Novel pro
Aab74496	White lup
Adg32062	Mutant B_
Aau02023	B. thurin
Aap81136	Bovine Pr
Adf89799	M. trunca
Aar70235	P. falcip
Aaw22481	Plasmodiu
Aay77903	P. falcip
Aay28503	HGFH3 Hum
Aab93013	Human pro

536	30	69.8	706	4	AAB93964	Aab93964 Human pro
537	30	69.8	706	8	ADQ15128	Adq15128 Human can
538	30	69.8	741	8	ADX00937	Adx00937 Wheat eth
539	30	69.8	743	4	ABB52985	Abb52985 Escherich
540	30	69.8	743	4	ABB52951	Abb52951 Escherich
541	30	69.8	778	7	ADB80089	Adb80089 Mycobacte
542	30	69.8	822	7	ADE08716	Ade08716 Novel pro
543	30	69.8	866	8	ABM84987	Abm84987 Human dia
544	30	69.8	866	9	AEA62657	Aea62657 Mitochond
545	30	69.8	869	4	ABG19554	Abg19554 Novel hum
546	30	69.8	1017	8	ADU25440	Adu25440 L. acidop
547	30	69.8	1048	4	ABB58976	Abb58976 Drosophil
548	30	69.8	1064	5	AAO21223	Aao21223 Alpha-iso
549	30	69.8	1093	5	AAO21235	Aao21235 Alpha-iso
550	30	69.8	1093	6	ABP70651	Abp70651 Bacillus
551	30	69.8	1093	6	ADA26480	Ada26480 Alpha-iso
552	30	69.8	1093	6	ABP57725	Abp57725 Protein #
553	30	69.8	1149	7	ADF07021	Adf07021 Bacterial
554	30	69.8	1162	8	ADO71744	Ado71744 BFLP1698
555	30	69.8	1162	8	ADO71745	Ado71745 BFLP1698
556	30	69.8	1229	2	AAR54074	Aar54074 CryET5. 2
557	30	69.8	1229	2	AAW35259	Aaw35259 Bacillus
558	30	69.8	1229	2	AAW17699	Aaw17699 CryET5. 3
559	30	69.8	1229	2	AAW87633	Aaw87633 CryET5 pr
560	30	69.8	1229	2	AAY30923	Aay30923 B. thurin
561	30	69.8	1229	8	ADK98479	Adk98479 B thuring
562	30	69.8	1230	8	ADK98484	Adk98484 B thuring
563	30	69.8	1230	8	ADK98489	Adk98489 B thuring
564	30	69.8	1230	8	ADK98481	Adk98481 B thuring
565	30	69.8	1230	8	ADK98491	Adk98491 B thuring
566	30	69.8	1230	8	ADK98487	Adk98487 B thuring
567	30	69.8	1288	5	AAE20285	Aae20285 Human Trp
568	30	69.8	1675	4	AAU00418	Aau00418 Mouse cel
569	30	69.8	1689	4	AAU00415	Aau00415 Mouse cel
570	30	69.8	2182	2	AAW22476	Aaw22476 Plasmodiu
571	30	69.8	2182	3	AAY77906	Aay77906 Plasmodiu
572	30	69.8	2311	5	ABG95034	Abg95034 Human tra
573	30	69.8	2520	8	ADN11586	Adn11586 Human CD9
574	30	69.8	2565	8	ADN11585	Adn11585 Human CD9
575	30	69.8	2641	9	ADZ12955	Adz12955 Human can
576	30	69.8	3010	9	ADX40804	Adx40804 HCV polym
577	30	69.8	3478	6	ABU11580	Abu11580 Human MDD
578	30	69.8	3660	4	ABG12812	Abg12812 Novel hum
579	30	69.8	3910	2	AAR38470	Aar38470 ALL-1 pro
580	30	69.8	3910	2	AAR66462	Aar66462 ALL-1 (ac
581	30	69.8	3969	2	AAR52971	Aar52971 Product o
582	30	69.8	3969	7	ADC27507	Adc27507 Human MLL
583	30	69.8	3969	8	ADK60223	Adk60223 Angiogene
584	30	69.8	3969	8	ADK60524	Adk60524 Angiogene
585	30	69.8	3969	8	ADP73147	Adp73147 Angiogene
586	30	69.8	3969	9	AEA06464	Aea06464 Human MLL
587	30	69.8	4183	7	ABM85419	Abm85419 Human pro
588	30	69.8	4419	8	ADN11590	Adn11590 Human CD9
589	30	69.8	4419	8	ADN11588	Adn11588 Human CD9
590	30	69.8	4464	8	ADN11587	Adn11587 Human CD9
591	30	69.8	4464	8	ADN11589	Adn11589 Human CD9
592	30	69.8	4485	9	ADZ12957	Adz12957 Human can
593	30	69.8	4529	5	AAU81016	Aau81016 Mouse alp
594	30	69.8	4544	2	AAR47861	Aar47861 Alpha 2-M
595	30	69.8	4544	2	AAR60517	Aar60517 Human alp
596	30	69.8	4544	4	AAM79091	Aam79091 Human pro
597	30	69.8	4544	5	AAU81019	Aau81019 Human alp
598	30	69.8	4544	6	ABP56839	Abp56839 Human LRP
599	30	69.8	4544	6	ABU89744	Abu89744 Protein d
600	30	69.8	4544	7	ADD14025	Add14025 Human src
601	30	69.8	4544	8	ADI27167	Adi27167 Human LRP
602	30	69.8	4544	8	ADL15636	Adl15636 Human lip
603	30	69.8	4544	8	ADN11584	Adn11584 Human CD9
604	30	69.8	4545	5	AAU74797	Aau74797 Mouse alp
605	30	69.8	4545	8	ADI27166	Adi27166 Mouse LRP
606	30	69.8	4545	8	ADI27170	Adi27170 Mouse LRP
607	30	69.8	4545	8	ADT49882	Adt49882 Murine LR
608	30	69.8	4545	9	ADZ12952	Adz12952 Murine ca
609	30	69.8	4563	4	ABB11353	Abb11353 Human LDL
610	30	69.8	4599	6	ABP56837	Abp56837 Human LRP
611	30	69.8	4599	8	ADI27168	Adi27168 Mouse LRP
612	30	69.8	4599	8	ADI27169	Adi27169 Mouse LRP
613	30	69.8	4599	9	AEA81490	Aea81490 Human low
614	30	69.8	4636	4	AAE11937	Aae11937 Human CG1
615	30	69.8	4636	8	ADS10474	Ads10474 Human the
616	30	69.8	7107	4	ABB58144	Abb58144 Drosophil
617	30	69.8	8943	8	ADQ89760	Adq89760 Antagonis
618	29.5	68.6	56	5	ABP11093	Abp11093 Human ORF
619	29	67.4	7	7	ABR82268	Abr82268 Anti-gang
620	29	67.4	7	7	ADC44344	Adc44344 Endotheli
621	29	67.4	7	8	ADP84123	Adp84123 Anti-mono
622	29	67.4	7	8	ADS31785	Ads31785 CDR2 regi
623	29	67.4	8	2	AAR36204	Aar36204 Hepatitis
624	29	67.4	18	9	ADV23171	Adv23171 HCV H77 i
625	29	67.4	18	9	ADV23170	Adv23170 HCV H77 i
626	29	67.4	22	4	AAM21156	Aam21156 Peptide #
627	29	67.4	22	4	ABB43474	Abb43474 Peptide #
628	29	67.4	22	4	AAM37367	Aam37367 Peptide #
629	29	67.4	22	4	ABB26438	Abb26438 Protein #
630	29	67.4	22	4	AAM77224	Aam77224 Human bon
631	29	67.4	22	4	AAM64406	Aam64406 Human bra
632	29	67.4	22	4	ABG58851	Abg58851 Human liv
633	29	67.4	22	5	ABG46235	Abg46235 Human pep
634	29	67.4	26	4	AAM18779	Aam18779 Peptide #
635	29	67.4	26	4	ABB37878	Abb37878 Peptide #
636	29	67.4	26	4	AAM31285	Aam31285 Peptide #
637	29	67.4	26	4	ABB23137	Abb23137 Protein #
638	29	67.4	26	4	AAM71008	Aam71008 Human bon
639	29	67.4	26	4	AAM58511	Aam58511 Human bra
640	29	67.4	26	4	ABG52723	Abg52723 Human liv
641	29	67.4	26	5	ABG40799	Abg40799 Human pep
642	29	67.4	30	5	AAU84785	Aau84785 HCV HepC1
643	29	67.4	37	2	AAY41156	Aay41156 HCV NS5B
644	29	67.4	38	6	ABP80434	Abp80434 N. gonorr
645	29	67.4	38	9	ADV76653	Adv76653 Human Trp
646	29	67.4	48	6	ABP77610	Abp77610 N. gonorr
647	29	67.4	49	8	ABO54925	Abo54925 Human gen
648	29	67.4	51	5	ABP34837	Abp34837 Human ORF
649	29	67.4	52	4	AAU45584	Aau45584 Propionib
650	29	67.4	52	4	AAU55419	Aau55419 Propionib
651	29	67.4	52	5	ABP29393	Abp29393 Streptoco
652	29	67.4	52	6	ABM51938	Abm51938 Propionib
653	29	67.4	52	6	ABM42103	Abm42103 Propionib
654	29	67.4	61	8	ADV16130	Adv16130 X. pelarg
655	29	67.4	64	1	AAP91302	Aap91302 Protein e
656	29	67.4	65	4	AAG99566	Aag99566 ERA bindi
657	29	67.4	65	4	AAU57939	Aau57939 Propionib
658	29	67.4	65	6	ABM54458	Abm54458 Propionib
659	29	67.4	66	4	ABB41401	Abb41401 Peptide #
660	29	67.4	66	4	AAM35193	Aam35193 Peptide #
661	29	67.4	66	4	AAM75075	Aam75075 Human bon
662	29	67.4	66	4	AAM62271	Aam62271 Human bra
663	29	67.4	66	4	ABG56839	Abg56839 Human liv
664	29	67.4	66	7	ADH85798	Adh85798 Enterococ
665	29	67.4	68	2	AAY02983	Aay02983 Fragment
666	29	67.4	68	7	ADA07818	Ada07818 Human sec
667	29	67.4	68	8	ADN41290	Adn41290 Novel hum
668	29	67.4	72	4	AAM95163	Aam95163 Human rep
669	29	67.4	72	4	ABB95864	Abb95864 Human tes
670	29	67.4	73	5	ABB97929	Abb97929 Human sec
671	29	67.4	79	4	AAU62603	Aau62603 Propionib
672	29	67.4	79	6	ABM59122	Abm59122 Propionib
673	29	67.4	83	4	AAU55144	Aau55144 Propionib
674	29	67.4	83	6	ABM51663	Abm51663 Propionib
675	29	67.4	84	2	AAR25872	Aar25872 HCV polyp
676	29	67.4	84	2	AAW41750	Aaw41750 Hepatitis
677	29	67.4	89	5	ABB77287	Abb77287 HCV bait
678	29	67.4	91	1	AAP92046	Aap92046 Sequence
679	29	67.4	91	1	AAP90163	Aap90163 Sequence
680	29	67.4	91	3	AAB18527	Aab18527 Protein e
681	29	67.4	91	8	ADN35950	Adn35950 HCV cDNA

682	29	67.4	95	2	AAR25894
683	29	67.4	108	8	ADT75006
684	29	67.4	112	7	ABR82259
685	29	67.4	112	7	ABR82263
686	29	67.4	112	8	ADP84128
687	29	67.4	112	8	ADP84132
688	29	67.4	112	8	ADS31794
689	29	67.4	112	8	ADS31790
690	29	67.4	115	4	AAU66213
691	29	67.4	115	6	ABM62732
692	29	67.4	115	6	ABR41323
693	29	67.4	115	8	ADT74992
694	29	67.4	116	4	AAU49642
695	29	67.4	116	6	ABM46161
696	29	67.4	122	3	AAB40386
697	29	67.4	122	5	ABP03434
698	29	67.4	123	4	AAU53824
699	29	67.4	123	6	ABM50343
700	29	67.4	126	4	ABB17899
701	29	67.4	127	5	ABB77286
702	29	67.4	128	1	AAP90826
703	29	67.4	129	3	AAB40757
704	29	67.4	129	5	ABP00240
705	29	67.4	132	7	ABR82265
706	29	67.4	132	8	ADP84134
707	29	67.4	132	8	ADS31796
708	29	67.4	137	8	ADY09068
709	29	67.4	141	5	ABP09777
710	29	67.4	142	2	AAR11278
711	29	67.4	142	2	AAR66627
712	29	67.4	142	2	AAY14974
713	29	67.4	142	2	AAW30587
714	29	67.4	142	2	AAY01618
715	29	67.4	142	2	AAY01613
716	29	67.4	142	2	ADF66066
717	29	67.4	142	2	ADF66056
718	29	67.4	144	7	ABM87811
719	29	67.4	152	1	AAP92045
720	29	67.4	152	1	AAP90162
721	29	67.4	157	7	AAE39893
722	29	67.4	157	8	ADQ48423
723	29	67.4	158	6	ABM65861
724	29	67.4	163	7	ABO80352
725	29	67.4	166	8	ADX95421
726	29	67.4	170	7	ABO78942
727	29	67.4	173	8	ADP29846
728	29	67.4	179	4	ABB68539
729	29	67.4	181	8	ADH22364
730	29	67.4	181	8	ADN47390
731	29	67.4	183	4	AAU16567
732	29	67.4	183	6	ABU55636
733	29	67.4	194	7	ADF04067
734	29	67.4	197	6	ADA34444
735	29	67.4	201	7	ADC84539
736	29	67.4	203	5	ADK34478
737	29	67.4	204	4	AAU58505
738	29	67.4	204	6	ABM55024
739	29	67.4	209	4	AAU41048
740	29	67.4	209	6	ABM37567
741	29	67.4	213	6	ADA55444
742	29	67.4	213	7	ABO74645
743	29	67.4	218	7	ABR82261
744	29	67.4	218	8	ADP84136
745	29	67.4	218	8	ADP84130
746	29	67.4	218	8	ADS31792
747	29	67.4	220	7	ABO61836
748	29	67.4	222	8	ADN26577
749	29	67.4	224	2	AAR25873
750	29	67.4	224	2	AAW41751
751	29	67.4	227	7	ADC94216
752	29	67.4	237	8	ADS28565
753	29	67.4	239	7	ABO72504
754	29	67.4	247	2	AAR25874

Aar25894	HK19. 9/2
Adt75006	Light cha
Abr82259	Anti-gang
Abr82263	Anti-gang
Adp84128	Armenian
Adp84132	Armenian
Ads31794	Light var
Ads31790	Light var
Aau66213	Propionib
Abm62732	Propionib
Abr41323	Human DIT
Adt74992	Light cha
Aau49642	Propionib
Abm46161	Propionib
Aab40386	Human ORF
Abp03434	Human ORF
Aau53824	Propionib
Abm50343	Propionib
Abb17899	Human ner
Abb77286	HCV bait
Aap90826	Protein s
Aab40757	Human ORF
Abp00240	Human ORF
Abr82265	Anti-gang
Adp84134	Armenian
Ads31796	Light var
Ady09068	Plant ful
Abp09777	Human ORF
Aar11278	Hepatitis
Aar66627	Hepatitis
Aay14974	HCV J1 NS
Aaw30587	Hepatitis
Aay01618	Protein e
Aay01613	Consensus
Adf66066	Hepatitis
Adf66056	Hepatitis
Abm87811	Rice abio
Aap92045	Sequence
Aap90162	Sequence
Aae39893	Human lip
Adq48423	LH2 domai
Abm65861	Propionib
Abo80352	Pseudomon
Adx95421	Plant ful
Abo78942	Pseudomon
Adp29846	Human sec
Abb68539	Drosophil
Adh22364	Human rec
Adn47390	Thermococ
Aau16567	Human nov
Abu55636	Human nov
Adf04067	Bacterial
Ada34444	Acinetoba
Adc84539	Rice RNas
Adk34478	Novel hum
Aau58505	Propionib
Abm55024	Propionib
Aau41048	Propionib
Abm37567	Propionib
Ada55444	Human pro
Abo74645	Pseudomon
Abr82261	Chimeric
Adp84136	Anti-mono
Adp84130	Anti-mono
Ads31792	Chimeric
Abo61836	Klebsiell
Adn26577	Bacterial
Aar25873	HCV polyp
Aaw41751	Hepatitis
Adc94216	E. faeciu
Ads28565	Bacterial
Abo72504	Pseudomon
Aar25874	HCV polyp

755	29	67.4	247	2	AAW41752
756	29	67.4	251	2	AAR25895
757	29	67.4	251	8	ADL04620
758	29	67.4	252	7	ADC32813
759	29	67.4	253	8	ADX71563
760	29	67.4	264	6	ABM65052
761	29	67.4	265	6	ABU11742
762	29	67.4	270	2	AAR25896
763	29	67.4	271	6	ABU35719
764	29	67.4	272	4	AAG74539
765	29	67.4	273	8	ADS42583
766	29	67.4	276	4	AAM39310
767	29	67.4	302	8	ADP45399
768	29	67.4	308	2	AAW52194
769	29	67.4	308	4	AAB92940
770	29	67.4	308	6	ABP56625
771	29	67.4	308	8	ADS88208
772	29	67.4	308	9	ADX07315
773	29	67.4	323	4	ABB60462
774	29	67.4	323	7	ADM03762
775	29	67.4	328	6	ABU31734
776	29	67.4	330	7	ADB85261
777	29	67.4	330	9	AEA20952
778	29	67.4	338	6	ABU41563
779	29	67.4	338	8	ADY12880
780	29	67.4	342	7	ABO65458
781	29	67.4	345	6	AAE35991
782	29	67.4	345	7	ADK63376
783	29	67.4	350	3	AAY91062
784	29	67.4	350	8	ADO01506
785	29	67.4	365	2	AAR38283
786	29	67.4	365	2	AAR38284
787	29	67.4	365	2	AAR67590
788	29	67.4	365	2	AAR67592
789	29	67.4	369	4	AAM41096
790	29	67.4	370	4	ABG10040
791	29	67.4	381	4	AAB60088
792	29	67.4	381	4	AAB94595
793	29	67.4	381	6	ABP99671
794	29	67.4	381	8	ADS10814
795	29	67.4	381	8	ADS10767
796	29	67.4	383	4	AAU16147
797	29	67.4	383	4	ABB11961
798	29	67.4	383	6	ABU55216
799	29	67.4	383	8	ADS12066
800	29	67.4	383	8	ADS12021
801	29	67.4	385	3	AAB15759
802	29	67.4	385	6	ABG76096
803	29	67.4	385	8	ADF29048
804	29	67.4	385	8	ADP22588
805	29	67.4	386	8	ADN26073
806	29	67.4	387	2	AAR21569
807	29	67.4	387	2	AAR33636
808	29	67.4	387	2	AAR33598
809	29	67.4	387	2	AAR33578
810	29	67.4	387	4	AAB51376
811	29	67.4	387	7	ABW01862
812	29	67.4	387	8	ADO29284
813	29	67.4	389	2	AAR29905
814	29	67.4	389	2	AAR29876
815	29	67.4	389	2	AAR29906
816	29	67.4	389	2	AAR29904
817	29	67.4	392	7	ABO80714
818	29	67.4	402	6	ABP75924
819	29	67.4	406	8	ADP45394
820	29	67.4	433	4	ABG08555
821	29	67.4	433	7	ABO75634
822	29	67.4	446	8	ABM81783
823	29	67.4	451	7	ADH89293
824	29	67.4	451	7	ADH89295
825	29	67.4	451	8	ADG44082
826	29	67.4	451	8	ADG44080
827	29	67.4	455	7	ABU63513

Aaw41752	Hepatitis
Aar25895	HK20. 9/2
Adl04620	M. catarr
Adc32813	Human nov
Adx71563	Plant ful
Abm65052	Propionib
Abu11742	Human MDD
Aar25896	HK21. 9/2
Abu35719	Protein e
Aag74539	Human col
Ads42583	Bacterial
Aam39310	Human pol
Adp45399	Human col
Aaw52194	Human gly
Aab92940	Human pro
Abp56625	Human ste
Ads88208	Human pro
Adx07315	Cyclin-de
Abb60462	Drosophil
Adm03762	Human pro
Abu31734	Protein e
Adb85261	Human pot
Aea20952	Novel hum
Abu41563	Protein e
Ady12880	Plant ful
Abo65458	Klebsiell
Aae35991	Saccharom
Adk63376	Disease t
Aay91062	Streptomy
Ado01506	N. bentha
Aar38283	NANB hepa
Aar38284	NANB hepa
Aar67590	Hepatitis
Aar67592	Hepatitis
Aam41096	Human pol
Abg10040	Novel hum
Aab60088	Human tra
Aab94595	Human pro
Abp99671	Human sec
Ads10814	Human the
Ads10767	Human the
Aau16147	Human nov
Abb11961	Human K c
Abu55216	Human nov
Ads12066	Human the
Ads12021	Human the
Aab15759	Rat D4 re
Abg76096	Rat dopam
Adf29048	Rat dopam
Adp22588	Sea-squir
Adn26073	Bacterial
Aar21569	HCV CKS-N
Aar33636	HCV CKS-N
Aar33598	HCV CKS-N
Aar33578	HCV CKS-N
Aab51376	HCV recom
Abw01862	HCV-CKS-N
Ado29284	Mouse GPC
Aar29905	HCV NS4-N
Aar29876	HCV NS4-N
Aar29906	HCV NS4-N
Aar29904	HCV NS4-N
Abo80714	Pseudomon
Abp75924	Human sec
Adp45394	Human col
Abg08555	Novel hum
Abo75634	Pseudomon
Abm81783	Tumour-as
Adh89293	A. thalia
Adh89295	A. thalia
Adg44082	A. thalia
Adg44080	A. thalia
Abu63513	Novel alk

828	29	67.4	455	8	ADN20757	Adn20757 Bacterial
829	29	67.4	459	6	ABM65568	Abm65568 Propionib
830	29	67.4	462	2	AAR58592	Aar58592 Hepatitis
831	29	67.4	462	8	ADL17783	Adl17783 Hepatitis
832	29	67.4	470	4	AAU44222	Aau44222 Propionib
833	29	67.4	470	6	ABM40741	Abm40741 Propionib
834	29	67.4	471	7	ADK41683	Adk41683 Maize ami
835	29	67.4	477	8	ADQ67717	Adq67717 Novel hum
836	29	67.4	484	7	ADK41685	Adk41685 Maize ami
837	29	67.4	484	8	ADM47951	Adm47951 Polypepti
838	29	67.4	492	4	ABB62773	Abb62773 Drosophil
839	29	67.4	498	6	ABU27977	Abu27977 Protein e
840	29	67.4	501	2	AAY49543	Aay49543 Human PRO
841	29	67.4	501	3	AAY51933	Aay51933 Human PRO
842	29	67.4	501	3	AAY51940	Aay51940 Human PRO
843	29	67.4	501	7	ADJ58631	Adj58631 Human PRO
844	29	67.4	501	9	AEA16700	Aea16700 Human SH2
845	29	67.4	513	5	ABB84258	Abb84258 Human act
846	29	67.4	513	7	ADK41727	Adk41727 Soybean a
847	29	67.4	513	7	ADK41725	Adk41725 Soybean a
848	29	67.4	513	8	ADJ48628	Adj48628 Oil-assoc
849	29	67.4	525	8	ADP45395	Adp45395 Human col
850	29	67.4	527	9	ADV96657	Adv96657 Hepatitis
851	29	67.4	531	8	ADN24127	Adn24127 Bacterial
852	29	67.4	545	5	AAG79559	Aag79559 HCV decre
853	29	67.4	567	7	ADM69007	Adm69007 HCV NS5B
854	29	67.4	571	9	AEB86383	Aeb86383 Amino aci
855	29	67.4	571	9	AEB86382	Aeb86382 Amino aci
856	29	67.4	571	9	AEB86384	Aeb86384 Amino aci
857	29	67.4	573	8	ADN26740	Adn26740 Bacterial
858	29	67.4	573	8	ADN26562	Adn26562 Bacterial
859	29	67.4	575	8	ADU80984	Adu80984 Hepatitis
860	29	67.4	575	8	ADU80981	Adu80981 Hepatitis
861	29	67.4	575	8	ADU80983	Adu80983 Hepatitis
862	29	67.4	575	8	ADU80986	Adu80986 Hepatitis
863	29	67.4	575	8	ADU80985	Adu80985 Hepatitis
864	29	67.4	575	8	ADU80982	Adu80982 Hepatitis
865	29	67.4	575	8	ADU80979	Adu80979 Hepatitis
866	29	67.4	575	8	ADU80980	Adu80980 Hepatitis
867	29	67.4	575	8	ADU80987	Adu80987 Hepatitis
868	29	67.4	576	6	AAO26417	Aao26417 Mutant RN
869	29	67.4	576	6	AAO26419	Aao26419 Mutant RN
870	29	67.4	576	6	AAO26418	Aao26418 Mutant RN
871	29	67.4	576	6	ABG72214	Abg72214 HCV mutan
872	29	67.4	576	8	ADH74494	Adh74494 HCV RNA-d
873	29	67.4	576	9	ADU80741	Adu80741 Hepatitis
874	29	67.4	576	9	ADU80735	Adu80735 Hepatitis
875	29	67.4	577	9	ADV91037	Adv91037 Hepatitis
876	29	67.4	578	5	AAG79558	Aag79558 HCV decre
877	29	67.4	578	6	ABP71662	Abp71662 HCV NS5Bd
878	29	67.4	579	4	AAB60131	Aab60131 Hepatitis
879	29	67.4	580	8	ADO19023	Ado19023 C-termina
880	29	67.4	580	8	ADS28549	Ads28549 Bacterial
881	29	67.4	584	4	ABG09029	Abg09029 Novel hum
882	29	67.4	590	2	AAW37130	Aaw37130 Hepatitis
883	29	67.4	590	2	AAY25292	Aay25292 HCV trunc
884	29	67.4	591	2	AAW01679	Aaw01679 NS5B prot
885	29	67.4	591	2	AAY25291	Aay25291 HCV NS5B
886	29	67.4	591	2	AAY29827	Aay29827 Human hep
887	29	67.4	591	3	AAY59538	Aay59538 HCV RNA p
888	29	67.4	591	4	AAB60130	Aab60130 Hepatitis
889	29	67.4	591	5	AAG79557	Aag79557 HCV decre
890	29	67.4	591	5	AAG79560	Aag79560 HCV NS5B
891	29	67.4	591	5	ABB05637	Abb05637 Hepatitis
892	29	67.4	591	6	AAO26416	Aao26416 Protein d
893	29	67.4	591	6	ABP71663	Abp71663 HCV His-N
894	29	67.4	591	6	ABP71665	Abp71665 HCV His-N
895	29	67.4	591	9	ADV91038	Adv91038 Hepatitis
896	29	67.4	592	2	AAY41144	Aay41144 HCV NS5B
897	29	67.4	592	2	AAY41148	Aay41148 HCV NS5B
898	29	67.4	592	2	AAY41147	Aay41147 HCV NS5B
899	29	67.4	592	2	AAY41149	Aay41149 HCV NS5B
900	29	67.4	592	2	AAY41150	Aay41150 HCV NS5B
901	29	67.4	592	2	AAY41146	Aay41146 HCV NS5B
902	29	67.4	592	2	AAY41145	Aay41145 HCV NS5B
903	29	67.4	592	3	ABB78822	Abb78822 Hepatitis
904	29	67.4	592	8	ADO36215	Ado36215 Hepatitis
905	29	67.4	592	8	ADO79389	Ado79389 Hepatitis
906	29	67.4	592	9	ADV66344	Adv66344 Hepatitis
907	29	67.4	592	9	ABM97125	Abm97125 M. xanthu
908	29	67.4	593	2	AAW14794	Aaw14794 Recombina
909	29	67.4	593	2	AAW14789	Aaw14789 Hepatitis
910	29	67.4	601	4	ABG24076	Abg24076 Novel hum
911	29	67.4	601	8	ADO19021	Ado19021 Full-leng
912	29	67.4	605	4	AAB93421	Aab93421 Human pro
913	29	67.4	612	2	AAW14792	Aaw14792 Modified
914	29	67.4	612	2	AAW14791	Aaw14791 Modified
915	29	67.4	612	2	AAW14793	Aaw14793 Modified
916	29	67.4	612	2	AAW14790	Aaw14790 Recombina
917	29	67.4	614	4	AAG93258	Aag93258 Human pro
918	29	67.4	621	5	AAG79556	Aag79556 HCV decre
919	29	67.4	621	5	AAE18903	Aae18903 Hepatitis
920	29	67.4	621	6	ABP71699	Abp71699 HCV NS5B
921	29	67.4	621	6	ABR41892	Abr41892 Hepatitis
922	29	67.4	621	6	ABP97967	Abp97967 Amino aci
923	29	67.4	624	4	AAB94379	Aab94379 Human pro
924	29	67.4	624	7	ADC31102	Adc31102 Human nov
925	29	67.4	627	5	AAG79561	Aag79561 HCV decre
926	29	67.4	627	5	ADG19078	Adg19078 HCV NS5B
927	29	67.4	654	6	ABJ19399	Abj19399 Human int
928	29	67.4	666	8	ADR89439	Adr89439 cry40Aa1.
929	29	67.4	668	8	ADS74103	Ads74103 Virulent
930	29	67.4	675	9	ABM91625	Abm91625 M. xanthu
931	29	67.4	690	8	ADR89404	Adr89404 AXMI-008
932	29	67.4	693	8	ADR89402	Adr89402 AXMI-008.
933	29	67.4	695	8	ADU07703	Adu07703 Amino aci
934	29	67.4	697	4	AAE07290	Aae07290 Human neu
935	29	67.4	745	4	AAE07289	Aae07289 Human neu
936	29	67.4	762	9	ADZ72267	Adz72267 Plasmodiu
937	29	67.4	773	4	AAU45423	Aau45423 Propionib
938	29	67.4	773	6	ABM41942	Abm41942 Propionib
939	29	67.4	791	4	AAE07292	Aae07292 Human neu
940	29	67.4	825	8	ADP23636	Adp23636 PRO polyp
941	29	67.4	830	4	ABB66347	Abb66347 Drosophil
942	29	67.4	838	4	AAU52698	Aau52698 Propionib
943	29	67.4	838	6	ABM49217	Abm49217 Propionib
944	29	67.4	839	4	AAE07291	Aae07291 Human neu
945	29	67.4	849	8	ADN26256	Adn26256 Bacterial
946	29	67.4	855	9	AEB27345	Aeb27345 Pinus rad
947	29	67.4	866	7	ADB70266	Adb70266 C. neofor
948	29	67.4	868	2	AAR07454	Aar07454 Second op
949	29	67.4	888	7	ABO75041	Abo75041 Pseudomon
950	29	67.4	899	4	ABG25235	Abg25235 Novel hum
951	29	67.4	923	6	ABU39177	Abu39177 Protein e
952	29	67.4	961	5	AAU80188	Aau80188 Human TSP
953	29	67.4	963	6	ADA55051	Ada55051 Human pro
954	29	67.4	963	7	ADJ70698	Adj70698 Human hea
955	29	67.4	966	5	AAU80189	Aau80189 Human TSP
956	29	67.4	967	4	ABG24097	Abg24097 Novel hum
957	29	67.4	980	4	ABG10445	Abg10445 Novel hum
958	29	67.4	1035	8	ADJ50326	Adj50326 Oil-assoc
959	29	67.4	1038	4	AAE02357	Aae02357 Hepacivir
960	29	67.4	1038	4	AAE02356	Aae02356 Hepacivir
961	29	67.4	1040	5	AAE19896	Aae19896 Hepatitis
962	29	67.4	1040	7	ABW00347	Abw00347 Hepatitis
963	29	67.4	1075	8	ADN21139	Adn21139 Bacterial
964	29	67.4	1082	4	ABG29167	Abg29167 Novel hum
965	29	67.4	1146	4	AAE00961	Aae00961 Chicken l
966	29	67.4	1146	9	AEA10571	Aea10571 M. degrad
967	29	67.4	1152	6	ABM67949	Abm67949 Photorhab
968	29	67.4	1175	4	AAE07294	Aae07294 Human neu
969	29	67.4	1259	4	AAE07283	Aae07283 Human neu
970	29	67.4	1286	5	ABP70076	Abp70076 Human NOV
971	29	67.4	1298	4	AAE07293	Aae07293 Human neu
972	29	67.4	1307	4	AAE07282	Aae07282 Human neu
973	29	67.4	1321	8	ADN23423	Adn23423 Bacterial

974	29	67.4	1372	8	ADN23424	Adn23424 Bacterial
975	29	67.4	1411	2	AAR29533	Aar29533 HCV NS4-N
976	29	67.4	1771	4	AAB62631	Aab62631 HCV NS35
977	29	67.4	1771	4	AAB62634	Aab62634 Amino aci
978	29	67.4	1771	4	AAB62635	Aab62635 Amino aci
979	29	67.4	1771	4	AAB62632	Aab62632 HCV delNS
980	29	67.4	1892	4	AAB62636	Aab62636 Amino aci
981	29	67.4	1892	8	ADI34636	Adi34636 HCVmodifi
982	29	67.4	1892	8	ADO00774	Ado00774 HCV NS345
983	29	67.4	1911	4	AAB62638	Aab62638 Amino aci
984	29	67.4	1921	4	AAB62639	Aab62639 Amino aci
985	29	67.4	1944	4	AAB62637	Aab62637 Amino aci
986	29	67.4	1985	5	AAO18001	Aao18001 Hepatitis
987	29	67.4	1985	5	AAE15729	Aae15729 Hepatitis
988	29	67.4	1985	5	AAE15731	Aae15731 Hepatitis
989	29	67.4	1985	5	AAE15720	Aae15720 Hepatitis
990	29	67.4	1985	5	AAE15717	Aae15717 Hepatitis
991	29	67.4	1985	5	AAE15727	Aae15727 Hepatitis
992	29	67.4	1985	5	AAE15728	Aae15728 Hepatitis
993	29	67.4	1985	5	AAE15722	Aae15722 Hepatitis
994	29	67.4	1985	5	AAE15730	Aae15730 Hepatitis
995	29	67.4	1985	6	ABU09574	Abu09574 HCV Met-N
996	29	67.4	1985	6	ABU09575	Abu09575 HCV Met-N
997	29	67.4	1985	8	ADJ57846	Adj57846 HCV repli
998	29	67.4	1985	8	ADR38450	Adr38450 Hepatitis
999	29	67.4	1985	9	AEB17075	Aeb17075 Hepatitis
1000	29	67.4	1986	8	ADR38451	Adr38451 Hepatitis

ALIGNMENTS

RESULT 1
AAR97314
ID AAR97314 standard; peptide; 7 AA.
XX
AC AAR97314;
XX
DT 15-OCT-1996 (first entry)
XX
DE Humanised monoclonal antibody light chain CDR.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Mus musculus.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Claim 5; Page 38; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. This sequence is a murine derived CDR region which corresponds
CC to CDR 2 in the light chain of the humanised MAb. See AAR97313-97333
XX
SQ Sequence 7 AA;

Query Match 100.0%; Score 43; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 1 WTSTRHT 7

RESULT 2
AAB86085
ID AAB86085 standard; peptide; 7 AA.
XX
AC AAB86085;
XX
DT 17-JUL-2001 (first entry)
XX
DE H. pylori catalase derived antibody HP25/6m/1B5 light chain CDR2.
XX
KW Catalase; beta-urease; antibody; antigen; detection; infection; epitope;
KW acid-resistant microorganism; complementarity determining region; CDR;
KW feces; heavy chain; light chain.
XX
OS Unidentified.
XX
PN WO200127612-A2.
XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-EP010057.
XX
PR 12-OCT-1999; 99EP-00120351.
PR 16-MAR-2000; 2000EP-00105592.
PR 31-MAR-2000; 2000EP-00107028.
PR 10-MAY-2000; 2000EP-00110110.
XX
PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
XX
PI Reiter C, Cullmann G, Lakner M, Truee A, Dehnert S, Schwartz G;
XX
DR WPI; 2001-282086/29.
DR N-PSDB; AAF88112.
XX
PT Detecting infections by acid-resistant microorganisms, particularly for
PT diagnosing Helicobacter pylori, comprises immunochromatographic detection
PT of antigen in feces.
XX
PS Claim 26; Page 26; 90pp; German.
XX
CC This invention describes a novel method for detecting infection by an
CC acid-resistant microorganism (A), in a mammal, using
CC immunochromatography. The method is used to diagnose infection by an acid
CC -resistant microorganism (A), in a mammal, such as Helicobacter,
CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
CC H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,
CC inexpensive and non-invasive, and may indicate the stage of infection. A
CC test strip used in the method may include a filter to eliminate particles
CC present in the sample and only a single receptor provides a reasonably
CC secure diagnosis, with specificity and selectivity improved by detecting
CC several epitopes (of catalase) or different antigens (catalase and beta-
CC urease). The method can be automated. This sequence represents a
CC complementarity determining region (CDR) from an antibody raised against
CC the H. pylori catalase or beta-urease antigen which is used to illustrate
CC the method of the invention

```
XX
SQ   Sequence 7 AA;

  Query Match             100.0%;  Score 43;  DB 4;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db          1 WTSTRHT 7


RESULT 3
AAB86053
ID   AAB86053 standard; peptide; 7 AA.
XX
AC   AAB86053;
XX
DT   17-JUL-2001  (first entry)
XX
DE   H. pylori catalase derived antibody HP25/6m/1B5 light chain CDR2.
XX
KW   Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;
KW   infection; acid-resistant microorganism; fecal; antibody; diagnosis;
KW   antibacterial; complementarity determining region.
XX
OS   Unidentified.
XX
PN   WO200127613-A2.
XX
PD   19-APR-2001.
XX
PF   12-OCT-2000; 2000WO-EP010058.
XX
PR   12-OCT-1999;   99EP-00120351.
PR   16-MAR-2000; 2000EP-00105592.
PR   31-MAR-2000; 2000EP-00107028.
PR   10-MAY-2000; 2000EP-00110110.
XX
PA   (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
XX
PI   Reiter C,  Cullmann G,  Heppner P,  Ringeis A,  Mueller H,  Haindl E;
XX
DR   WPI; 2001-282087/29.
DR   N-PSDB; AAF88055.
XX
PT   Detecting infections by acid-resistant microorganisms, particularly for
PT   diagnosing Helicobacter pylori, comprises an immunoassay on a fecal
PT   sample.
XX
PS   Claim 21; Page 16; 89pp; German.
XX
CC   This invention describes a novel method for detecting, in a mammal,
CC   infection by an acid-resistant microorganism (A) which comprises reacting
CC   a fecal sample with: (i) a receptor (R) such that a complex is formed
CC   with an antigen (Ag) of (A); or (ii) two different R so that a three-part
CC   complex is formed with Ag, and the formation of a complex detected. R are
CC   specific for an Ag which, after passage through the intestines, at least
CC   in some mammals, retains a native (or corresponding) structure against
CC   which the mammal produces antibodies (when immunized or infected with
CC   (A), or its extracts, lysates or derived proteins (or fragments) or
CC   synthetic peptides). The products of the invention have antibacterial
CC   activity. The method is used to diagnose infection by Helicobacter,
CC   Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
CC   H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the
CC   progress of treatment. Receptors, particularly antibodies, directed
CC   against Ag can be used therapeutically for treatment of infections. The
CC   method requires only one R to provide a reasonably secure diagnosis
CC   (although use of two R improves sensitivity), so is relatively
CC   inexpensive and more easily standardized. Also it is direct, non-
CC   invasive, suitable for automation and may indicate the stage of an
CC   infection. This sequence represents a complementarity determining region
CC   (CDR) from an antibody generated against a Helicobacter pylori antigen
CC   (catalase or beta-urease) which is used to illustrate the method of the
CC   invention
XX
SQ   Sequence 7 AA;

  Query Match             100.0%;  Score 43;  DB 4;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db          1 WTSTRHT 7


RESULT 4
ADM95103
ID   ADM95103 standard; peptide; 7 AA.
XX
AC   ADM95103;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Murine MN-14 MAb light chain variable region CDR2.
XX
KW   non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW   complementarity determining region; pancreatic cancer; breast cancer;
KW   ovarian cancer.
XX
OS   Mus sp.
XX
PN   WO2004032962-A1.
XX
PD   22-APR-2004.
XX
PF   11-OCT-2002; 2002WO-US032307.
XX
PR   08-OCT-2002; 2002US-0416531P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-364813/34.
XX
PT   Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT   comprises administering, either concurrently or sequentially, Class III
PT   anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT   therapeutic agent(s).
XX
PS   Claim 6; SEQ ID NO 21; 88pp; English.
XX
CC   The invention relates to a method of treating a non-medullary thyroid
CC   carcinoma or treating medullary thyroid carcinoma involves administering
CC   to a subject, either concurrently or sequentially, a Class III anti-CEA
CC   (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC   least one therapeutic agent. The antibody or its fragment comprises the
CC   complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC   antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC   medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC   ovarian cancer, in a subject. This sequence corresponds to the CDR2 of
CC   the murine MN-14 antibody light chain variable region and used to
CC   generate the humanised/chimeric antibody of the invention.
XX
SQ   Sequence 7 AA;

  Query Match             100.0%;  Score 43;  DB 8;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db          1 WTSTRHT 7
```

```
RESULT 5
ADM98312
ID   ADM98312 standard; peptide; 7 AA.
XX
AC   ADM98312;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 antibody light chain variable region CDR2 peptide.
XX
KW   carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; humanised;
KW   murine; mouse; antibody; MN-14; non-medullary thyroid carcinoma;
KW   medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW   hepatocellular carcinoma; breast cancer; lung cancer;
KW   antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW   apoptosis.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   WO2004032857-A2.
XX
PD   22-APR-2004.
XX
PF   08-OCT-2003; 2003WO-US031801.
XX
PR   08-OCT-2002; 2002US-0416531P.
PR   11-OCT-2002; 2002WO-US032307.
PR   02-MAY-2003; 2003US-0467161P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-340797/31.
XX
PT   Treating non-medullary or medullary thyroid carcinoma, involves
PT   administering to subject, either concurrently or sequentially, anti-
PT   carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS   Claim 8; Page 76; 122pp; English.
XX
CC   This invention relates to methods for treating cancers that express
CC   carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC   therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC   antibodies that can be used following administration of an agent that
CC   will increase antibody effector functions or following administration of
CC   an amount of interferon effective to upregulate CEA expression in tumour
CC   cells. The present invention describes the anti-CEA antibody as a class
CC   III humanised murine monoclonal antibody that retains specificity for CEA
CC   binding and is preferably an MN-14 antibody or fragment thereof.
CC   Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC   composition useful for the treatment of non-medullary or medullary
CC   thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC   carcinoma, as well as breast or lung cancer. Furthermore, it can
CC   stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC   mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC   cell growth and angiogenesis. This peptide sequence is a CDR region of
CC   the humanised murine MN-14 antibody of the invention.
XX
SQ   Sequence 7 AA;

  Query Match             100.0%;  Score 43;  DB 8;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db          1 WTSTRHT 7


RESULT 6
```

```
AAR97337
ID   AAR97337 standard; protein; 106 AA.
XX
AC   AAR97337;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Humanised antibody variable light chain (MN14HuVK).
XX
KW   Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW   complementary determining region; anti-carcinoembryonic antigen; CEA;
KW   diagnosis; imaging; therapy; immune response.
XX
OS   Mus musculus.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    24. .34
FT                   /label= CDR 1.
FT   Binding-site    50. .56
FT                   /label= CDR 2.
FT   Binding-site    89. .96
FT                   /label= CDR 3.
XX
PN   WO9611013-A1.
XX
PD   18-APR-1996.
XX
PF   28-SEP-1995;   95WO-US011964.
XX
PR   05-OCT-1994;   94US-00318157.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Hansen HJ,  Armour KL;
XX
DR   WPI; 1996-209653/21.
DR   N-PSDB; AAT29013.
XX
PT   New humanised anti-CEA monoclonal antibody - having engrafted murine
PT   CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS   Disclosure; Fig 8; 62pp; English.
XX
CC   New humanised monoclonal antibodies (MAbs) comprising the complementary
CC   determining regions (CDRs) of a parental murine class III anti-
CC   carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC   heterologous antibody which can be derived from any species including
CC   human, retain the anti-CEA binding specificity of the parental murine MAb
CC   but are less immunogenic in a human subject than the parental MAb. The
CC   humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC   -producing cancers and patients receiving the humanised antibodies and
CC   conjugates show improved therapeutic results, decreased immune responses
CC   and decreased immune-mediated adverse effects compared to the parent
CC   antibody. See AAR97313-97333 for the CDR sequence and framework regions
CC   of the humanised MAbs
XX
SQ   Sequence 106 AA;

  Query Match             100.0%;  Score 43;  DB 2;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 2.4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         50 WTSTRHT 56


RESULT 7
AAR97335
ID   AAR97335 standard; protein; 106 AA.
XX
AC   AAR97335;
```

XX
DT 15-OCT-1996 (first entry)
XX
DE Murine NEWM MN-14 variable region light chain.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Binding-site 24. .34
FT /label= CDR 1.
FT Binding-site 50. .56
FT /label= CDR 2.
FT Binding-site 89. .96
FT /label= CDR 3.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
DR N-PSDB; AAT29011.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Example 7; Fig 2; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. See AAR97313-97333 for the CDR sequence and framework regions
CC of the humanised MAbs
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 43; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 50 WTSTRHT 56

RESULT 8
AAB86108
ID AAB86108 standard; protein; 106 AA.
XX
AC AAB86108;
XX
DT 17-JUL-2001 (first entry)
XX
DE H. pylori catalase antibody HP25/2m/1BS V region light chain.
XX
KW Catalase; beta-urease; antibody; antigen; detection; infection; epitope;
KW acid-resistant microorganism; complementarity determining region; CDR;
KW feces; heavy chain; light chain.
XX
OS Unidentified.
XX
PN WO200127612-A2.
XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-EP010057.
XX
PR 12-OCT-1999; 99EP-00120351.
PR 16-MAR-2000; 2000EP-00105592.
PR 31-MAR-2000; 2000EP-00107028.
PR 10-MAY-2000; 2000EP-00110110.
XX
PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
XX
PI Reiter C, Cullmann G, Lakner M, Truee A, Dehnert S, Schwartz G;
XX
DR WPI; 2001-282086/29.
DR N-PSDB; AAF88154.
XX
PT Detecting infections by acid-resistant microorganisms, particularly for
PT diagnosing Helicobacter pylori, comprises immunochromatographic detection
PT of antigen in feces.
XX
PS Claim 31; Fig 4; 90pp; German.
XX
CC This invention describes a novel method for detecting infection by an
CC acid-resistant microorganism (A), in a mammal, using
CC immunochromatography. The method is used to diagnose infection by an acid
CC -resistant microorganism (A), in a mammal, such as Helicobacter,
CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
CC H. hepatica, C. jejuni and M. tuberculosis. The method is rapid, simple,
CC inexpensive and non-invasive, and may indicate the stage of infection. A
CC test strip used in the method may include a filter to eliminate particles
CC present in the sample and only a single receptor provides a reasonably
CC secure diagnosis, with specificity and selectivity improved by detecting
CC several epitopes (of catalase) or different antigens (catalase and beta-
CC urease). The method can be automated. This sequence represents a
CC Helicobacter pylori catalase derived antibody V-region light chain
CC fragment used to illustrate the method of the invention
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 43; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 50 WTSTRHT 56

RESULT 9
AAB86070
ID AAB86070 standard; protein; 106 AA.
XX
AC AAB86070;
XX
DT 17-JUL-2001 (first entry)
XX
DE H. pylori catalase antibody HP25/6m/1B5 V-region light chain.
XX
KW Heavy chain; light chain; catalase; beta-urease; detection; CDR; antigen;
KW infection; acid-resistant microorganism; fecal; antibody; diagnosis;
KW antibacterial; complementarity determining region; V-region.
XX
OS Unidentified.
XX
PN WO200127613-A2.

XX
PD 19-APR-2001.
XX
PF 12-OCT-2000; 2000WO-EP010058.
XX
PR 12-OCT-1999; 99EP-00120351.
PR 16-MAR-2000; 2000EP-00105592.
PR 31-MAR-2000; 2000EP-00107028.
PR 10-MAY-2000; 2000EP-00110110.
XX
PA (CONN-) CONNEX GES OPTIMIERUNG VON FORSCHUNG & E.
XX
PI Reiter C, Cullmann G, Heppner P, Ringeis A, Mueller H, Haindl E;
XX
DR WPI; 2001-282087/29.
DR N-PSDB; AAF88097.
XX
PT Detecting infections by acid-resistant microorganisms, particularly for
PT diagnosing Helicobacter pylori, comprises an immunoassay on a fecal
PT sample.
XX
PS Claim 27; Fig 4; 89pp; German.
XX
CC This invention describes a novel method for detecting, in a mammal,
CC infection by an acid-resistant microorganism (A) which comprises reacting
CC a fecal sample with: (i) a receptor (R) such that a complex is formed
CC with an antigen (Ag) of (A); or (ii) two different R so that a three-part
CC complex is formed with Ag, and the formation of a complex detected. R are
CC specific for an Ag which, after passage through the intestines, at least
CC in some mammals, retains a native (or corresponding) structure against
CC which the mammal produces antibodies (when immunized or infected with
CC (A), or its extracts, lysates or derived proteins (or fragments) or
CC synthetic peptides). The products of the invention have antibacterial
CC activity. The method is used to diagnose infection by Helicobacter,
CC Campylobacter or Mycobacterium, particularly H. pylori (most preferred),
CC H. hepatica, C. jejuni and M. tuberculosis, and also to monitor the
CC progress of treatment. Receptors, particularly antibodies, directed
CC against Ag can be used therapeutically for treatment of infections. The
CC method requires only one R to provide a reasonably secure diagnosis
CC (although use of two R improves sensitivity), so is relatively
CC inexpensive and more easily standardized. Also it is direct, non-
CC invasive, suitable for automation and may indicate the stage of an
CC infection. This sequence represents a Helicobacter pylori anti-catalase
CC derived antibody HP25/6m/1BM V-region light chain fragment which is
CC described in the method of the invention
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 43; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 50 WTSTRHT 56

RESULT 10
ADM95097
ID ADM95097 standard; protein; 106 AA.
XX
AC ADM95097;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 MAb light chain variable region.
XX
KW non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW complementarity determining region; pancreatic cancer; breast cancer;
KW ovarian cancer.
XX
OS Mus sp.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-364813/34.
DR N-PSDB; ADM95096.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Disclosure; Fig 12A-B; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the murine MN-
CC 14 antibody light chain variable region.
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 43; DB 8; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 50 WTSTRHT 56

RESULT 11
ADM95100
ID ADM95100 standard; protein; 106 AA.
XX
AC ADM95100;
XX
DT 15-JUL-2004 (first entry)
XX
DE Humanised murine MN-14 MAb light chain variable region.
XX
KW non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW complementarity determining region; pancreatic cancer; breast cancer;
KW ovarian cancer.
XX
OS Mus sp.
OS Homo sapiens.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX

DR WPI; 2004-364813/34.
DR N-PSDB; ADM95098.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Claim 14; Fig 16A; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the humanised
CC murine MN-14 antibody light chain variable region.
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 43; DB 8; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 50 WTSTRHT 56

RESULT 12
ADM98320
ID ADM98320 standard; protein; 106 AA.
XX
AC ADM98320;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 antibody light chain variable region protein.
XX
KW carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW antibody; MN-14; non-medullary thyroid carcinoma;
KW medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW hepatocellular carcinoma; breast cancer; lung cancer;
KW antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW apoptosis.
XX
OS Mus sp.
XX
PN WO2004032857-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031801.
XX
PR 08-OCT-2002; 2002US-0416531P.
PR 11-OCT-2002; 2002WO-US032307.
PR 02-MAY-2003; 2003US-0467161P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-340797/31.
DR N-PSDB; ADM98319.
XX
PT Treating non-medullary or medullary thyroid carcinoma, involves
PT administering to subject, either concurrently or sequentially, anti-
PT carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS Disclosure; Fig 12; 122pp; English.
XX
CC This invention relates to methods for treating cancers that express
CC carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC antibodies that can be used following administration of an agent that
CC will increase antibody effector functions or following administration of
CC an amount of interferon effective to upregulate CEA expression in tumour
CC cells. The present invention describes the anti-CEA antibody as a class
CC III humanised murine monoclonal antibody that retains specificity for CEA
CC binding and is preferably an MN-14 antibody or fragment thereof.
CC Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC composition useful for the treatment of non-medullary or medullary
CC thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC carcinoma, as well as breast or lung cancer. Furthermore, it can
CC stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC cell growth and angiogenesis. This polypeptide sequence is murine MN-14
CC antibody light chain variable region protein of the invention.
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 43; DB 8; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 50 WTSTRHT 56

RESULT 13
ADM98322
ID ADM98322 standard; protein; 106 AA.
XX
AC ADM98322;
XX
DT 15-JUL-2004 (first entry)
XX
DE Humanised murine MN-14 antibody light chain variable region protein.
XX
KW carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW antibody; MN-14; non-medullary thyroid carcinoma;
KW medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW hepatocellular carcinoma; breast cancer; lung cancer;
KW antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW apoptosis; humanised.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO2004032857-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031801.
XX
PR 08-OCT-2002; 2002US-0416531P.
PR 11-OCT-2002; 2002WO-US032307.
PR 02-MAY-2003; 2003US-0467161P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-340797/31.
DR N-PSDB; ADM98321.
XX
PT Treating non-medullary or medullary thyroid carcinoma, involves
PT administering to subject, either concurrently or sequentially, anti-
PT carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS Disclosure; Fig 23a; 122pp; English.
XX

CC This invention relates to methods for treating cancers that express
CC carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC antibodies that can be used following administration of an agent that
CC will increase antibody effector functions or following administration of
CC an amount of interferon effective to upregulate CEA expression in tumour
CC cells. The present invention describes the anti-CEA antibody as a class
CC III humanised murine monoclonal antibody that retains specificity for CEA
CC binding and is preferably an MN-14 antibody or fragment thereof.
CC Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC composition useful for the treatment of non-medullary or medullary
CC thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC carcinoma, as well as breast or lung cancer. Furthermore, it can
CC stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC cell growth and angiogenesis. This polypeptide sequence is the humanised
CC murine MN-14 antibody light chain variable region protein of the
CC invention.
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 43; DB 8; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 50 WTSTRHT 56

RESULT 14
ADD05266
ID ADD05266 standard; protein; 108 AA.
XX
AC ADD05266;
XX
DT 01-JAN-2004 (first entry)
XX
DE Female mouse sex hormone of the invention #2.
XX
KW female sex hormone.
XX
OS Mus sp.
XX
PN WO2003074704-A1.
XX
PD 12-SEP-2003.
XX
PF 28-FEB-2003; 2003WO-JP002311.
XX
PR 01-MAR-2002; 2002JP-00055669.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Katagiri M, Fujimoto S, Goda Y;
XX
DR WPI; 2003-731681/69.
DR N-PSDB; ADD05265.
XX
PT Novel proteins for binding, identifying and concentrating female sex
PT hormones.
XX
PS Claim 1; SEQ ID NO 4; 101pp; Japanese.
XX
CC The present invention relates to proteins that bind to female sex
CC hormones. The method is useful for binding, identifying and concentrating
CC female sex hormones. The present invention represents a female sex
CC hormone of the invention.
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 43; DB 7; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 50 WTSTRHT 56

RESULT 15
ADM80357
ID ADM80357 standard; protein; 108 AA.
XX
AC ADM80357;
XX
DT 03-JUN-2004 (first entry)
XX
DE Murine hormone disruptor E2-73 antibody (scFv) protein SeqID 4.
XX
KW antibody; mouse; murine; scFv; hormone disruptor; alkylphenol;
KW resin component; chlorophenol; immunological isolation;
KW environmental protection.
XX
OS Mus sp.
XX
PN WO2003101611-A1.
XX
PD 11-DEC-2003.
XX
PF 30-MAY-2003; 2003WO-JP006840.
XX
PR 31-MAY-2002; 2002JP-00159728.
XX
PA (NIEN-) JAPAN ENVIROCHEMICALS LTD.
PA (ENVI-) ENVIRONMENT PURIFICATION RES INST INC.
XX
PI Saito K, Shiraishi T, Goda Y;
XX
DR WPI; 2004-043011/04.
DR N-PSDB; ADM80356.
XX
PT Polymer-molded support carrying anti-hormone-disrupting-substance
PT antibody for immunological isolation, concentration or clean-up of such
PT trace hormone disruptors in samples, applicable in environmental
PT protection.
XX
PS Example 7; SEQ ID NO 4; 133pp; Japanese.
XX
CC This invention relates to a novel material useful for the isolation of
CC hormone disrupting substances (i.e. hormone disruptors). Specifically, it
CC refers to a material that comprises a polymer-molded support carrying an
CC anti-hormone disruptor antibody covalently linked via a graft chain to
CC the support, which can be used to capture and subsequently recover the
CC substances of interest. The present invention provides a method for
CC selectively and efficiently concentrating hormone disruptors including
CC alkylphenols, resin components, chlorophenols and female, male or thyroid
CC hormones from environmental samples. In particular, the method is useful
CC for the immunological isolation, concentration or clean-up of such trace
CC hormone disruptors that occur in river water, such that it is a method
CC applicable for environmental protection and the analytical sciences. This
CC polypeptide is a murine hormone disruptor antibody (scFv) protein
CC sequence of the invention.
XX
SQ Sequence 108 AA;

Query Match 100.0%; Score 43; DB 8; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 50 WTSTRHT 56

RESULT 16

```
ABR42756
ID   ABR42756 standard; protein; 115 AA.
XX
AC   ABR42756;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14 Vkappa region.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Disclosure; Fig 12; 62pp; English.
XX
CC   The present sequence is the protein sequence of the light chain variable
CC   region of anti-carcinoembryonic antigen (CEA) humanized monoclonal
CC   antibody hMN-14. scFv constructs comprising the hMN-14 Vkappa and VH
CC   regions are used in novel multivalent, monospecific binding proteins
CC   (diabody, triabody and tetrabody) of the invention (see also ABR42754,
CC   ABR42757 and ABR42758). Claimed binding proteins are specific for a
CC   tumour-associated antigen, and are used in the diagnosis and treatment of
CC   a tumour, carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma,
CC   lymphoma or myeloma, or a cancer selected from acute lymphoblastic
CC   leukaemia, acute myelogenous leukaemia, biliary, breast, cervical,
CC   chronic lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 115 AA;

  Query Match           100.0%;  Score 43;  DB 6;  Length 115;
  Best Local Similarity  100.0%;  Pred. No. 2.6;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         50 WTSTRHT 56


RESULT 17
ABG76490
ID   ABG76490 standard; protein; 232 AA.
XX
AC   ABG76490;
XX
DT   13-MAY-2003  (first entry)
XX
DE   Light chain variable, VL, region of antibody hMN14.
XX
KW   CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW   colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW   human; zeta signalling chain; CD8alpha hinge; humanised antibody;
KW   light chain variable region; VL.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT   Protein         20. .232
FT                   /label= Mature_VL_of_hMN14
XX
PN   US2002165360-A1.
XX
PD   07-NOV-2002.
XX
PF   10-DEC-2001; 2001US-00006771.
XX
PR   30-NOV-2000; 2000US-0250087P.
PR   30-NOV-2000; 2000US-0250090P.
XX
PA   (JUNG/) JUNGHANS R P.
XX
PI   Junghans RP;
XX
DR   WPI; 2003-298705/29.
DR   N-PSDB; ABX13170.
XX
PT   New chimeric molecule from humanized antibody against carcinoembryonic
PT   antigen and having signaling molecules of T cells and other effector
PT   cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS   Disclosure; Page 10-11; 20pp; English.
XX
CC   The invention relates to a chimaeric molecule comprising the
CC   carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC   as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC   chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC   which the cysteine residues have been mutated, with the IgTCR molecule
CC   occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC   appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC   NK (not defined) or other effector cells are useful in treating patients
CC   with cancers expressing the CEA antigen, together with other or with
CC   heterologous constructs to engage additional stimulatory and functional
CC   properties of the effector cells to enhance the anti-tumour therapeutic
CC   efficacy. The cancer disorder includes colorectal, breast and lung
CC   cancers. The present sequence represents the light chain variable, VL,
CC   region of antibody hMN14. The VL protein is humanised (complementarity
CC   determining region-grafted) and has a leader peptide
XX
SQ   Sequence 232 AA;

  Query Match           100.0%;  Score 43;  DB 6;  Length 232;
  Best Local Similarity  100.0%;  Pred. No. 5.6;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         69 WTSTRHT 75


RESULT 18
ADE64204
ID   ADE64204 standard; protein; 232 AA.
XX
AC   ADE64204;
XX
```

DT 29-JAN-2004 (first entry)
XX
DE MN14LC protein related to a novel antibody library.
XX
KW antibody library; retroviral vector; antibody light chain;
KW antibody heavy chain; human therapy; multiplicity of infection; MOI;
KW plasmid; GATEWAY vector; MN14LC.
XX
OS Unidentified.
XX
PN WO2003083077-A2.
XX
PD 09-OCT-2003.
XX
PF 28-MAR-2003; 2003WO-US009662.
XX
PR 28-MAR-2002; 2002US-0368808P.
PR 10-APR-2002; 2002US-0371299P.
PR 28-MAR-2003; 2003US-00371299.
XX
PA (GALA-) GALA DESIGN INC.
XX
PI Bremel RD, Eakle K, Imboden M;
XX
DR WPI; 2003-804051/75.
DR N-PSDB; ADE64208.
XX
PT New antibody library comprising cells comprising at least one integrated
PT retroviral vector expressing an antibody light or heavy chain, useful in
PT preparing a composition for diagnosing or treating disorders.
XX
PS Disclosure; Fig 8; 57pp; English.
XX
CC This invention relates to a new antibody library which comprises at least
CC 100 cells, each of which comprises at least one integrated retroviral
CC vector expressing an antibody light or heavy chain. Antibodies are of
CC increasing importance in human therapy, assay procedures and diagnostic
CC methods and a need exists for efficient methods of generating and
CC screening antibody libraries containing large numbers of antibodies. The
CC antibody library of the invention addresses this need, with the
CC additional advantage of strict control over multiplicity of infection
CC (MOI), and is useful in preparing a composition for diagnosing or
CC treating a wide variety of disorders. The present sequence is the amino
CC acid sequence of the MN14LC protein, which was encoded by the Gateway
CC retroviral vectors used in the exemplification of the invention.
XX
SQ Sequence 232 AA;

Query Match 100.0%; Score 43; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 69 WTSTRHT 75

RESULT 19
ADF60817
ID ADF60817 standard; protein; 232 AA.
XX
AC ADF60817;
XX
DT 12-FEB-2004 (first entry)
XX
DE hMN-14 light chain amino acid sequence.
XX
KW Immunomodulatory; antidiabetic; immunosuppressive; cardiovascular;
KW neuroprotective; nootropic; fungicide; virucide; antimalarial;
KW antihelmintic; antiparasitic; haemostatic; muscular; antiinflammatory;
KW dermatological; antipyretic; antirheumatic; cytostatic; mutant;
KW bispecific antibody; immunoglobulin G; IgG; scFvs; Fvs; CH2 domain;
KW immune; autoimmune; disease; organ graft rejection; cardiovascular;
KW neurological; Alzheimer's disease; graft vs host disease;
KW systemic lupus erythematosus; diabetes mellitus.
XX
OS Homo sapiens.
XX
PN WO2003074569-A2.
XX
PD 12-SEP-2003.
XX
PF 03-MAR-2003; 2003WO-GB000871.
XX
PR 01-MAR-2002; 2002US-0361037P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (MCCA/) MCCALL J D.
XX
PI Qu Z, Hansen H, Goldenberg DM;
XX
DR WPI; 2003-902725/82.
DR N-PSDB; ADF60816.
XX
PT Mutant bispecific antibody which is rapidly cleared from a patient's
PT body, useful as a pretargeting agent in methods for diagnosing or
PT treating diseases, such as autoimmune disease, and disease caused by
PT infectious agents.
XX
PS Example; Fig 2; 68pp; English.
XX
CC The invention relates to a mutant bispecific antibody (mbAb1) comprising
CC at least a human hinge constant region from immunoglobulin G (IgG), two
CC single chain variable fragments (scFvs), and two variable fragments
CC (Fvs), where the constant region contains one or more amino acid
CC mutations in the heavy chain 2 (CH2) domain. The methods and antibody of
CC the invention are used to diagnose or treat an immune dysregulation
CC disease, an autoimmune disease, organ graft rejection, cardiovascular
CC disease, neurological disease (Alzheimer's disease) or graft vs. host
CC disease. The methods are also useful for treating a disease caused by a
CC fungus, virus, parasite, or bacterium. The methods may also be used for
CC intraoperative or endoscopic diagnosis to identify diseased tissue. The
CC autoimmune diseases that may be diagnosed or treated include acute or
CC chronic idiopathic thrombocytopenic purpura, dermatomyositis, Sydenham's
CC chorea, myasthenia gravis, systemic lupus erythematosus, lupus nephritis,
CC rheumatic fever, polyglandular syndromes and diabetes mellitus. The
CC current sequence represents the hMN-14 light chain amino acid sequence.
XX
SQ Sequence 232 AA;

Query Match 100.0%; Score 43; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 69 WTSTRHT 75

RESULT 20
AAW02278
ID AAW02278 standard; protein; 250 AA.
XX
AC AAW02278;
XX
DT 25-MAR-2003 (revised)
DT 29-OCT-1996 (first entry)
XX
DE 741F8 anti-c-erbB-2 two single chain Fv construct.
XX
KW 741F8; anti-c-erbB-2; monoclonal antibody; single chain Fv; sFv;
KW construct; polypeptide linker; C-terminal amino acid sequence;
KW in vivo imaging; drug targetting experiment; homodimer; increased;
KW binding avidity; tissue retention time.
XX
OS Homo sapiens.

```
XX
FH   Key             Location/Qualifiers
PT   Peptide         122. .135
FT                   /label= linker
PT   Peptide         246. .250
FT                   /note= "claimed C-terminal tail to facilitate
FT                   crosslinking of two sFv polypeptides"
XX
PN   US5534254-A.
XX
PD   09-JUL-1996.
XX
PF   07-OCT-1993;   93US-00133804.
XX
PR   06-FEB-1992;   92US-00831967.
XX
PA   (CHIR ) CHIRON CORP.
PA   (CREA-) CREATIVE BIOMOLECULES INC.
XX
PI   Oppermann H,  Ring DB,  Huston JS,  Houston LL;
XX
DR   WPI; 1996-333194/33.
DR   N-PSDB; AAT36878.
XX
PT   Compsns. contg. antigen-targetting antibody fragment constructs -
PT   comprising dimer of single-chain Fv fragments.
XX
PS   Claim 25; Col 27-28; 30pp; English.
XX
CC   The variable heavy (VH) and variable light (VL) genes of the 741F8 anti-c
CC   -erbB-2 monoclonal antibody (MAb), were isolated from the cDNA of the
CC   parental 741F8 hybridoma line. A two single chain Fv (sFv) gene was
CC   constructed by connecting the VH and VL genes with a DNA sequence
CC   endcoding a polypeptide linker. A synthetic DNA duplex encoding the C-
CC   terminal amino acid sequence, (Gly)4-Cys was inserted, and the resulting
CC   741F8 anti-c-erbB-2 two sFv inserted into an expression vector. The
CC   resulting gene, which encodes the present sequence, was transformed into
CC   E. coli, and protein expression induced by the addn. of IPTG to the
CC   culture medium. A compsn. comprising a carrier and the 2 sFv protein
CC   prod. can be used for in vivo imaging, and drug targetting experiments.
CC   The 2 sFv protein prod. is a homodimer, in which both fragments target
CC   the same antigen, therefore giving greater binding avidity and longer
CC   tissue retention times, compared to individual sFv protein prod.
CC   fragments. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 250 AA;

  Query Match             100.0%;  Score 43;  DB 2;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 6;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        185 WTSTRHT 191


RESULT 21
AAW29261
ID   AAW29261 standard; protein; 250 AA.
XX
AC   AAW29261;
XX
DT   25-MAR-2003  (revised)
DT   07-JAN-1998  (first entry)
XX
DE   Anti-c-erbB-2 single chain antibody 741F8.
XX
KW   Adenovirus; E1A; transactivator; transcription activator; stimulate;
KW   expression vector; single-chain binding protein; VA1; enhance; PCR;
KW   translation; production; immortal; eukaryotic cell; scFv; primer;
KW   single-chain antibody fragment; imaging; tumour; breast cancer;
KW   ovarian cancer; c-erbB-2 antigen; digoxin intoxication.
XX
OS   Synthetic.
XX
PN   US5658763-A.
XX
PD   19-AUG-1997.
XX
PF   05-JUN-1995;   95US-00463675.
XX
PR   25-OCT-1993;   93US-00143498.
XX
PA   (CREA-) CREATIVE BIOMOLECULES INC.
XX
PI   Oppermann H,  Dorai H;
XX
DR   WPI; 1997-424235/39.
DR   N-PSDB; AAT91837.
XX
PT   Producing single chain binding protein in immortalised eukaryotic cells -
PT   which comprise protein coding sequences, a transcription activator and
PT   translation promotion sequences, provides high expression at low copy
PT   number.
XX
PS   Example 2; Col 29-32; 24pp; English.
XX
CC   This sequence is a single chain anti-c-erbB-2 antibody (scFv) derived
CC   from hybridoma 741F8. The protein product includes a C-terminal tail Gly4
CC   -Cys in some constructs. Single-chain antibodies can be produced using a
CC   novel method which comprises culturing an immmortalised eukaryotic cell
CC   having transfected DNA sequences (encoding the protein of interest),
CC   integrated into its genome. In particular expression effector vectors
CC   containing a non-native reporter DNA (encoding the scFv) and viral
CC   sequences to promote transcription and translation (e.g. the adenovirus
CC   E1A and VA1 genes as shown in AAT91831 and AAT91834 respectively) are
CC   used. The scFv that is produced, when properly folded, has a structure
CC   with mono- or bi-functional binding activity. The method is especially
CC   used to produce single-chain antibody fragments (scFv), e.g. for imaging
CC   tumours or delivering therapeutic agents to them, particularly breast and
CC   ovarian cancers that express the c-erbB-2 antigen. Other scFv are used in
CC   model studies and for treating digoxin intoxication. (Updated on 25-MAR-
CC   2003 to correct PF field.)
XX
SQ   Sequence 250 AA;

  Query Match             100.0%;  Score 43;  DB 2;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 6;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        185 WTSTRHT 191


RESULT 22
AAW22400
ID   AAW22400 standard; protein; 250 AA.
XX
AC   AAW22400;
XX
DT   25-MAR-2003  (revised)
DT   09-OCT-1997  (first entry)
XX
DE   Single chain antibody 741F8 protein sequence.
XX
KW   Production; single-chain; binding protein; antibody; eukaryote; virus;
KW   transcription activator; promoter; expression; adenovirus; E1A; PCR;
KW   polymerase chain reaction; amplification; primer; herpes simplex virus;
KW   thymidine kinase; vector; enhancer; translation; heterologous.
XX
OS   Synthetic.
XX
PN   US5631158-A.
XX
PD   20-MAY-1997.
```

XX
PF 05-JUN-1995; 95US-00461184.
XX
PR 25-OCT-1993; 93US-00143498.
XX
PA (CREA-) CREATIVE BIOMOLECULES INC.
XX
PI Oppermann H, Dorai H;
XX
DR WPI; 1997-288577/26.
DR N-PSDB; AAT78879.
XX
PT Production of cell line for producing single-chain binding protein -
PT using construct containing DNA encoding viral transcription activator
PT protein.
XX
PS Example 2; Col 29-32; 24pp; English.
XX
CC The invention relates to methods of increasing production of a single-
CC chain binding protein, especially a single chain antibody, by generating
CC eukaryotic cell lines containing DNA encoding either a viral
CC transcription activator protein that acts on and stimulates a viral
CC promoter controlling the expression of DNA encoding the single-chain
CC binding protein, such as the adenovirus Ad2 E1A protein encoded by the
CC sequence AAT78873, or an RNA sequence able to promote translation of the
CC RNA transcript from the heterologous gene, such as the adenoviral VA1
CC gene (AAT78876). The sequence presented here is the amino acid sequence
CC of the anti-c-erbB2 single chain antibody 741. The coding sequence was
CC constructed by amplifying the variable heavy and light chain genes which
CC were then cloned into a pUC vector. For secretion from mammalian cells,
CC the sequence is preceded by the signal peptide sequence from the
CC monoclonal antibody 520C9 (AAT78880) or from PacI (AAT78881). (Updated on
CC 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 250 AA;

Query Match 100.0%; Score 43; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 185 WTSTRHT 191

RESULT 23
AAW47012
ID AAW47012 standard; protein; 250 AA.
XX
AC AAW47012;
XX
DT 13-JUL-1998 (first entry)
XX
DE Single chain binding site molecule (sFv) 741F8.
XX
KW Single chain binding site molecule 7414F8; sFv 741F8; large scale;
KW transactivating transcription activator; viral transcription promoter;
KW protein production; non-native gene; hard to express gene.
XX
OS Synthetic.
XX
PN US5733782-A.
XX
PD 31-MAR-1998.
XX
PF 05-JUN-1995; 95US-00464589.
XX
PR 25-OCT-1993; 93US-00143498.
XX
PA (CREA-) CREATIVE BIOMOLECULES INC.
XX
PI Oppermann H, Dorai H;
XX
DR WPI; 1998-229831/20.
DR N-PSDB; AAV22398.
XX
PT Immortalised eukaryotic cell comprising transfected DNa sequences -
PT useful for enhanced production of proteins encoded by non native genes.
XX
PS Example 2; Col 31-32; 24pp; English.
XX
CC The present sequence represents single chain binding site molecule (sFv).
CC The sequence was expressed to exemplify the invention, which is a method
CC for the expression of poorly expressed genes in an immortalised
CC eukaryotic cell. This cell contains transfected DNA sequences operatively
CC integrated into its genome. The transfected DNA sequences encode a viral
CC transcription promoter linked to a non-native reporter sequence encoding
CC a single chain binding protein. The promoter is activated by a viral
CC transcription activator protein. The cell allows the production on a
CC commercial scale of proteins encoded by non-native hard to express genes
XX
SQ Sequence 250 AA;

Query Match 100.0%; Score 43; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 185 WTSTRHT 191

RESULT 24
AAW53168
ID AAW53168 standard; protein; 250 AA.
XX
AC AAW53168;
XX
DT 16-JUL-1998 (first entry)
XX
DE 741F8 anti-c-erbB-2 sFv' dimeric construct protein sequence.
XX
KW Antigen imaging; single chain Fv; sFv; linker; dimeric; cancer; c-erbB-2;
KW tumour; diagnosis.
XX
OS Synthetic.
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 122. .135
FT /note= "linker peptide"
FT Peptide 246. .250
FT /note= "Gly4-Cys C-terminal tail"
XX
PN US5753204-A.
XX
PD 19-MAY-1998.
XX
PF 05-JUN-1995; 95US-00461838.
XX
PR 06-FEB-1992; 92US-00831967.
PR 07-OCT-1993; 93US-00133804.
XX
PA (CHIR) CHIRON CORP.
PA (CREA-) CREATIVE BIOMOLECULES INC.
XX
PI Oppermann H, Ring DB, Huston JS, Houston LL;
XX
DR WPI; 1998-311318/27.
DR N-PSDB; AAV21796.
XX
PT Imaging of antigens in vivo - using dimers of single-chain antibody Fv
PT fragments.
XX
PS Example 1; Col 25-28; 30pp; English.
XX

CC This represents the protein sequence of a 741F8 sFv' (single chain Fv) C-
CC terminal Gly4-Cys construct. This was constructed by connecting the Vh
CC and Vl genes with a DNA sequence encoding a 14 residue polypeptide
CC linker. 741F8 is a monoclonal antibody useful in targeting c-erbB-2
CC antigen. This dimeric construct can be used in the methods of invention
CC of imaging a preselected antigen expressed in a mammal. The methods are
CC used in magnetic resonance imaging of c-erbB-2 or related antigens in
CC cancer diagnosis. The biosynthetic constructs have enhanced properties as
CC in vivo targetting agents in comparison with intact monoclonal antibodies
CC or their Fab fragments. The dimeric constructs permit the in vivo
CC targetting of an epitope on an antigen with greater apparent avidity,
CC including greater tumour specificity, tumour localisation and tumour
CC retention properties than that of the Fab fragment having the same CDRS
CC as the construct
XX
SQ Sequence 250 AA;

Query Match 100.0%; Score 43; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 185 WTSTRHT 191

RESULT 25
AAW80422
ID AAW80422 standard; protein; 250 AA.
XX
AC AAW80422;
XX
DT 28-JAN-1999 (first entry)
XX
DE Anti-c-erbB-2 sFv' protein sequence.
XX
KW Anti-c-erbB-2 sFv'; c-erbB-2; antigen; tumour cell; antibody 741F8;
KW targeted delivery; antigen-expressing cell.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 122. .135
FT /note= "linker"
XX
PN US5837846-A.
XX
PD 17-NOV-1998.
XX
PF 05-JUN-1995; 95US-00461386.
XX
PR 06-FEB-1992; 92US-00831967.
PR 07-OCT-1993; 93US-00133804.
XX
PA (CREA-) CREATIVE BIOMOLECULES INC.
PA (CHIR) CHIRON CORP.
XX
PI Oppermann H, Houston LL, Huston JS, Ring DB;
XX
DR WPI; 1999-023541/02.
DR N-PSDB; AAV63397.
XX
PT Nucleic acid encoding single-chain Fv fragment specific for antigens -
PT and having C-terminal tail for crosslinking to form dimer with improved
PT pharmacokinetic properties, used to deliver drugs and imaging agents,
PT especially to tumours.
XX
PS Example 1; Col 27-30; 29pp; English.
XX
CC The present sequence represents an anti-c-erbB-2 sFv'. c-erbB-2 is an
CC antigen that is overexpressed on the surface of tumour cells. An antibody
CC designated 741F78 binds c-erbB-2. Variable heavy and light sequences of
CC antibody 741F8 are connected, together with a linker, to produce the
CC present single chain Fv gene. Anti-c-erbB-2 sFv' exemplifies the
CC invention. Dimers of the single chain Fv are used for targeted delivery
CC of drugs or imaging agents (e.g. cytotoxins, prodrugs or 99m-technetium)
CC to antigen-expressing cells, particularly for treatment or diagnosis of
CC tumours (especially of ovary or breast)
XX
SQ Sequence 250 AA;

Query Match 100.0%; Score 43; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 185 WTSTRHT 191

RESULT 26
ABW00714
ID ABW00714 standard; protein; 250 AA.
XX
AC ABW00714;
XX
DT 15-JAN-2004 (first entry)
XX
DE 741F8 sFv' C-terminal Gly4-Cys protein.
XX
KW Cell proliferation; cytotoxic agent; drug targetting; single-chain Fv;
KW sFv.
XX
OS Unidentified.
XX
PN US2002168375-A1.
XX
PD 14-NOV-2002.
XX
PF 21-JUN-2001; 2001US-00887853.
XX
PR 06-FEB-1992; 92US-00831967.
PR 07-OCT-1993; 93US-00133804.
PR 05-JUN-1995; 95US-00462641.
PR 26-APR-2000; 2000US-00558741.
XX
PA (CHIR) CHIRON CORP.
XX
PI Huston JS, Houston LL, Ring DB, Oppermann H;
XX
DR WPI; 2003-765156/72.
DR N-PSDB; AAD61483.
XX
PT Novel binding protein formulation for targeting epitope on antigen in
PT mammal, comprising dimeric biosynthetic construct having conformation
PT permitting binding of antigen by binding site of each polypeptide chain.
XX
PS Example 1; Page 15-16; 30pp; English.
XX
CC The invention relates to a binding protein formulation for targetting an
CC epitope on an antigen expressed in mammal. The formulation comprises of
CC dimeric biosynthetic construct having conformation permitting binding of
CC antigen by binding site of each polypeptide chain. The invention is
CC useful for imaging a preselected antigen in a mammal expressing the
CC antigen. It is also useful for targetting drugs that inhibits cell
CC proliferation and cytotoxic agents that kill cells. The present sequence
CC is 741F8 sFv' C-terminal Gly4-Cys protein. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 250 AA;

Query Match 100.0%; Score 43; DB 7; Length 250;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WTSTRHT 7
              |||||||
Db        185 WTSTRHT 191
```

RESULT 27
ADY60804
ID ADY60804 standard; protein; 250 AA.
XX
AC ADY60804;
XX
DT 02-JUN-2005 (first entry)
XX
DE 741F8 sFv' construct protein SEQ ID NO:2.
XX
KW gene therapy; tumor; cytostatic.
XX
OS Synthetic.
XX
PN US2005058638-A1.
XX
PD 17-MAR-2005.
XX
PF 10-OCT-2003; 2003US-00683547.
XX
PR 21-MAY-1987; 87US-00052800.
PR 30-JUN-1988; 88US-00213671.
PR 06-FEB-1992; 92US-00831967.
PR 12-MAR-1992; 92US-00850228.
PR 19-OCT-1993; 93US-00139901.
PR 18-DEC-1995; 95US-00575724.
PR 26-APR-2000; 2000US-00558741.
XX
PA (HUST/) HUSTON J S.
PA (OPPE/) OPPERMANN H.
XX
PI Huston JS, Oppermann H;
XX
DR WPI; 2005-222160/23.
DR N-PSDB; ADY60803.
XX
PT New isolated biosynthetic polypeptides comprising antigen binding sites,
PT useful as diagnostic or therapeutic reagents for in vivo imaging and drug
PT targeting experiments, or for diagnosing or treating tumors or
PT malignancies.
XX
PS Example 1; SEQ ID NO 2; 35pp; English.
XX
CC The invention relates to an isolated polypeptide that includes an antigen
CC -binding site. Also described: (1) an isolated polypeptide comprising:
CC (a) two variable domain sequences, each variable domain sequence
CC independently comprising at least one group of 3 complementarity
CC determining regions (CDRs) interposed between framework regions (FRs),
CC which variable domains are linked to a polypeptide linker to form a
CC single polypeptide chain in which the FRs and CDRs together define a
CC variable region binding domain which can be immunologically reactive with
CC an antigen; and (b) an amino acid sequence that is a part of the single
CC polypeptide chain, and has a biological activity independent of the
CC immunological reactivity; (2) DNA sequences encoding the above
CC polypeptide; (3) vectors including the above DNA sequences; and (4)
CC methods for employing the above DNA and vectors for producing the
CC polypeptides. The polypeptide is useful as a diagnostic or therapeutic
CC reagent for in vivo imaging and drug targeting experiments. The
CC polypeptide may be used for diagnosing or treating tumors or
CC malignancies. The present sequence represents an sFv construct designated
CC 741F8 sFv', which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 250 AA;

```
  Query Match             100.0%;  Score 43;  DB 9;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 6;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 WTSTRHT 7
              |||||||
Db        185 WTSTRHT 191
```

RESULT 28
ABR42757
ID ABR42757 standard; protein; 256 AA.
XX
AC ABR42757;
XX
DT 26-AUG-2003 (first entry)
XX
DE Anti-CEA humanized monoclonal antibody hMN-14-0.
XX
KW Humanized; monoclonal antibody; antibody; hMN-14-0;
KW carcinoembryonic antigen; CEA; tumour; cytostatic; triabody.
XX
OS Homo sapiens.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1. .23
FT /label= Signal_peptide
FT /note= "pelB"
FT Region 23. .141
FT /label= hMN-14VH
FT Protein 24. .256
FT /label= hMN-14-0
FT Region 142. .250
FT /label= hMN-14Vkappa
FT Region 251. .256
FT /label= 6xHis_tag
XX
PN WO2003033654-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032718.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
PR 08-JAN-2002; 2002US-0345641P.
PR 22-AUG-2002; 2002US-0404919P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg DM;
XX
DR WPI; 2003-513460/48.
DR N-PSDB; ACC58722.
XX
PT New multivalent, monospecific binding protein comprising two or more
PT binding sites having affinity for the same single target antigen, where
PT each binding site is associated with scFv fragments, useful for
PT diagnosing or treating tumor.
XX
PS Claim 39; Fig 13; 62pp; English.
XX
CC The present sequence is the protein sequence of hMN-14-0, which is
CC designed to form an hMN-14 triabody. The hMN-14-0 polypeptide comprises
CC the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC Vkappa without a peptide linker. The use of the zero linker enables the
CC secreted polypeptide to form a triabody, forming 3 binding sites for CEA.
CC The polypeptide also includes a pelB signal peptide, which precedes the
CC VH moiety to facilitate synthesis of the polypeptide in the periplasmic
CC space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC purification. This monospecific triabody is an example of claimed
CC multivalent binding proteins specific for a tumour-associated antigen.

```
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 256 AA;

  Query Match             100.0%;  Score 43;  DB 6;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 6.2;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        191 WTSTRHT 197


RESULT 29
ABR42758
ID   ABR42758 standard; protein; 257 AA.
XX
AC   ABR42758;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-1G.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-1G;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; tetrabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .257
FT                   /label= hMN-14-0
FT   Region          142
FT                   /label= 1G_linker
FT   Region          143. .251
FT                   /label= hMN-14Vkappa
FT   Region          252. .257
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 48; Fig 14; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-1G, which is
CC   designed to form an hMN-14 tetrabody. The hMN-14-1G polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa via a single glycine residues. Use of the 1G linker enables some
CC   of the the secreted polypeptide to form a tetrabody with 4 binding sites
CC   for CEA. The polypeptide also includes a pelB signal peptide, which
CC   precedes the VH moiety to facilitate synthesis of the polypeptide in the
CC   periplasmic space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific tetrabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 257 AA;

  Query Match             100.0%;  Score 43;  DB 6;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 6.2;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        192 WTSTRHT 198


RESULT 30
ABR42289
ID   ABR42289 standard; protein; 261 AA.
XX
AC   ABR42289;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Diabody 679-scFv-L5 polypeptide (VH-I3Q/C101S mutant).
XX
KW   Diabody; antibody; 679-scFv-L5; histamine-succinyl-glycyl; HSG;
KW   affinity enhancement system; tumour; targeting; mutant; mutein.
XX
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB signal peptide"
FT   Misc-difference 3
FT                   /note= "wild-type Ile substituted by Gln"
FT   Protein         23. .268
FT                   /label= 679-scFv-L5
FT   Region          23. .142
FT                   /label= 679VH(I3Q/C101S)
FT   Misc-difference 101
FT                   /note= "wild-type Cys substituted by Ser"
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .260
FT                   /label= 679Vk
FT   Region          261. .268
FT                   /label= 6His_tag
XX
PN   WO2003033653-A2.
```

XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032717.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (IBCP-) IBC PHARM.
XX
PI Chang CK, Rossi E;
XX
DR WPI; 2003-393513/37.
DR N-PSDB; ACC57803.
XX
PT New kit comprising a multivalent, multi-specific binding protein and a
PT carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT for treating cancer, and cardiovascular, immune, inflammatory, or
PT infectious diseases.
XX
PS Disclosure; Fig 28; 87pp; English.
XX
CC The present sequence is the protein sequence of a 679 mutant diabody in
CC which antibody 679 VH has a Gln for Ile amino acid substitution at
CC position 3 and a Ser for Gln amino acid substitution at position 101.
CC Murine monoclonal antibody 679 binds with high affinity to molecules
CC containing the moiety histamine-succinyl-glycyl (HSG). The present
CC polypeptide comprises: 679 VH(I3Q) linked to 679 Vk via a peptide linker
CC (enables the secreted polypeptide to dimerise into a diabody, forming 2
CC sites for HSG); a pelB leader signal peptide (facilitates transport of
CC the polypeptide into the periplasmic space of Escherichia coli); and 6
CC His residues (allows purification by IMAC). The 679 diabody was expressed
CC in E. coli at a level of 10 ug/l of culture, compared with 1 ug/l for the
CC non-mutant polypeptide. The invention provides a bispecific diabody
CC comprising an HSG binding site and a carcinoembryonic antigen (CEA)
CC binding site. The HSG antigen binding site may comprise the VH and Vk
CC polypeptides of 679 MAb. These diabodies are produced via recombinant DNA
CC technology and create a novel affinity enhancement system that shows
CC specific affinity for HSG and CEA. They pre-target CEA positive tumours
CC for subsequent specific delivery of therapeutic radioisotopes carried by
CC HSG-carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC cardiovascular diseases and inflammatory diseases can be detected or
CC treated using the methods of the invention
XX
SQ Sequence 261 AA;

Query Match 100.0%; Score 43; DB 6; Length 261;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 196 WTSTRHT 202

RESULT 31
ABR42754
ID ABR42754 standard; protein; 261 AA.
XX
AC ABR42754;
XX
DT 26-AUG-2003 (first entry)
XX
DE Anti-CEA humanized monoclonal antibody hMN-14-scFv-L5.
XX
KW Humanized; monoclonal antibody; antibody; hMN-14-scFv-15;
KW carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS Homo sapiens.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.

XX
FH Key Location/Qualifiers
FT Peptide 1. .23
FT /label= Signal_peptide
FT /note= "pelB"
FT Region 23. .141
FT /label= hMN-14VH
FT Protein 24. .261
FT /label= hMN-14-scFv-L5
FT Region 142. .146
FT /label= Linker
FT Region 147. .255
FT /label= hMN-14Vkappa
FT Region 256. .261
FT /label= 6xHis_tag
XX
PN WO2003033654-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032718.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
PR 08-JAN-2002; 2002US-0345641P.
PR 22-AUG-2002; 2002US-0404919P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg DM;
XX
DR WPI; 2003-513460/48.
DR N-PSDB; ACC58721.
XX
PT New multivalent, monospecific binding protein comprising two or more
PT binding sites having affinity for the same single target antigen, where
PT each binding site is associated with scFv fragments, useful for
PT diagnosing or treating tumor.
XX
PS Claim 31; Fig 11; 62pp; English.
XX
CC The present sequence is the protein sequence of hMN-14-scFv-L5, which was
CC designed to form an hMN-14 diabody. The hMN-14-scFv-L5 polypeptide
CC comprises the C-terminal end of anti-carcinoembryonic antigen (CEA)
CC humanized monoclonal antibody hMN-14 VH linked to the N-terminal part of
CC hMN-14 Vkappa by a peptide linker that enables the secreted polypeptide
CC to dimerize into a diabody, forming 2 binding sites for CEA. The
CC polypeptide also includes a pelB signal peptide, which precedes the VH
CC moiety to facilitate synthesis of the polypeptide in the periplasmic
CC space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC purification. In the claimed monospecific diabody, each scFv comprises
CC the present sequence. The diabody is an example of claimed multivalent
CC binding proteins specific for a tumour-associated antigen. The binding
CC proteins are used in the diagnosis and treatment of a tumour, carcinoma,
CC melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma or myeloma,
CC or a cancer selected from acute lymphoblastic leukaemia, acute
CC myelogenous leukaemia, biliary, breast, cervical, chronic lymphocytic
CC leukaemia, chronic myelogenous leukaemia, colorectal, endometrial,
CC oesophageal, gastric, head and neck, Hodgkin's lymphoma, lung, medullary
CC thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic, prostate and
CC bladder
XX
SQ Sequence 261 AA;

Query Match 100.0%; Score 43; DB 6; Length 261;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||||||
Db 196 WTSTRHT 202

```
RESULT 32
ABR83645
ID   ABR83645 standard; protein; 261 AA.
XX
AC   ABR83645;
XX
DT   16-OCT-2003  (first entry)
XX
DE   hMN14-scFv-L5 amino acid sequence.
XX
KW   Multispecific binding protein; multivalent; target antigen; cytostatic;
KW   immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW   immunotherapy; autoimmune disease; infectious disease;
KW   cardiovascular disease; inflammatory disease.
XX
OS   Escherichia coli.
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003057829-A2.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-US038985.
XX
PR   26-DEC-2001; 2001US-0342103P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg D;
XX
DR   WPI; 2003-607997/57.
DR   N-PSDB; ACF57430.
XX
PT   Novel multivalent, multi-specific binding protein useful for treating
PT   cancer, has first binding site having affinity towards hapten group and
PT   second and third binding sites each having affinity towards target
PT   antigen.
XX
PS   Claim 11; Fig 6; 43pp; English.
XX
CC   The present invention describes a multivalent, multi-specific binding
CC   protein (I) comprising a first binding site having an affinity towards a
CC   hapten group and a second and a third binding sites each having affinity
CC   towards a target antigen, which may be the same or a different target
CC   antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC   and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC   useful for delivering a diagnostic agent, a therapeutic agent, or its
CC   combination to a target, which involves administering (I) to a subject,
CC   waiting for a sufficient amount of time for an amount of the non-binding
CC   protein to clear the subject's blood stream, and administering to the
CC   subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC   agent, or its combination, that binds to a binding site of the binding
CC   protein. (I) is also useful for detecting or treating a human disorder,
CC   preferably cancer, autoimmune diseases, infectious diseases,
CC   cardiovascular diseases and inflammatory diseases. The present sequence
CC   represents a hMN14-scFv-L5 amino acid sequence, which is used in the
CC   exemplification of the present invention
XX
SQ   Sequence 261 AA;

  Query Match             100.0%;  Score 43;  DB 6;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 6.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        196 WTSTRHT 202


RESULT 33
ABR42295
ID   ABR42295 standard; protein; 262 AA.
XX
AC   ABR42295;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS2 polypeptide #1.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BS2_polypeptide#1
FT   Region          24. .142
FT                   /label= 679_VH(I3Q)
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
FT                   /label= hMN14_VH
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57809.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 34; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #1 of novel
CC   bispecific diabody BS2 comprising the VH region of monoclonal antibody
CC   679 and the Vk region of monoclonal antibody hMN14. The 679VH moiety
CC   includes I3Q and C101S mutations, which improve solubility. Mouse
CC   antibody 679 binds with high affinity to molecules containing the moiety
CC   histamine-succinyl-glycyl (HSG). Humanised antibody hMN14 binds
CC   specifically to carcinoembryonic antigen (CEA). The bispecific diabody
CC   can be produced using recombinant DNA methods, e.g. in Escherichia coli
CC   host cells. It provides a novel affinity enhancement system that shows
CC   specific affinity for HSG and CEA. Such bispecific diabodies pre-target
CC   CEA positive tumours for subsequent specific delivery of therapeutic
CC   radioisotopes carried by HSG-carrying peptides. Cancer, autoimmune
CC   diseases, infectious disease, cardiovascular diseases and inflammatory
CC   diseases can be detected or treated using the methods of the invention
XX
SQ   Sequence 262 AA;
```

```
  Query Match           100.0%;  Score 43;  DB 6;  Length 262;
  Best Local Similarity  100.0%;  Pred. No. 6.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        197 WTSTRHT 203


RESULT 34
ABR42293
ID   ABR42293 standard; protein; 262 AA.
XX
AC   ABR42293;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS1.5 polypeptide #1.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BS1.5_polypeptide#1
FT   Region          24. .142
FT                   /label= 679_VH(I3Q)
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
FT                   /label= hMN14_VH
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 32; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #1 of a
CC   novel bispecific diabody comprising the VH region of monoclonal antibody
CC   679 and the Vk region of monoclonal antibody hMN14. The 679VH region
CC   includes an I3Q mutation which improves solubility. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen. The bispecific diabody can be produced using
CC   recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC   a novel affinity enhancement system that shows specific affinity for HSG
CC   and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC   subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC   carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 262 AA;

  Query Match           100.0%;  Score 43;  DB 6;  Length 262;
  Best Local Similarity  100.0%;  Pred. No. 6.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        197 WTSTRHT 203


RESULT 35
ABR42298
ID   ABR42298 standard; protein; 262 AA.
XX
AC   ABR42298;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS1.5H polypeptide #1.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BS1.5H_polypeptide#1
FT   Region          24. .142
FT                   /label= 679_VH(I3Q)
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
FT                   /label= hMN14_VH
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57812.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
```

```
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 37; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #1 of novel
CC   bispecific diabody BS1.5H comprising the VH region of monoclonal antibody
CC   679 and the Vk region of monoclonal antibody hMN14. The 679VH moiety
CC   includes an I3Q mutation, which improves solubility. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). A humanised version of its VH and Vk sequences
CC   have been used in BS1.5H. Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC   using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC   provides a novel affinity enhancement system that shows specific affinity
CC   for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC   tumours for subsequent specific delivery of therapeutic radioisotopes
CC   carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC   disease, cardiovascular diseases and inflammatory diseases can be
CC   detected or treated using the methods of the invention
XX
SQ   Sequence 262 AA;

  Query Match             100.0%;  Score 43;  DB 6;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 6.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        197 WTSTRHT 203


RESULT 36
ABR42290
ID   ABR42290 standard; protein; 262 AA.
XX
AC   ABR42290;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Diabody hMN14-scFv-L5 polypeptide.
XX
KW   Diabody; antibody; hMN14-scFv-L5; carcinoembryonic antigen; CEA;
KW   affinity enhancement system; tumour; targeting.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB signal peptide"
FT   Protein         23. .262
FT                   /label= hMN14-scFv-L5
FT   Region          23. .141
FT                   /label= hMN14VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .253
FT                   /label= 679Vk
FT   Region          257. .262
FT                   /label= 6His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 10; Fig 29; 87pp; English.
XX
CC   The present sequence is the protein sequence of a hMN14 diabody,
CC   designated hMN14-scFv-L5. Humanised monoclonal antibody hMN14 binds
CC   specifically to carcinoembryonic antigen (CEA). hMN14-scFv-L5 comprises:
CC   hMN14 VH linked to 679 Vk via a peptide linker (enables the secreted
CC   polypeptide to dimerise into a diabody, forming 2 sites for HSG); a pelB
CC   leader signal peptide (facilitates transport of the polypeptide into the
CC   periplasmic space of Escherichia coli); and 6 His residues (allows
CC   purification by IMAC). The invention provides a bispecific diabody
CC   comprising a histamine-succinyl-glycyl (HSG) binding site and a CEA
CC   binding site. The CEA binding site may comprise the VH and Vk
CC   polypeptides of hMN14 MAb. These diabodies are produced via recombinant
CC   DNA technology and create a novel affinity enhancement system that shows
CC   specific affinity for HSG and CEA. They pre-target CEA positive tumours
CC   for subsequent specific delivery of therapeutic radioisotopes carried by
CC   HSG-carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 262 AA;

  Query Match             100.0%;  Score 43;  DB 6;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 6.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        197 WTSTRHT 203


RESULT 37
ABR42291
ID   ABR42291 standard; protein; 262 AA.
XX
AC   ABR42291;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody polypeptide #1.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BSI_polypeptide#1
FT   Region          24. .142
FT                   /label= 679_VH
```

```
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
FT                   /label= hMN14_VH
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57805.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 30; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #1 of a
CC   novel bispecific diabody comprising the VH region of monoclonal antibody
CC   679 and the Vk region of monoclonal antibody hMN14. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen. The bispecific diabody can be produced using
CC   recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC   a novel affinity enhancement system that shows specific affinity for HSG
CC   and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC   subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC   carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 262 AA;

  Query Match             100.0%;  Score 43;  DB 6;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 6.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        197 WTSTRHT 203


RESULT 38
ADU26571
ID   ADU26571 standard; protein; 358 AA.
XX
AC   ADU26571;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric hBS14 polypeptide 2.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26573.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 2; SEQ ID NO 12; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
CC   activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC   site of inflammation (caused by infectious agent). (I) is useful in
CC   antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric hBS14 polypeptide 2 containing heavy and light chain variable
CC   regions.
XX
SQ   Sequence 358 AA;

  Query Match             100.0%;  Score 43;  DB 8;  Length 358;
  Best Local Similarity   100.0%;  Pred. No. 8.8;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         51 WTSTRHT 57


RESULT 39
ADU26561
ID   ADU26561 standard; protein; 363 AA.
XX
AC   ADU26561;
```

XX
DT 27-JAN-2005 (first entry)
XX
DE Chimeric BS14hp polypeptide 2.
XX
KW cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW neoplasm; fungal infection; viral infection; bacterial infection;
KW mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW autoimmune disease; myocardial infarction; ischemic heart disease;
KW atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .6
FT		/note= "signal peptide"
FT	Protein	7. .363
FT		/note= "mature protein"
FT	Region	30. .40
FT		/note= "CDR1hMN14Vk"
FT	Region	56. .62
FT		/note= "CDR2hMN14Vk"
FT	Region	95. .102
FT		/note= "CDR3hMN14Vk"
FT	Region	114. .119
FT		/note= "linker region"
FT	Region	150. .154
FT		/note= "CDR1hMN14Vh"
FT	Region	169. .185
FT		/note= "CDR2hMN14Vh"
FT	Region	218. .227
FT		/note= "CDR3hMN14Vh"
FT	Region	238. .242
FT		/note= "linker region"
FT	Region	266. .282
FT		/note= "CDR1h679Vk"
FT	Region	298. .304
FT		/note= "CDR2h679Vk"
FT	Region	337. .344
FT		/note= "CDR3h679Vk"

XX
PN WO2004094613-A2.
XX
PD 04-NOV-2004.
XX
PF 22-APR-2004; 2004WO-US012662.
XX
PR 22-APR-2003; 2003US-0464532P.
PR 24-NOV-2003; 2003US-0525391P.
XX
PA (IBCP-) IBC PHARM.
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Rossi EA, Chang C, Mcbride WJ;
XX
DR WPI; 2004-795560/78.
DR N-PSDB; ADU26569.
XX
PT Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT chains having immunoglobulin variable domains, to form complex having
PT three antigen binding sites.
XX
PS Example 1; SEQ ID NO 2; 148pp; English.
XX
CC The invention relates to a polyvalent protein complex (PPC) (I),
CC comprising a first and second polypeptide chains having immunoglobulin
CC variable domains, where the first and second polypeptide chains form a
CC complex having three antigen binding sites, and where each binding site
CC comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC useful in pretargeting method of treating or diagnosing, or treating and
CC diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC also useful for diagnosing a non-neoplastic disease or disorder where the
CC disease or disorder is caused by a fungus, a virus, a bacterium, a
CC mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC infarction, ischemic heart disease, atherosclerotic plaques, graft
CC rejection, Alzheimer's disease or inflammation caused by accretion of
CC activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC site of inflammation (caused by infectious agent). (I) is useful in
CC antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC molecule, and immunostaining technique. This sequence corresponds to the
CC chimeric BS14HP polypeptide 2 containing heavy and light chain variable
CC regions. The encoded polypeptide is designated alpha-factor-hMN-14Vk-
CC GGGGS-hMN-14Vh-LEGGGS-h679Vk-6-His where the hMN14 is from a humanized
CC antibody that binds specifically to the carcinoembryonic antigen and the
CC h679 is a monoclonal antibody that binds the tri-peptide moiety histamine
CC -succinyl-glycyl (HSG).
XX
SQ Sequence 363 AA;

Query Match 100.0%; Score 43; DB 8; Length 363;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WTSTRHT 7
              |||||||
Db         56 WTSTRHT 62
```

RESULT 40
ADU26570
ID ADU26570 standard; protein; 364 AA.
XX
AC ADU26570;
XX
DT 27-JAN-2005 (first entry)
XX
DE Chimeric hBS14 polypeptide 1.
XX
KW cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW neoplasm; fungal infection; viral infection; bacterial infection;
KW mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW autoimmune disease; myocardial infarction; ischemic heart disease;
KW atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
OS Synthetic.
XX
PN WO2004094613-A2.
XX
PD 04-NOV-2004.
XX
PF 22-APR-2004; 2004WO-US012662.

```
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26572.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 2; SEQ ID NO 11; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
CC   activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC   site of inflammation (caused by infectious agent). (I) is useful in
CC   antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric hBS14 polypeptide 1 containing heavy and light chain variable
CC   regions.
XX
SQ   Sequence 364 AA;

  Query Match             100.0%;  Score 43;  DB 8;  Length 364;
  Best Local Similarity   100.0%;  Pred. No. 9;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        175 WTSTRHT 181


RESULT 41
ADU26560
ID   ADU26560 standard; protein; 370 AA.
XX
AC   ADU26560;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric  BS14HP polypeptide 1.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .7
FT                   /note= "signal peptide"
FT   Protein         8. .370
FT                   /note= "mature protein"
FT   Region          38. .42
FT                   /note= "CDR1h679Vh"
FT   Region          57. .68
FT                   /note= "CDR2h679Vh"
FT   Region          106. .115
FT                   /note= "CDR3h679Vh"
FT   Region          127. .131
FT                   /note= "linker region"
FT   Region          155. .165
FT                   /note= "CDR1hMN14Vk"
FT   Region          181. .187
FT                   /note= "CDR2hMN14Vk"
FT   Region          220. .227
FT                   /note= "CDR3hMN14Vk"
FT   Region          239. .244
FT                   /note= "linker region"
FT   Region          275. .279
FT                   /note= "CDR1hMN14Vh"
FT   Region          294. .310
FT                   /note= "CDR2hMN14Vh"
FT   Region          343. .352
FT                   /note= "CDR3hMN14Vh"
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26568.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 1; SEQ ID NO 1; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
```

CC activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC site of inflammation (caused by infectious agent). (I) is useful in
CC antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC molecule, and immunostaining technique. This sequence corresponds to the
CC chimeric BS14HP polypeptide 1 containing heavy and light chain variable
CC regions. The encoded polypeptide is designated alpha-factor-h679Vh-GGGGS-
CC hMN-14Vk-LEGGGS-hMN-14Vh-6-His where the hMN14 is from a humanized
CC antibody that binds specifically to the carcinoembryonic antigen and the
CC h679 is a monoclonal antibody that binds the tri-peptide moiety histamine
CC -succinyl-glycyl (HSG).
XX
SQ Sequence 370 AA;

Query Match 100.0%; Score 43; DB 8; Length 370;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
||||||| |
Db 181 WTSTRHT 187

RESULT 42
ABR83649
ID ABR83649 standard; protein; 391 AA.
XX
AC ABR83649;
XX
DT 16-OCT-2003 (first entry)
XX
DE TS1 VL chain amino acid sequence.
XX
KW Multispecific binding protein; multivalent; target antigen; cytostatic;
KW immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW immunotherapy; autoimmune disease; infectious disease;
KW cardiovascular disease; inflammatory disease.
XX
OS Escherichia coli.
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003057829-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US038985.
XX
PR 26-DEC-2001; 2001US-0342103P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg D;
XX
DR WPI; 2003-607997/57.
DR N-PSDB; ACF57434.
XX
PT Novel multivalent, multi-specific binding protein useful for treating
PT cancer, has first binding site having affinity towards hapten group and
PT second and third binding sites each having affinity towards target
PT antigen.
XX
PS Claim 48; Fig 9A-B; 43pp; English.
XX
CC The present invention describes a multivalent, multi-specific binding
CC protein (I) comprising a first binding site having an affinity towards a
CC hapten group and a second and a third binding sites each having affinity
CC towards a target antigen, which may be the same or a different target
CC antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC useful for delivering a diagnostic agent, a therapeutic agent, or its
CC combination to a target, which involves administering (I) to a subject,
CC waiting for a sufficient amount of time for an amount of the non-binding
CC protein to clear the subject's blood stream, and administering to the
CC subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC agent, or its combination, that binds to a binding site of the binding
CC protein. (I) is also useful for detecting or treating a human disorder,
CC preferably cancer, autoimmune diseases, infectious diseases,
CC cardiovascular diseases and inflammatory diseases. The present sequence
CC represents the TS1 VL chain amino acid sequence, which is used in the
CC exemplification of the present invention
XX
SQ Sequence 391 AA;

Query Match 100.0%; Score 43; DB 6; Length 391;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
||||||| |
Db 326 WTSTRHT 332

RESULT 43
ABG76488
ID ABG76488 standard; protein; 443 AA.
XX
AC ABG76488;
XX
DT 13-MAY-2003 (first entry)
XX
DE Humanised anti-CEA antibody, hMN14.
XX
KW CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW human; zeta signalling chain; CD8alpha hinge; humanised antibody.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
PN US2002165360-A1.
XX
PD 07-NOV-2002.
XX
PF 10-DEC-2001; 2001US-00006771.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250090P.
XX
PA (JUNG/) JUNGHANS R P.
XX
PI Junghans RP;
XX
DR WPI; 2003-298705/29.
DR N-PSDB; ABX13168.
XX
PT New chimeric molecule from humanized antibody against carcinoembryonic
PT antigen and having signaling molecules of T cells and other effector
PT cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS Disclosure; Page 7-8; 20pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the
CC carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC which the cysteine residues have been mutated, with the IgTCR molecule
CC occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC NK (not defined) or other effector cells are useful in treating patients
CC with cancers expressing the CEA antigen, together with other or with
CC heterologous constructs to engage additional stimulatory and functional
CC properties of the effector cells to enhance the anti-tumour therapeutic
CC efficacy. The cancer disorder includes colorectal, breast and lung
CC cancers. The present sequence represents the chimaeric molecule of the

```
CC   invention
XX
SQ   Sequence 443 AA;

  Query Match             100.0%;  Score 43;  DB 6;  Length 443;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         69 WTSTRHT 75


RESULT 44
ABG74240
ID   ABG74240 standard; protein; 443 AA.
XX
AC   ABG74240;
XX
DT   23-OCT-2003  (revised)
DT   22-APR-2003  (first entry)
XX
DE   Chimaeric hMN14/T-cell receptor.
XX
KW   Retroviral vector; T-cell receptor; hMN14; antibody; IgTCR; receptor;
KW   cytostatic; dermatological; neuroprotective; immunostimulant; GD3;
KW   ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4; 3E11;
KW   prostate-specific membrane antigen; zeta signalling chain; human; cancer;
KW   melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer;
KW   mouse; CD8alpha hinge.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
XX
PN   US2002132983-A1.
XX
PD   19-SEP-2002.
XX
PF   10-DEC-2001; 2001US-00006773.
XX
PR   30-NOV-2000; 2000US-0250087P.
PR   30-NOV-2000; 2000US-0250089P.
XX
PA   (JUNG/) JUNGHANS R P.
XX
PI   Junghans RP;
XX
DR   WPI; 2003-208946/20.
DR   N-PSDB; ABX16565.
XX
PT   New chimeric molecule useful in treating patients with disorders, such as
PT   melanoma, neuroendocrine disorders, prostate and small cell lung cancer
PT   comprises GD3 and/or PSMA binding domains of antibody.
XX
PS   Disclosure; Page 7-8; 35pp; English.
XX
CC   The invention relates to a chimaeric molecule comprising the GD3
CC   (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC   variable gene sequences, or the PSMA (prostate-specific membrane antigen)
CC   binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC   sequences, the zeta signalling chain of the T cell receptor and an
CC   intervening CD8alpha hinge in which cysteine residues have been mutated.
CC   The chimaeric molecules expressed in T cells or NK cells or other
CC   effector cells are useful in treating patients with cancers expressing
CC   the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC   and/or together with each other or with heterologous constructs to engage
CC   additional stimulatory and functional properties of the effector cells to
CC   enhance the antitumour therapeutic efficacy (claimed). They are
CC   particularly useful in disorders including melanoma, neuroendocrine
CC   tumours and prostate and small cell lung cancer. The present sequence is
CC   a hMN14 antibody (specific to CEA antigen) in a fusion protein with the
CC   modified CD8alpha hinge and the T-cell receptor zeta chain (IgTCR)
CC   encoded by a retroviral vector. The hMN14 antibody coding region is
CC   replaced with the MB3.6, 3D8, 4D4 or 3E11 genes of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 443 AA;

  Query Match             100.0%;  Score 43;  DB 6;  Length 443;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         69 WTSTRHT 75


RESULT 45
AAR39573
ID   AAR39573 standard; protein; 667 AA.
XX
AC   AAR39573;
XX
DT   25-MAR-2003  (revised)
DT   07-FEB-1994  (first entry)
XX
DE   Sequence of 741 sFV-PE40.
XX
KW   Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;
KW   exotoxin.
XX
OS   Pseudomonas.
XX
PN   WO9316185-A2.
XX
PD   19-AUG-1993.
XX
PF   05-FEB-1993;   93WO-US001055.
XX
PR   06-FEB-1992;   92US-00831967.
XX
PA   (CREA-) CREATIVE BIOMOLECULES INC.
PA   (CETU ) CETUS ONCOLOGY CORP.
XX
PI   Huston JS,  Houston LL,  Ring DB,  Oppermann H;
XX
DR   WPI; 1993-272889/34.
DR   N-PSDB; AAQ46088.
XX
PT   New single chain Fv polypeptide binding to C-erbB-2 tumour antigen - for
PT   imaging or treating breast or ovarian cancer etc.
XX
PS   Example; Page 71-74; 87pp; English.
XX
CC   c-erbB-2 refers to a protein antigen expressed on the surface of tumour
CC   cells. such as breast and ovarian tumour cells, which is an approx.
CC   200,000 mol. wt. acidic glycoprotein having an isolelectric pt. of about
CC   5.3 (see AAQ46083, AAR39568). A single chain Fv (sFv) is a covalently
CC   linked VH-VL heterodimer which is expressed from a gene fusion including
CC   VH- and VL- encoding genes connected by a peptide-encoding linker. Such
CC   linker sequences are set forth in AA residues 116-135 in AAR39569, which
CC   includes part of the 16 AA linker sequences in AAR39572. Using AAQ46084
CC   for the 520C9 monoclonal antibody, a single chain polypeptide can be
CC   produced having a binding affinity for a c-erbB-2 related antigen. In
CC   another design, the pseudomonal exotoxin fragment analogous to ricin A
CC   chain, PE40, is fused to the carboxy terminus of the antic-c-erbB-2 741
CC   sFv. the resulting 741F8 sFv-PE40 is a single-chain Fv-toxin fusion
CC   protein, which was constructed with an 18 residue short FB leader which
CC   initially was left on the protein. 'X' in AAR39573 refers to posn. of
CC   stop codon in cDNA. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 667 AA;

  Query Match             100.0%;  Score 43;  DB 2;  Length 667;
  Best Local Similarity   100.0%;  Pred. No. 17;
```

```
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        185 WTSTRHT 191


RESULT 46
ADY97271
ID   ADY97271 standard; protein; 669 AA.
XX
AC   ADY97271;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Exemplary antibody fusion protein SEQ ID NO:3.
XX
KW   antibody engineering; fusion protein; cytostatic; antimicrobial;
KW   virucide; antibacterial; cancer; infection.
XX
OS   Synthetic.
XX
PN   US2005069552-A1.
XX
PD   31-MAR-2005.
XX
PF   28-JUL-2004; 2004US-00900928.
XX
PR   28-JUL-2003; 2003US-0490569P.
XX
PA   (BLEC/) BLECK G T.
PA   (YORK/) YORK D.
PA   (COLL/) COLLINS I.
XX
PI   Bleck GT,  York D,  Collins I;
XX
DR   WPI; 2005-261600/27.
DR   N-PSDB; ADY97269.
XX
PT   Composition useful as cancer vaccine, comprises polypeptide having
PT   antibody heavy chain fused to antibody light chain, or multivalent
PT   antibody having two polypeptides with antibody heavy chain fused to
PT   antibody light chain.
XX
PS   Disclosure; SEQ ID NO 3; 101pp; English.
XX
CC   The invention describes a composition (I) comprising: (a) a polypeptide
CC   comprising at least one antibody heavy chain fused to at least one
CC   antibody light chain; or (b) a multivalent antibody comprising at least
CC   two polypeptides, where each of the polypeptides comprises at least one
CC   antibody heavy chain fused to at least one antibody light chain. Also
CC   described: (1) a composition (II) comprising a nucleic acid comprising at
CC   least one antibody heavy chain gene and at least one antibody light chain
CC   gene, where the nucleic acid encodes a polypeptide comprising at least
CC   one antibody heavy chain fused to at least one antibody light chain; (2)
CC   a method (M1) of binding an antigen, involves providing a polypeptide
CC   comprising at least one antibody heavy chain fused to at least one
CC   antibody light chain, and contacting the polypeptide with a sample having
CC   an antigen under conditions such that the polypeptide binds to the
CC   antigen; (3) a method (M2), which involves providing a vector comprising
CC   a bicistronic expression construct comprising genes encoding an antibody
CC   heavy chain gene and an antibody light chain gene, and altering the
CC   nucleic acid sequence of a splice acceptor sequence or a splice donor
CC   sequence in the antibody light chain gene or the antibody heavy chain
CC   gene under conditions such that splicing is prevented at the splice
CC   acceptor sequence or donor sequence; (4) a nucleic acid sequence produced
CC   by (M2); (5) a vector (III) comprising a modified antibody heavy or light
CC   gene, where modification eliminates a splice donor or acceptor sequence
CC   in antibody heavy or light chain gene; and (6) a host cell comprising
CC   (III). (I) is useful in in vitro binding assays for identifying antigens
CC   in a mixture or determining the presence or absence of expression of a
CC   particular protein. (I) is also useful as vaccine for treating cancer and
CC   infections caused by pathogens e.g. virus or bacteria. The present
CC   sequence represents an exemplary antibody fusion protein from the present
CC   invention.
XX
SQ   Sequence 669 AA;

  Query Match             100.0%;  Score 43;  DB 9;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 17;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        506 WTSTRHT 512


RESULT 47
AAE27930
ID   AAE27930 standard; protein; 238 AA.
XX
AC   AAE27930;
XX
DT   27-DEC-2002  (first entry)
XX
DE   Human C5E10 antibody light chain protein.
XX
KW   Human; CC49 antibody; C2B8 antibody; tumour associated antigen; TAG-72;
KW   neoplasm; neoplastic disorder; haematologic neoplasm; colon cancer;
KW   non-Hodgkin's lymphoma; haematologic malignancy; tumour.
XX
OS   Homo sapiens.
XX
PN   WO200260955-A2.
XX
PD   08-AUG-2002.
XX
PF   29-JAN-2002; 2002WO-US002373.
XX
PR   29-JAN-2001; 2001US-0264318P.
PR   16-NOV-2001; 2001US-0331481P.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Braslawsky GR,  Hanna N,  Chinn P;
XX
DR   WPI; 2002-698547/75.
DR   N-PSDB; AAD45759.
XX
PT   Novel domain deleted CC49 antibody reactive with tumor associated antigen
PT   -72, or C2B8 antibody reactive with CD20, useful for treating
PT   myelosuppressed patient suffering from a neoplastic disorder.
XX
PS   Example 3; Fig 8B; 74pp; English.
XX
CC   The present invention relates to domain deleted CC49 or C2B8 antibodies.
CC   Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain
CC   deleted sequence in which CH2 domain has been deleted and are reactive
CC   with tumour associated antigen (TAG)-72. The C2B8 antibodies are reactive
CC   with CD20 and comprise a heavy chain having a sequence of a derived
CC   domain deleted C2B8 construct where the CH2 domain has been deleted.
CC   Sequences of the invention are useful for imaging a neoplasm. They are
CC   also useful for treating myelosuppressed patients suffering from
CC   neoplastic disorder such as haematologic neoplasm, preferably non-
CC   Hodgkin's lymphoma. Antibodies of the invention are also used to treat
CC   neoplastic disorder, colon cancer and haematologic malignancy. They are
CC   useful for reducing tumour size, inhibiting tumour growth and/or
CC   prolonging the survival time of tumour-bearing animals and for treating
CC   tumours. The present sequence is human C5E10 light chain protein. This
CC   sequence is used in the exemplification of the invention
XX
SQ   Sequence 238 AA;

  Query Match             90.7%;  Score 39;  DB 5;  Length 238;
  Best Local Similarity   85.7%;  Pred. No. 32;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 WTSTRHT 7
              |:|||||
Db         74 WSSTRHT 80
```

RESULT 48
ABB82839
ID ABB82839 standard; protein; 238 AA.
XX
AC ABB82839;
XX
DT 31-MAR-2003 (first entry)
XX
DE Antibody C5E10 light chain.
XX
KW C5E10; antibody; cytostatic; antiallergic; antianemic; antiasthmatic;
KW vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic;
KW thyromimetic; hepatotropic; haemostatic; antileprotic; antibacterial;
KW neuroprotective; antipsoriatic; antirheumatic; antiarthritic; antiulcer;
KW dermatological; immunosuppressive; antiinflammatory.
XX
OS Homo sapiens.
XX
PN WO200296948-A2.
XX
PD 05-DEC-2002.
XX
PF 29-JAN-2002; 2002WO-US002374.
XX
PR 29-JAN-2001; 2001US-0264318P.
PR 16-NOV-2001; 2001US-0331481P.
PR 21-DEC-2001; 2001US-0341858P.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Braslawsky GR, Hanna N, Chinn P, Hariharan K;
XX
DR WPI; 2003-140446/13.
DR N-PSDB; ABZ24023.
XX
PT Novel dimeric antibody useful for treating immune disorder and neoplastic
PT disorder, has several non-covalently associated monomeric subunits.
XX
PS Example 3; Fig 8B; 78pp; English.
XX
CC The invention relates to a dimeric antibody (I) comprising several
CC monomeric subunits, where the monomeric subunits are non-covalently
CC associated. (I) is useful for treating a disorder, especially immune
CC disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
CC resistant Hodgkin's disease high grade, low grade and intermediate grade
CC non-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
CC lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular
CC lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
CC AIDS-related lymphomas, monocytic B cell lymphoma, angioimmunoblastic
CC lymphoadenopathy, small lymphocytic, follicular, diffuse large cell,
CC diffuse small cleaved cell, large cell immunoblastic lymphoblastoma,
CC small, non-cleaved, Burkitt's and non-Burkitt's, follicular, mixed small
CC cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
CC detailed description of the various uses of (I)). The present sequence
CC represents the antibody C5E10 light chain
XX
SQ Sequence 238 AA;

```
  Query Match             90.7%;  Score 39;  DB 6;  Length 238;
  Best Local Similarity   85.7%;  Pred. No. 32;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db         74 WSSTRHT 80
```

RESULT 49
ABU07879
ID ABU07879 standard; protein; 239 AA.
XX
AC ABU07879;
XX
DT 14-MAY-2003 (first entry)
XX
DE Venezuelan equine encephalitis virus ScFv antibody MA116-6.
XX
KW Venezuelan equine encephalitis virus; VEE; ScFv; antibody;
KW single chain variable fragment; immunotherapeutic; immunodiagnostic;
KW MA116-6 single chain variable fragment antibody; gene therapy.
XX
OS Mus sp.
XX
PN CA2374027-A1.
XX
PD 13-SEP-2002.
XX
PF 08-MAR-2002; 2002CA-02374027.
XX
PR 13-MAR-2001; 2001US-0275103P.
PR 21-DEC-2001; 2001US-0341843P.
XX
PA (MIND) CANADA MIN NAT DEFENCE.
XX
PI Fulton RE, Nagata LP, Alvi AZ;
XX
DR WPI; 2003-094224/09.
DR N-PSDB; ABX12649.
XX
PT New recombinant ScFv antibody from a well-characterized monoclonal
PT antibody, useful for the diagnosis and treatment of Venezuelan equine
PT encephalitis.
XX
PS Disclosure; Fig 12; 72pp; English.
XX
CC The invention describes a new recombinant A116-16 single chain variable
CC fragment (ScFv) antibody (I) against Venezuelan equine encephalitis
CC (VEE). The recombinant MA116-15 ScFv antibody is useful as a diagnostic
CC reagent for detection and identification of VEE. The other recombinant
CC antibodies are useful as immunotherapeutic and/or immunodiagnostic
CC reagents for VEE. The antibodies are also useful for gene therapy. This
CC is the amino acid sequence of an anti-venezuelan equine enchephalitis
CC (VEE) virus single chain variable fragment antibody
XX
SQ Sequence 239 AA;

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  Query Match             90.7%;  Score 39;  DB 6;  Length 239;
  Best Local Similarity   85.7%;  Pred. No. 32;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        181 WSSTRHT 187
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RESULT 50
ABU07882
ID ABU07882 standard; protein; 240 AA.
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AC ABU07882;
XX
DT 14-MAY-2003 (first entry)
XX
DE Venezuelan equine encephalitis virus ScFv antibody MA116-16.
XX
KW Venezuelan equine encephalitis virus; VEE; ScFv; antibody;
KW single chain variable fragment; immunotherapeutic; immunodiagnostic;
KW MA116-16 single chain variable fragment antibody; gene therapy.
XX
OS Mus sp.

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PN CA2374027-A1.
XX
PD 13-SEP-2002.
XX
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CC antibodies are useful as immunotherapeutic and/or immunodiagnostic
CC reagents for VEE. The antibodies are also useful for gene therapy. This
CC is the amino acid sequenece of an anti-venezuelan equine enchephalitis
CC (VEE) virus single chain variable fragment antibody
XX
SQ Sequence 240 AA;

Query Match 90.7%; Score 39; DB 6; Length 240;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 WTSTRHT 7
              |:|||||
Db        182 WSSTRHT 188
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Search completed: March 23, 2006, 01:51:58
Job time : 91.8904 secs

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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:54:26 ; Search time 9.68493 Seconds
(without alignments)
69.543 Million cell updates/sec

Title: US-10-755-382-21
Perfect score: 43
Sequence: 1 WTSTRHT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	38	88.4	117	2	S42466	Ig kappa chain V r
2	38	88.4	131	2	PL0207	anti-idiotypic ant
3	38	88.4	152	2	S30751	Ig kappa chain pre
4	37	86.0	738	2	T01897	ethylene-response
5	36	83.7	461	2	B69676	alkaline phosphata
6	36	83.7	736	2	T06271	probable ethylene-
7	34	79.1	195	2	T32807	hypothetical prote
8	34	79.1	488	2	S64140	hypothetical prote
9	34	79.1	546	2	A69166	5-methylcytosine-s
10	34	79.1	745	2	T07184	subtilisin-like pr
11	34	79.1	745	2	JC6119	subtilisin-like pr
12	34	79.1	939	2	E82121	peptidase, insulin
13	32	74.4	91	2	G90732	hypothetical prote
14	32	74.4	91	2	A85583	unknown protein en
15	32	74.4	268	2	E86962	probable oxidoredu
16	32	74.4	268	2	E70551	probable oxidoredu
17	32	74.4	358	2	AF3187	flavin-dependent o
18	32	74.4	369	2	S38744	serotonin receptor
19	32	74.4	370	2	I48231	serotonin receptor
20	32	74.4	407	2	AE1073	phosphopentomutase
21	32	74.4	407	2	F91296	phosphopentomutase
22	32	74.4	407	2	H86137	phosphopentomutase
23	32	74.4	407	2	S56607	phosphopentomutase
24	32	74.4	434	2	AG1697	hypothetical prote
25	32	74.4	572	1	DEECPC	pyruvate dehydroge
26	32	74.4	572	2	A85599	pyruvate oxidase p
27	32	74.4	572	2	E90748	pyruvate oxidase [
28	32	74.4	607	2	AB0915	probable transfera
29	32	74.4	712	2	T33231	hypothetical prote
30	32	74.4	995	2	A88483	protein C05D11.1 [
31	32	74.4	2363	2	T38841	probable pre-mRNA
32	32	74.4	2616	2	A57096	nudel protein prec
33	31	72.1	26	2	A58955	metalloendoprotein
34	31	72.1	88	2	A30503	Ig gamma-2b chain
35	31	72.1	104	2	JC7376	hardening-inducibl
36	31	72.1	112	2	B30503	Ig gamma-2a chain
37	31	72.1	167	2	T35320	probable membrane
38	31	72.1	198	2	S30968	major tail protein
39	31	72.1	205	1	CYBOB	beta-crystallin B2
40	31	72.1	205	2	JC2009	beta-crystallin B2
41	31	72.1	205	2	JC4964	beta-B2-crystallin
42	31	72.1	207	2	A39757	beta-crystallin B2
43	31	72.1	223	1	QQBE26	BZLF2 protein - hu
44	31	72.1	247	2	AI3555	histidine utilizat
45	31	72.1	273	2	H75393	conserved hypothet
46	31	72.1	291	2	A36051	H+/K+-exchanging A
47	31	72.1	305	2	T24736	hypothetical prote
48	31	72.1	315	2	T17340	hypothetical prote
49	31	72.1	405	1	G2MSBM	Ig gamma-2b chain
50	31	72.1	408	2	A47041	probable transposa
51	31	72.1	454	2	T05168	hypothetical prote
52	31	72.1	474	1	G2MS11	Ig gamma-2b chain
53	31	72.1	475	2	S01321	Ig gamma-2b chain
54	31	72.1	630	2	T07966	probable ethylene
55	31	72.1	636	2	T03439	probable ethylene-
56	31	72.1	694	2	S67296	probable membrane
57	31	72.1	726	2	T02901	MSP1 protein homol
58	31	72.1	750	2	T08994	6-phosphofructo-2-
59	31	72.1	1130	2	T23104	hypothetical prote
60	31	72.1	1133	2	T23103	hypothetical prote
61	31	72.1	1139	2	S44800	F10E9.8 protein -
62	31	72.1	1144	2	A54810	TMV resistance pro
63	31	72.1	1148	2	T18770	probable calcium c
64	31	72.1	1228	2	S00873	parasporal crystal
65	31	72.1	1536	2	E72310	hypothetical prote
66	31	72.1	1663	2	T28923	hypothetical prote
67	31	72.1	1844	1	RRWPTM	genome polyprotein
68	31	72.1	1844	2	S01956	hypothetical prote
69	31	72.1	1985	2	S19151	hypothetical prote
70	31	72.1	2599	2	F90608	ABC transporter pe
71	30	69.8	197	2	JC6544	tumor-associated a
72	30	69.8	205	2	S05015	beta-crystallin B2
73	30	69.8	210	2	S42417	probable transcrip
74	30	69.8	210	2	S42419	probable transcrip
75	30	69.8	212	2	T27834	hypothetical prote
76	30	69.8	220	2	T24319	hypothetical prote
77	30	69.8	223	2	C85928	hypothetical prote
78	30	69.8	223	2	AB0859	conserved hypothet
79	30	69.8	223	2	A91083	hypothetical prote
80	30	69.8	223	2	AH0409	conserved hypothet
81	30	69.8	223	2	B65059	hypothetical prote
82	30	69.8	246	2	AG0743	conserved hypothet
83	30	69.8	246	2	C38113	yebC protein - Esc
84	30	69.8	246	2	F90950	hypothetical prote
85	30	69.8	246	2	B85799	hypothetical prote
86	30	69.8	251	2	AB0597	biotin synthesis p
87	30	69.8	341	2	H83162	probable amino aci
88	30	69.8	356	2	A47128	carminomycin 4-O-m
89	30	69.8	378	2	C64091	adenine glycosylas
90	30	69.8	383	1	H64601	conserved hypothet
91	30	69.8	425	2	F97108	probable glycosylt
92	30	69.8	434	2	B72410	alkaline phosphata
93	30	69.8	474	2	C90070	alkaline phosphata
94	30	69.8	499	2	A46039	steroid 11beta-mon
95	30	69.8	500	2	I56601	cytochrome P450 al
96	30	69.8	500	2	B41552	steroid 11beta-mon
97	30	69.8	500	2	A41552	aldosterone syntha
98	30	69.8	501	1	A60005	glycoprotein A pre
99	30	69.8	501	1	VGBEMA	glycoprotein A pre
100	30	69.8	501	1	VGBEMB	glycoprotein A pre
101	30	69.8	505	1	VGBEMH	glycoprotein gp57-
102	30	69.8	506	2	JN0615	steroid 11beta-mon

103	30	69.8	552	2	F69817	conserved hypothet
104	30	69.8	598	2	A72124	phosphomannomutase
105	30	69.8	598	2	A86498	phosphomannomutase
106	30	69.8	605	2	T49780	related to beta tr
107	30	69.8	606	2	JC5604	ABC-transporting p
108	30	69.8	643	2	T19549	hypothetical prote
109	30	69.8	644	2	T33132	hypothetical prote
110	30	69.8	675	1	KXBOS	plasma protein S p
111	30	69.8	710	2	H44490	retrovirus-related
112	30	69.8	729	2	T23769	hypothetical prote
113	30	69.8	750	2	AE2860	xanthine dehydroge
114	30	69.8	778	2	B70667	hypothetical prote
115	30	69.8	779	2	D97637	xanthine dehydroge
116	30	69.8	779	2	G87573	xanthine dehydroge
117	30	69.8	857	2	S16133	dimethylglycine de
118	30	69.8	888	2	A71720	hypothetical prote
119	30	69.8	1063	2	A53164	glutamate dehydrog
120	30	69.8	1638	2	D87749	protein unc-73b [i
121	30	69.8	1742	2	S24600	projectin - fruit
122	30	69.8	2182	2	T28634	variant-specific s
123	30	69.8	2236	1	QZFF	rudimentary protei
124	30	69.8	2488	2	T42739	guanine nucleotide
125	30	69.8	3010	1	GNWVTW	genome polyprotein
126	30	69.8	3869	2	A48205	All-1 protein +GTE
127	30	69.8	3968	2	A44265	trithorax homolog
128	30	69.8	4543	1	A53102	alpha-2-macroglobu
129	30	69.8	4544	1	S02392	alpha-2-macroglobu
130	30	69.8	4545	1	S25111	alpha-2-macroglobu
131	30	69.8	6658	2	T13931	projectin - fruit
132	29	67.4	78	2	PS0085	hypothetical prote
133	29	67.4	166	2	JC6003	intracellular prot
134	29	67.4	204	2	B98131	hypothetical prote
135	29	67.4	204	2	AG3156	conserved hypothet
136	29	67.4	206	2	C83590	probable transcrip
137	29	67.4	212	2	C90786	probable tet opero
138	29	67.4	212	2	A85646	probable tet opero
139	29	67.4	212	2	C64843	probable transcrip
140	29	67.4	237	2	E82674	3'-phosphoadenosin
141	29	67.4	259	2	PS0102	genome polyprotein
142	29	67.4	263	2	S01360	salivary glue prot
143	29	67.4	271	2	B86918	hypothetical prote
144	29	67.4	275	2	D97525	hypothetical prote
145	29	67.4	284	2	PS0104	genome polyprotein
146	29	67.4	286	2	G70537	hypothetical prote
147	29	67.4	308	2	I56573	synaptic glycoprot
148	29	67.4	308	2	T50639	synaptic glycoprot
149	29	67.4	308	2	T50638	synaptic glycoprot
150	29	67.4	317	2	T35869	probable transfera
151	29	67.4	340	2	AI0097	galactose operon r
152	29	67.4	342	2	AE0867	galactose operon r
153	29	67.4	343	1	RPECG	gal operon repress
154	29	67.4	343	2	A85936	repressor of galET
155	29	67.4	343	2	F91090	repressor of galET
156	29	67.4	345	2	S64476	hypothetical prote
157	29	67.4	347	2	D83554	hypothetical prote
158	29	67.4	365	2	JQ0879	NS5 protein - hepa
159	29	67.4	365	2	JQ0880	NS5 protein - hepa
160	29	67.4	380	2	S62525	hypothetical prote
161	29	67.4	386	2	F95911	probable hydrocarb
162	29	67.4	387	2	I49246	D4 dopamine recept
163	29	67.4	395	2	T34908	redV protein - Str
164	29	67.4	403	2	T30464	hypothetical prote
165	29	67.4	411	2	G86923	probable hydrolase
166	29	67.4	430	2	T28870	hypothetical prote
167	29	67.4	451	2	F86169	hypothetical prote
168	29	67.4	480	2	T20168	hypothetical prote
169	29	67.4	490	2	I52410	cytochrome P450 II
170	29	67.4	490	2	A32140	steroid 15beta-mon
171	29	67.4	490	2	A36122	cytochrome P450 2C
172	29	67.4	519	2	T31292	glycolate oxidase
173	29	67.4	531	2	T29920	hypothetical prote
174	29	67.4	580	2	G82693	glutaminyl-tRNA sy
175	29	67.4	600	2	H75516	probable maltoolig
176	29	67.4	618	2	D88483	protein let-721 [i
177	29	67.4	684	2	AE3251	virA/G regulated p
178	29	67.4	722	2	T19568	hypothetical prote
179	29	67.4	747	2	T06580	subtilisin-like pr
180	29	67.4	778	2	B95984	probable xanthine
181	29	67.4	791	2	B46171	coat protein - Lei
182	29	67.4	796	2	T21460	hypothetical prote
183	29	67.4	808	2	G83210	conserved hypothet
184	29	67.4	855	2	C82983	hypothetical prote
185	29	67.4	905	2	F82734	serine proteinase
186	29	67.4	910	2	H82826	serine proteinase
187	29	67.4	1321	2	A60165	sodium channel pro
188	29	67.4	1321	2	T29308	hypothetical prote
189	29	67.4	1372	2	T29309	hypothetical prote
190	29	67.4	1505	2	S26765	genome polyprotein
191	29	67.4	2057	2	F90109	splicing factor Pr
192	29	67.4	2344	1	RRWWRH	genome polyprotein
193	29	67.4	2344	2	S64740	genome polyprotein
194	29	67.4	2344	2	S55399	genome polyprotein
195	29	67.4	3010	1	A45573	genome polyprotein
196	29	67.4	3010	1	GNWVCJ	genome polyprotein
197	29	67.4	3010	1	GNWVTC	genome polyprotein
198	29	67.4	3010	1	S18030	genome polyprotein
199	29	67.4	3011	1	GNWVC3	genome polyprotein
200	29	67.4	3011	1	GNWVCH	genome polyprotein
201	29	67.4	3011	1	S40770	genome polyprotein
202	29	67.4	3097	2	T28635	glutamate synthase
203	29	67.4	5105	2	T32650	hypothetical prote
204	28	65.1	103	2	T46667	hypothetical prote
205	28	65.1	106	2	E75632	hypothetical prote
206	28	65.1	135	1	W4BP77	gene 4.7 protein -
207	28	65.1	135	2	T45887	hypothetical prote
208	28	65.1	142	2	C82829	conserved hypothet
209	28	65.1	146	2	F71263	probable flavodoxi
210	28	65.1	159	2	A87283	hypothetical prote
211	28	65.1	170	2	B53274	complement factor
212	28	65.1	180	2	D72629	hypothetical prote
213	28	65.1	181	2	E82333	oligoribonuclease
214	28	65.1	186	2	A90000	hypothetical prote
215	28	65.1	189	2	H82529	hypothetical prote
216	28	65.1	194	2	T44862	transcription regu
217	28	65.1	199	2	AC2673	hypothetical prote
218	28	65.1	199	2	A97455	probable acetyltra
219	28	65.1	203	2	B82493	hypothetical prote
220	28	65.1	204	2	AD2607	conserved hypothet
221	28	65.1	204	2	C97389	hypothetical prote
222	28	65.1	234	2	D87629	transcription regu
223	28	65.1	238	2	T23867	hypothetical prote
224	28	65.1	242	2	T46543	hypothetical prote
225	28	65.1	250	2	B71321	conserved hypothet
226	28	65.1	256	2	AH1148	hypothetical prote
227	28	65.1	257	2	F86697	hypothetical prote
228	28	65.1	257	2	C84207	hypothetical prote
229	28	65.1	257	2	AH1507	hypothetical membr
230	28	65.1	262	2	T27381	hypothetical prote
231	28	65.1	268	2	A81079	conserved hypothet
232	28	65.1	268	2	A81864	probable NMA1686 [
233	28	65.1	271	1	A89124	probable phosphoes
234	28	65.1	285	2	B88546	protein R107.2 [im
235	28	65.1	286	2	S30872	hypothetical prote
236	28	65.1	288	2	S18990	probable acyl-CoA
237	28	65.1	293	1	DAPSPC	biphenyl-2,3-diol
238	28	65.1	295	2	T33388	hypothetical prote
239	28	65.1	297	2	AG3487	transcription regu
240	28	65.1	303	2	T35930	hypothetical prote
241	28	65.1	317	2	H70566	hypothetical prote
242	28	65.1	347	2	E89788	hypothetical prote
243	28	65.1	357	2	S28058	serotonin receptor
244	28	65.1	357	2	I37107	5-HT5A serotonin r
245	28	65.1	357	2	B47472	5-hydroxytryptamin
246	28	65.1	360	1	E64130	alanine racemase (
247	28	65.1	361	2	E84506	probable N-acetylg
248	28	65.1	365	2	F96003	conserved hypothet

249	28	65.1	367	2	S74900	histidinol-phospha
250	28	65.1	367	2	E84855	hypothetical prote
251	28	65.1	368	2	AB2602	conserved hypothet
252	28	65.1	368	2	B97384	probable integral
253	28	65.1	369	2	C82211	4-hydroxyphenylpyr
254	28	65.1	375	2	H82329	alanine racemase,
255	28	65.1	378	2	A45680	G protein-coupled
256	28	65.1	378	2	B55735	lymphocyte-specifi
257	28	65.1	378	2	A55735	G protein-coupled
258	28	65.1	397	2	T44477	hypothetical prote
259	28	65.1	403	2	T39697	DNAJ protein - fis
260	28	65.1	411	2	T03154	DNA polymerase pro
261	28	65.1	412	2	D95941	conserved hypothet
262	28	65.1	417	2	AF3448	hypothetical membr
263	28	65.1	421	2	G72074	hypothetical prote
264	28	65.1	421	2	A86550	hypothetical prote
265	28	65.1	421	2	G81594	conserved hypothet
266	28	65.1	423	2	G96554	hypothetical prote
267	28	65.1	440	2	F86385	probable lysine an
268	28	65.1	448	2	T06698	hypothetical prote
269	28	65.1	456	2	E69391	hypothetical prote
270	28	65.1	473	2	D82884	glycyl-tRNA synthe
271	28	65.1	505	2	A87314	phospholipase D fa
272	28	65.1	511	2	S58399	cellutagmin I sytV
273	28	65.1	515	2	A46374	reserpine-sensitiv
274	28	65.1	535	2	E96730	hypothetical prote
275	28	65.1	544	2	F69350	L-lactate permease
276	28	65.1	545	2	A87136	hypothetical prote
277	28	65.1	571	2	T52164	nucleotide phospho
278	28	65.1	573	2	AH0165	pyruvate dehydroge
279	28	65.1	584	2	S76424	hypothetical prote
280	28	65.1	591	2	H70755	probable oppA prot
281	28	65.1	615	2	S38088	hypothetical prote
282	28	65.1	616	2	C95861	probable ABC trans
283	28	65.1	624	2	T39102	hypothetical prote
284	28	65.1	648	2	T08898	envelope-like - so
285	28	65.1	673	2	A49878	coagulation factor
286	28	65.1	690	2	F71239	hypothetical prote
287	28	65.1	698	2	D90541	atp synthase beta
288	28	65.1	709	2	A35364	carcinoembryonic a
289	28	65.1	710	2	T46589	ropy-2 protein [im
290	28	65.1	716	2	A75595	hypothetical prote
291	28	65.1	722	2	T20362	glycerol-3-phospha
292	28	65.1	725	2	D75294	hypothetical prote
293	28	65.1	745	2	E75354	DNA helicase II -
294	28	65.1	761	1	BBMS	complement factor
295	28	65.1	764	1	BBHU	complement factor
296	28	65.1	796	2	T16424	hypothetical prote
297	28	65.1	830	2	I50455	prolactin receptor
298	28	65.1	831	2	JQ1655	prolactin receptor
299	28	65.1	832	2	T49494	condensin complex
300	28	65.1	840	1	S69204	pheromone response
301	28	65.1	889	2	A41259	potassium transpor
302	28	65.1	926	2	T29323	hypothetical prote
303	28	65.1	998	2	S77225	sensory transducti
304	28	65.1	1007	2	E72489	hypothetical prote
305	28	65.1	1019	2	T50251	hypothetical coile
306	28	65.1	1036	2	S73601	protein P200 - Myc
307	28	65.1	1132	1	QSBPL	host specificity p
308	28	65.1	1142	1	GNVUPH	M polyprotein prec
309	28	65.1	1148	1	GNVUNE	M polyprotein prec
310	28	65.1	1148	1	JQ1604	M polyprotein prec
311	28	65.1	1162	2	T37889	probable nuclear p
312	28	65.1	1234	2	E83415	methionine synthas
313	28	65.1	1257	2	AC2841	methionine synthas
314	28	65.1	1259	2	E97618	methionine synthas
315	28	65.1	1330	1	VCBES5	major capsid prote
316	28	65.1	1385	2	S61236	major capsid prote
317	28	65.1	1405	1	DJZPA	DNA-directed DNA p
318	28	65.1	1440	2	JC6312	protein-tyrosine-p
319	28	65.1	1457	1	A48066	protein-tyrosine-p
320	28	65.1	1488	2	AG2136	polyketide synthas
321	28	65.1	1499	2	AC2555	hypothetical prote
322	28	65.1	1524	2	G84721	hypothetical prote
323	28	65.1	1750	2	G84649	hypothetical prote
324	28	65.1	1782	2	S45289	vitellogenin precu
325	28	65.1	2109	2	T31352	hypothetical prote
326	27.5	64.0	323	2	S59373	cyclin homolog UME
327	27.5	64.0	405	2	T37963	caffeine-induced d
328	27.5	64.0	414	1	E70708	cytochrome P450 Rv
329	27	62.8	65	1	TIVIVC	venom basic protei
330	27	62.8	65	2	T03452	nonstructural prot
331	27	62.8	88	2	AF1023	hypothetical prote
332	27	62.8	94	2	T18030	hypothetical prote
333	27	62.8	95	2	JQ0134	hypothetical 10.8K
334	27	62.8	97	2	C87697	hypothetical prote
335	27	62.8	98	2	PL0034	photosystem I chai
336	27	62.8	99	2	C46518	Ig L1 chain V regi
337	27	62.8	102	2	D71042	hypothetical prote
338	27	62.8	105	2	AB0318	conserved hypothet
339	27	62.8	115	2	B46518	Ig L1 chain V regi
340	27	62.8	115	2	T10849	y4hO protein - Rhi
341	27	62.8	127	2	AG2241	hypothetical prote
342	27	62.8	132	2	T36665	hypothetical prote
343	27	62.8	133	2	F90305	transposase, proba
344	27	62.8	140	2	S34667	hypothetical prote
345	27	62.8	142	2	B82223	hypothetical prote
346	27	62.8	142	2	B24653	hemoglobin beta ch
347	27	62.8	148	2	A82591	conserved hypothet
348	27	62.8	151	2	D84495	hypothetical prote
349	27	62.8	164	2	D83172	hypothetical prote
350	27	62.8	165	2	C75480	hypothetical prote
351	27	62.8	170	2	T15452	hypothetical prote
352	27	62.8	171	2	AC2539	hypothetical prote
353	27	62.8	175	2	T08948	hypothetical prote
354	27	62.8	186	2	G75272	probable ribosomal
355	27	62.8	188	1	A39553	adrenodoxin precur
356	27	62.8	190	2	B87664	hypothetical prote
357	27	62.8	196	2	G84513	hypothetical prote
358	27	62.8	198	2	S31937	coat protein - Myc
359	27	62.8	198	2	E72802	major tail subunit
360	27	62.8	200	2	B69859	hypothetical prote
361	27	62.8	203	2	T41380	hypothetical prote
362	27	62.8	207	2	S60006	Mad4 protein - mou
363	27	62.8	209	2	AG2841	outer membrane pro
364	27	62.8	209	2	H82415	DnaJ-related prote
365	27	62.8	210	2	S73646	hypothetical prote
366	27	62.8	210	2	AD0547	RhtC-like transpor
367	27	62.8	213	2	AF2869	transcription regu
368	27	62.8	213	2	H97645	probable tet opero
369	27	62.8	214	2	AG1276	hypothetical prote
370	27	62.8	214	2	AG1639	hypothetical prote
371	27	62.8	219	2	AG2036	hypothetical prote
372	27	62.8	219	2	H97618	25K outer-membrane
373	27	62.8	221	2	E83625	probable transcrip
374	27	62.8	235	2	T03076	hypothetical prote
375	27	62.8	238	2	A86562	hypothetical prote
376	27	62.8	238	2	C72061	conserved hypothet
377	27	62.8	238	2	A81671	conserved hypothet
378	27	62.8	238	2	D71513	hypothetical prote
379	27	62.8	238	2	T16788	hypothetical prote
380	27	62.8	239	2	D64756	probable transcrip
381	27	62.8	242	2	T16349	hypothetical prote
382	27	62.8	242	2	B83468	hypothetical prote
383	27	62.8	247	2	AG0250	conserved hypothet
384	27	62.8	248	2	A71106	hypothetical prote
385	27	62.8	251	2	S72730	yfcA protein - Myc
386	27	62.8	251	2	F70500	hypothetical prote
387	27	62.8	254	2	T40688	hypothetical prote
388	27	62.8	259	2	B85066	hypothetical prote
389	27	62.8	261	2	I52518	sperm acrosome ant
390	27	62.8	262	2	AI2715	dehydrogenase Atu1
391	27	62.8	263	2	A21195	chymotrypsin (EC 3
392	27	62.8	263	2	JN0817	beta-hemolysin pre
393	27	62.8	277	2	D97497	pteridine reductas
394	27	62.8	277	2	AG1594	phage SPP1 hypothe

395	27	62.8	278	2	T03850	myb-related protei
396	27	62.8	278	2	G96015	conserved hypothet
397	27	62.8	279	2	S62364	L-2-chloropropioni
398	27	62.8	281	2	E75195	hypothetical prote
399	27	62.8	281	2	AG2975	2-haloalkanoic aci
400	27	62.8	281	2	D98307	hypothetical prote
401	27	62.8	283	2	T18662	hypothetical prote
402	27	62.8	288	2	S41382	pobR protein - Pse
403	27	62.8	290	2	S45349	L1 metallo-beta-la
404	27	62.8	298	2	S77536	lactose transport
405	27	62.8	300	2	T42343	hypothetical prote
406	27	62.8	305	2	C69609	cytochrome caa3 ox
407	27	62.8	305	2	T05072	hypothetical prote
408	27	62.8	312	2	T49764	hypothetical prote
409	27	62.8	314	2	T50871	hypothetical prote
410	27	62.8	315	2	F64129	probable phosphogl
411	27	62.8	321	2	G95218	hypothetical prote
412	27	62.8	321	2	E98082	hypothetical prote
413	27	62.8	326	2	A59232	ABA-responsive pro
414	27	62.8	327	2	T33540	hypothetical prote
415	27	62.8	331	2	B70837	hypothetical prote
416	27	62.8	332	2	T15561	G protein-coupled
417	27	62.8	345	2	T26698	hypothetical prote
418	27	62.8	345	2	G69492	hypothetical prote
419	27	62.8	346	2	D89981	hypothetical prote
420	27	62.8	347	2	T45551	NADH2 dehydrogenas
421	27	62.8	351	2	A34201	bone morphogenetic
422	27	62.8	353	2	AB2860	monooxygenase [imp
423	27	62.8	353	2	H97636	N5,N10-methylenete
424	27	62.8	356	2	AF2137	hypothetical prote
425	27	62.8	359	2	H89472	protein F52D2.1 [i
426	27	62.8	369	2	AD0985	probable endogluca
427	27	62.8	378	2	T33045	hypothetical prote
428	27	62.8	378	2	AH0036	conserved hypothet
429	27	62.8	379	2	A84235	acyl-CoA dehydroge
430	27	62.8	380	2	G85657	hypothetical prote
431	27	62.8	380	2	E90797	hypothetical prote
432	27	62.8	388	2	AE2641	aspartate aminotra
433	27	62.8	388	2	G85147	hypothetical prote
434	27	62.8	390	2	C42477	malY protein (EC 2
435	27	62.8	390	2	B90920	probable aminotras
436	27	62.8	390	2	G85768	probable aminotras
437	27	62.8	391	1	GZBPT4	baseplate protein
438	27	62.8	391	2	G97423	probable aspartate
439	27	62.8	393	2	S37073	bone morphogenetic
440	27	62.8	393	2	AD0674	probable aminotran
441	27	62.8	394	2	S45355	bone morphogenetic
442	27	62.8	398	2	S59905	myc2 protein - rai
443	27	62.8	404	2	S42831	F40F12.2 protein -
444	27	62.8	406	2	H84590	hypothetical prote
445	27	62.8	410	2	S41188	gene 40 protein -
446	27	62.8	413	2	H69255	hypothetical prote
447	27	62.8	416	2	F24723	tryptophan synthas
448	27	62.8	419	2	D42725	nitrile hydratase
449	27	62.8	421	2	AI2931	hypothetical prote
450	27	62.8	424	2	E87558	cytochrome P450 fa
451	27	62.8	428	2	T04743	cyclin cyc1 - Arab
452	27	62.8	431	2	T36319	probable aminotran
453	27	62.8	437	2	JU0185	PACAP/VIP receptor
454	27	62.8	437	2	E98350	hypothetical prote
455	27	62.8	439	2	C82349	3-deoxy-D-manno-oc
456	27	62.8	442	2	T42342	hypothetical prote
457	27	62.8	442	2	A57044	alpha-1,6-mannosyl
458	27	62.8	445	2	A27263	50K spicule matrix
459	27	62.8	447	2	S66256	alpha-1,6-mannosyl
460	27	62.8	449	2	S16319	secretin receptor
461	27	62.8	450	2	F82848	GTP-binding protei
462	27	62.8	454	2	E70637	hypothetical prote
463	27	62.8	454	2	F71313	probable V-type AT
464	27	62.8	458	2	C90513	conserved hypothet
465	27	62.8	460	2	S06022	regulatory protein
466	27	62.8	462	2	T41018	probable membrane
467	27	62.8	468	2	E69294	hypothetical prote
468	27	62.8	470	1	SYPSRA	threonine synthase
469	27	62.8	470	2	AC0020	uroporphyrin-III C
470	27	62.8	476	2	T45656	hypothetical prote
471	27	62.8	478	2	T45661	hypothetical prote
472	27	62.8	480	2	I65309	autoantigen p69 -
473	27	62.8	481	2	S70111	hypothetical prote
474	27	62.8	482	2	E70554	hypothetical prote
475	27	62.8	483	2	I55598	diabetes-associate
476	27	62.8	485	2	E88114	protein F53C3.9 [i
477	27	62.8	490	2	C70854	probable gltS prot
478	27	62.8	497	2	S37580	probable acyltrans
479	27	62.8	497	2	S37581	probable acyltrans
480	27	62.8	498	2	AE1103	lysyl-tRNA synthet
481	27	62.8	498	2	AE1465	lysyl-tRNA synthet
482	27	62.8	502	2	T45422	glutamyl-tRNA synt
483	27	62.8	509	2	D64435	hypothetical prote
484	27	62.8	515	2	T32175	hypothetical prote
485	27	62.8	528	2	H75513	probable sodium/pr
486	27	62.8	530	2	A86934	probable membrane
487	27	62.8	531	2	AH1131	hypothetical prote
488	27	62.8	531	2	AH1491	hypothetical prote
489	27	62.8	543	2	AB0460	ubiquinone biosynt
490	27	62.8	554	2	T51213	hypothetical prote
491	27	62.8	555	2	I38656	lymphoid-restricte
492	27	62.8	561	2	AH2314	lysyl-tRNA synthet
493	27	62.8	564	2	T28949	hypothetical prote
494	27	62.8	565	2	C86617	sulfate transporte
495	27	62.8	565	2	D72006	sulfate transporte
496	27	62.8	571	2	T00835	calcium-dependent
497	27	62.8	572	2	AG0608	pyruvate dehydroge
498	27	62.8	583	2	S67571	hypothetical prote
499	27	62.8	585	2	C82157	hypothetical prote
500	27	62.8	591	2	B97952	pyruvate oxidase (
501	27	62.8	591	2	F95084	pyruvate oxidase [
502	27	62.8	593	2	T31693	hypothetical prote
503	27	62.8	593	2	T10301	ribonucleotide red
504	27	62.8	598	2	A96685	probable RING zinc
505	27	62.8	608	2	T29778	hypothetical prote
506	27	62.8	619	2	H84416	hypothetical prote
507	27	62.8	622	2	H96684	probable RING zinc
508	27	62.8	622	2	B71326	probable V-type AT
509	27	62.8	631	2	T08051	probable ethylene
510	27	62.8	632	2	T18692	hypothetical prote
511	27	62.8	635	2	S73017	polyketide synthas
512	27	62.8	642	2	S53433	plasma protein S p
513	27	62.8	650	2	D96612	hypothetical prote
514	27	62.8	653	2	H86373	protein T23E23.16
515	27	62.8	663	2	E96705	hypothetical prote
516	27	62.8	673	2	S72440	X-Pro aminopeptida
517	27	62.8	685	2	G82022	methionine-tRNA li
518	27	62.8	706	2	T01351	subtilisin-like pr
519	27	62.8	706	2	D81236	nitrogen regulatio
520	27	62.8	706	2	E82009	probable two-compo
521	27	62.8	711	2	C70606	probable fadE34 pr
522	27	62.8	720	2	S71130	catalase (EC 1.11.
523	27	62.8	724	2	B82186	catalase/peroxidas
524	27	62.8	726	1	S73915	virulence-associat
525	27	62.8	735	1	JS0520	catalase (EC 1.11.
526	27	62.8	737	2	A87626	catalase/peroxidas
527	27	62.8	738	2	A48246	ethylene-response
528	27	62.8	740	2	T51619	probable ethylene
529	27	62.8	743	2	T02828	conserved hypothet
530	27	62.8	746	2	S74546	glycogen operon pr
531	27	62.8	747	2	T04188	subtilisin-like pr
532	27	62.8	749	2	A99438	hypothetical prote
533	27	62.8	751	4	T43873	catalase (EC 1.11.
534	27	62.8	751	4	T43874	catalase (EC 1.11.
535	27	62.8	751	4	T43878	catalase (EC 1.11.
536	27	62.8	751	4	T43880	catalase (EC 1.11.
537	27	62.8	751	4	T43881	catalase (EC 1.11.
538	27	62.8	752	4	T43877	catalase (EC 1.11.
539	27	62.8	753	4	T43882	catalase (EC 1.11.
540	27	62.8	760	1	C2MS	classical-compleme

541	27	62.8	774	2	T19244	hypothetical prote
542	27	62.8	783	2	A96825	hypothetical prote
543	27	62.8	800	2	T23780	hypothetical prote
544	27	62.8	801	1	MWXRR5	RNA 5 protein - ri
545	27	62.8	805	2	S68441	leptin receptor, s
546	27	62.8	806	2	A53256	nuclear protein bi
547	27	62.8	825	2	T13473	DNA-directed DNA p
548	27	62.8	827	2	T13468	DNA-directed DNA p
549	27	62.8	832	2	S55396	LI-cadherin - huma
550	27	62.8	842	1	JDVLVS	DNA-directed DNA p
551	27	62.8	843	1	JDVLJ3	DNA-directed DNA p
552	27	62.8	843	1	JDVLVR	DNA-directed DNA p
553	27	62.8	843	1	S43491	DNA-directed DNA p
554	27	62.8	843	1	A27340	complement C7 prec
555	27	62.8	843	2	S35527	DNA-directed DNA p
556	27	62.8	857	2	T37459	ribonucleotide red
557	27	62.8	874	4	GNHUER	retrovirus-related
558	27	62.8	877	2	T03098	p97 protein - Toxo
559	27	62.8	878	2	AE0478	phosphoenolpyruvat
560	27	62.8	879	2	I64133	phosphoenolpyruvat
561	27	62.8	883	1	QYEC	phosphoenolpyruvat
562	27	62.8	883	2	B86087	phosphoenolpyruvat
563	27	62.8	883	2	AD0936	phosphoenolpyruvat
564	27	62.8	883	2	E91239	phosphoenolpyruvat
565	27	62.8	888	2	I58378	tyrosine kinase -
566	27	62.8	892	2	S68439	leptin receptor, s
567	27	62.8	894	2	S68437	leptin receptor, s
568	27	62.8	899	2	A44879	retinoblastoma pro
569	27	62.8	900	2	S68440	leptin receptor, s
570	27	62.8	919	1	PXZP1P	H+-exporting ATPas
571	27	62.8	937	2	PQ0864	hypothetical prote
572	27	62.8	939	2	T32521	hypothetical prote
573	27	62.8	942	2	T19553	hypothetical prote
574	27	62.8	981	2	A41401	mineralocorticoid
575	27	62.8	984	2	A29513	mineralocorticoid
576	27	62.8	994	2	B82843	valyl-tRNA synthet
577	27	62.8	1040	2	AB2186	hypothetical prote
578	27	62.8	1051	2	D82428	chitodextrinase VC
579	27	62.8	1098	2	T08599	probable transcrip
580	27	62.8	1108	2	B96675	hypothetical prote
581	27	62.8	1125	1	OYURCP	speract receptor p
582	27	62.8	1159	2	H96674	hypothetical prote
583	27	62.8	1162	2	S68438	leptin receptor, s
584	27	62.8	1179	2	T04488	DNA topoisomerase
585	27	62.8	1193	2	A96675	hypothetical prote
586	27	62.8	1222	2	S40977	hypothetical prote
587	27	62.8	1227	2	A33638	erythrocyte anion
588	27	62.8	1232	2	I38496	anion exchanger 3
589	27	62.8	1234	2	C84465	hypothetical prote
590	27	62.8	1267	1	MWXR31	lambda 3 protein -
591	27	62.8	1267	1	MWXR32	lambda 3 protein -
592	27	62.8	1267	1	MWXR33	lambda 3 protein -
593	27	62.8	1357	2	S57052	hypothetical prote
594	27	62.8	1358	2	S64356	phosphoribosylform
595	27	62.8	1381	2	T31083	paranodin - rat
596	27	62.8	1385	2	T14158	neurexin IV - mous
597	27	62.8	1443	2	S05979	steroid hormone re
598	27	62.8	1446	2	S73013	polyketide synthas
599	27	62.8	1493	2	H71445	hypothetical prote
600	27	62.8	1530	2	H83865	glutamate synthase
601	27	62.8	1540	2	H87203	polyketide synthas
602	27	62.8	1585	2	T19121	probable protein-t
603	27	62.8	1614	2	T29861	hypothetical prote
604	27	62.8	1824	1	QRHUMT	microtubule-associ
605	27	62.8	1871	2	A87204	polyketide synthas
606	27	62.8	1876	2	C70749	probable ppsA prot
607	27	62.8	2025	2	T03884	hypothetical prote
608	27	62.8	2113	2	G91286	probable RNA helic
609	27	62.8	2113	2	C86128	probable helicase
610	27	62.8	2135	2	T14602	variant-specific s
611	27	62.8	2201	2	S73014	polyketide synthas
612	27	62.8	2228	2	T14029	variant-specific s
613	27	62.8	2245	2	T27511	hypothetical prote
614	27	62.8	2329	2	S44625	C50C3.6 protein -
615	27	62.8	2352	2	T06077	splicing factor PR
616	27	62.8	2359	2	B96832	hypothetical prote
617	27	62.8	2630	2	T08868	polyprotein P1 - A
618	27	62.8	3078	2	T28432	variant-specific s
619	26.5	61.6	342	2	B84220	hypothetical prote
620	26.5	61.6	413	2	T08297	conserved hypothet
621	26.5	61.6	447	2	AC1847	hypothetical prote
622	26	60.5	52	2	AC1374	hypothetical prote
623	26	60.5	60	2	AB1374	hypothetical CDS 1
624	26	60.5	68	2	T18874	hypothetical prote
625	26	60.5	76	2	H81272	probable acyl carr
626	26	60.5	81	2	PH1048	Ig light chain V r
627	26	60.5	87	2	T51758	hypothetical prote
628	26	60.5	90	2	C85905	hypothetical prote
629	26	60.5	90	2	E91060	hypothetical prote
630	26	60.5	90	2	A65037	hypothetical 9.9 k
631	26	60.5	92	2	S37532	Ig kappa chain V r
632	26	60.5	92	2	S37533	Ig kappa chain V r
633	26	60.5	92	2	S37530	Ig kappa chain V r
634	26	60.5	92	2	S37535	Ig kappa chain V r
635	26	60.5	92	2	S37531	Ig kappa chain V r
636	26	60.5	92	2	S37534	Ig kappa chain V r
637	26	60.5	92	2	S37529	Ig kappa chain V r
638	26	60.5	98	2	S19974	Ig kappa chain V r
639	26	60.5	101	2	PH0869	Ig kappa chain V r
640	26	60.5	101	2	PH1046	Ig light chain V r
641	26	60.5	101	2	S26337	Ig light chain V r
642	26	60.5	102	2	A34153	Ig kappa chain V-I
643	26	60.5	103	2	PH1047	Ig light chain V r
644	26	60.5	103	2	PH1051	Ig light chain V r
645	26	60.5	103	2	PH1052	Ig light chain V r
646	26	60.5	103	2	PH1050	Ig light chain V r
647	26	60.5	103	2	PH1054	Ig light chain V r
648	26	60.5	104	2	PH1101	Ig light chain V r
649	26	60.5	104	2	F38601	Ig kappa chain V r
650	26	60.5	104	2	PH1102	Ig light chain V r
651	26	60.5	104	2	PH1103	Ig light chain V r
652	26	60.5	104	2	PH1104	Ig light chain V r
653	26	60.5	105	2	G71294	hypothetical prote
654	26	60.5	106	2	A49138	IgA kappa rheumato
655	26	60.5	111	2	S03304	Ig kappa chain V r
656	26	60.5	111	2	G30502	Ig kappa chain V r
657	26	60.5	112	2	S09970	Ig kappa chain V-J
658	26	60.5	112	2	PL0265	Ig kappa chain V r
659	26	60.5	112	2	S43103	Ig kappa chain V-J
660	26	60.5	113	2	S34002	Ig kappa chain V r
661	26	60.5	113	2	S34003	Ig kappa chain V r
662	26	60.5	113	2	S30523	Ig kappa chain V r
663	26	60.5	113	2	PL0263	Ig kappa chain V r
664	26	60.5	113	2	T10018	hypothetical prote
665	26	60.5	114	1	K4HULN	Ig kappa chain V-I
666	26	60.5	114	2	S44119	Ig kappa chain V-J
667	26	60.5	114	2	S44116	Ig kappa chain V-J
668	26	60.5	114	2	AF3219	hypothetical prote
669	26	60.5	117	2	AH2986	hypothetical prote
670	26	60.5	118	2	PT0356	Ig kappa chain V r
671	26	60.5	120	2	S51147	antibody light cha
672	26	60.5	120	2	G33932	Ig kappa chain pre
673	26	60.5	120	2	T02037	acidic ribosomal p
674	26	60.5	121	1	K4HU	Ig kappa chain pre
675	26	60.5	124	2	G85070	hypothetical prote
676	26	60.5	129	2	S40329	Ig kappa chain V-J
677	26	60.5	129	2	S40347	Ig kappa chain - h
678	26	60.5	131	2	A84491	hypothetical prote
679	26	60.5	131	2	T36638	probable substrate
680	26	60.5	133	1	K4HUJI	Ig kappa chain pre
681	26	60.5	133	2	PS0023	Ig kappa chain pre
682	26	60.5	134	2	S49531	anti-Sm antibody V
683	26	60.5	134	2	PC1214	Ig kappa chain pre
684	26	60.5	137	2	T21078	hypothetical prote
685	26	60.5	138	2	A53261	Ig kappa chain pre
686	26	60.5	138	2	S26040	Ig kappa chain pre

687	26	60.5	140	1	QQMSIG	hypothetical Ig do
688	26	60.5	142	2	H82560	hypothetical prote
689	26	60.5	145	2	PL0014	Ig kappa chain pre
690	26	60.5	157	2	S26735	hypothetical prote
691	26	60.5	159	2	S32327	coat protein - Ses
692	26	60.5	160	2	F82635	outer membrane pro
693	26	60.5	161	2	JS0739	H+-transporting tw
694	26	60.5	165	2	S35195	hypothetical prote
695	26	60.5	170	2	F81014	lipopolysaccharide
696	26	60.5	171	2	S44737	C02C2.6 protein -
697	26	60.5	172	2	C84293	acetyltransferase
698	26	60.5	176	2	T47361	hypothetical prote
699	26	60.5	186	1	G69069	hypothetical prote
700	26	60.5	190	2	S04661	thioredoxin f prec
701	26	60.5	192	2	T09847	phosphoenolpyruvat
702	26	60.5	194	2	AH1371	peptidyl-prolyl ci
703	26	60.5	194	2	AF1741	peptidyl-prolyl ci
704	26	60.5	201	2	S09887	hypothetical prote
705	26	60.5	203	2	T36102	hypothetical prote
706	26	60.5	209	2	T01336	hypothetical prote
707	26	60.5	211	2	B71809	hypothetical prote
708	26	60.5	211	2	E64710	hypothetical prote
709	26	60.5	212	2	AC0633	probable transcrip
710	26	60.5	214	2	E70575	hypothetical prote
711	26	60.5	215	2	T16383	hypothetical prote
712	26	60.5	220	2	A31790	Ig kappa chain V r
713	26	60.5	221	2	B86200	hypothetical prote
714	26	60.5	221	2	T51867	hypothetical prote
715	26	60.5	229	2	S55963	hypothetical prote
716	26	60.5	240	2	S06084	Ig kappa chain pre
717	26	60.5	247	2	T05226	hypothetical prote
718	26	60.5	247	2	D75055	hypothetical prote
719	26	60.5	249	2	JQ2287	SPCP1 protein - so
720	26	60.5	250	2	T35875	hypothetical prote
721	26	60.5	251	2	S22202	tonoplast intrinsi
722	26	60.5	252	1	DGBEN8	uracil-DNA glucosi
723	26	60.5	252	2	C69172	conserved hypothet
724	26	60.5	253	2	S13718	probable membrane
725	26	60.5	253	2	T51819	gamma tonoplast in
726	26	60.5	253	2	E84289	hypothetical prote
727	26	60.5	256	2	A47062	pyocin negative re
728	26	60.5	256	2	G70830	hypothetical prote
729	26	60.5	257	2	T40655	hypothetical prote
730	26	60.5	258	2	A97991	hypothetical prote
731	26	60.5	258	2	E95121	phosphoesterase, p
732	26	60.5	264	2	AG2950	conserved hypothet
733	26	60.5	267	2	T47288	hypothetical prote
734	26	60.5	269	2	E87595	hydrolase, alpha/b
735	26	60.5	277	2	T34779	tRNA (guanine-N1)-
736	26	60.5	278	2	D98332	hypothetical prote
737	26	60.5	279	2	H81678	phospho-2-dehydro-
738	26	60.5	280	2	AC1398	conserved hypothet
739	26	60.5	280	2	AF1773	conserved hypothet
740	26	60.5	283	2	AB3633	nirV precursor [im
741	26	60.5	284	2	F84363	Brp-like homolog [
742	26	60.5	286	2	T49505	hypothetical prote
743	26	60.5	288	2	S58219	ABA-inducible prot
744	26	60.5	289	2	E84140	transcription regu
745	26	60.5	290	2	T48880	beta-lactamase (EC
746	26	60.5	291	2	S10329	aryl sulfotransfer
747	26	60.5	295	2	F70936	hypothetical prote
748	26	60.5	298	2	AB0526	glutamyl-tRNA synt
749	26	60.5	299	2	D95382	probable transcrip
750	26	60.5	300	2	T36182	probable phosphotr
751	26	60.5	305	2	E91146	probable periplasm
752	26	60.5	305	2	A85992	probable periplasm
753	26	60.5	305	2	F65119	hypothetical amino
754	26	60.5	305	2	D98198	hypothetical prote
755	26	60.5	308	2	H64737	glutamate-tRNA lig
756	26	60.5	308	2	D90647	probable tRNA synt
757	26	60.5	308	2	D85498	probable tRNA synt
758	26	60.5	310	2	D87634	conserved hypothet
759	26	60.5	313	2	S54474	hypothetical prote
760	26	60.5	317	2	T50881	2-alpha-hydroxy et
761	26	60.5	321	2	A58458	isopenicillin N sy
762	26	60.5	321	2	T04626	probable protein k
763	26	60.5	322	1	JQ1645	coat protein - pop
764	26	60.5	323	2	T49723	hypothetical prote
765	26	60.5	323	2	T02617	hypothetical prote
766	26	60.5	326	2	AD2479	hypothetical prote
767	26	60.5	326	2	C69341	cobalt transport A
768	26	60.5	328	2	T06547	probable phosphoen
769	26	60.5	328	2	H86348	hypothetical prote
770	26	60.5	331	2	E84770	probable serpin [i
771	26	60.5	332	2	T18923	hypothetical prote
772	26	60.5	333	2	PS0018	Ig gamma-2b chain
773	26	60.5	335	2	D71275	hypothetical prote
774	26	60.5	336	2	AB2763	conserved hypothet
775	26	60.5	336	2	A97544	nifr3/smm1 family
776	26	60.5	343	2	AG2978	desulfurizing enzy
777	26	60.5	347	2	H84608	probable RNA-bindi
778	26	60.5	348	2	T19007	hypothetical prote
779	26	60.5	355	2	A45177	chemokine (C-C) re
780	26	60.5	360	2	H70553	probable mcr prote
781	26	60.5	361	2	C84746	hypothetical prote
782	26	60.5	362	2	T05167	hypothetical prote
783	26	60.5	363	2	A82567	GumF protein XP236
784	26	60.5	364	2	T20843	hypothetical prote
785	26	60.5	366	2	F98304	dibenzothiophene d
786	26	60.5	368	2	T42748	probable threonine
787	26	60.5	368	2	C91180	endo-1,4-D-glucana
788	26	60.5	368	2	E86026	probable endogluca
789	26	60.5	368	2	S47752	cellulase (EC 3.2.
790	26	60.5	370	2	S68416	phosphoenolpyruvat
791	26	60.5	370	2	S68415	phosphoenolpyruvat
792	26	60.5	370	2	I40085	gtcS protein - Bac
793	26	60.5	371	2	S68413	phosphoenolpyruvat
794	26	60.5	371	2	S68414	phosphoenolpyruvat
795	26	60.5	373	2	T34699	hypothetical prote
796	26	60.5	378	2	AH0878	probable oxygen-in
797	26	60.5	379	2	T20394	hypothetical prote
798	26	60.5	380	2	D82088	chromate resistanc
799	26	60.5	380	2	C83719	hypothetical prote
800	26	60.5	380	2	T40853	probable cysteine
801	26	60.5	380	2	B90423	hypothetical prote
802	26	60.5	384	2	G95933	probable glycosylt
803	26	60.5	384	2	S37608	NADH2 dehydrogenas
804	26	60.5	385	1	C72230	probable exonuclea
805	26	60.5	385	2	F70604	probable fadE30 pr
806	26	60.5	385	2	B84447	hypothetical prote
807	26	60.5	385	2	AH2169	ABC transport syst
808	26	60.5	386	2	E75588	glutaryl-CoA dehyd
809	26	60.5	387	2	B82178	conserved hypothet
810	26	60.5	389	2	T05814	hypothetical prote
811	26	60.5	394	2	T08757	probable translati
812	26	60.5	397	2	A32370	cyclin B1 - Africa
813	26	60.5	397	2	T37955	hypothetical prote
814	26	60.5	398	2	AE0975	probable racemase
815	26	60.5	401	2	T02380	hypothetical prote
816	26	60.5	403	2	B35401	cytochrome P450 10
817	26	60.5	406	2	AC2593	phosphopentomutase
818	26	60.5	406	2	E97375	phosphopentomutase
819	26	60.5	406	2	D82087	phosphopentomutase
820	26	60.5	406	2	A47696	acetamidase - Myco
821	26	60.5	407	2	B84993	phosphopentomutase
822	26	60.5	407	2	AE0054	phosphopentomutase
823	26	60.5	413	2	T32691	hypothetical prote
824	26	60.5	417	2	T19381	hypothetical prote
825	26	60.5	424	2	F83556	hypothetical prote
826	26	60.5	424	2	S15146	hypothetical prote
827	26	60.5	426	2	AD0136	citrate (si)-synth
828	26	60.5	427	1	YKEC	citrate (si)-synth
829	26	60.5	427	2	E83984	isocitrate lyase B
830	26	60.5	427	2	H85572	citrate synthase [
831	26	60.5	427	2	AF0590	citrate synthase [
832	26	60.5	427	2	A99722	citrate synthase [

833	26	60.5	427	2	G70936	hypothetical prote
834	26	60.5	428	1	A42971	cytochrome P450ter
835	26	60.5	428	2	A81705	peptide ABC transp
836	26	60.5	430	1	HMIHMS	hemagglutinin-este
837	26	60.5	436	1	WZBEP9	gene 68 protein -
838	26	60.5	436	2	T42982	hypothetical prote
839	26	60.5	436	2	T39855	beta-transducin -
840	26	60.5	437	2	S34469	gamma-aminobutyric
841	26	60.5	438	2	A71323	hypothetical prote
842	26	60.5	439	2	JQ0997	hemagglutinin-este
843	26	60.5	440	2	JL0144	interleukin-6 rece
844	26	60.5	441	2	T42946	hypothetical prote
845	26	60.5	444	2	B83759	alkaline phosphata
846	26	60.5	444	2	A48538	endothelin-3 recep
847	26	60.5	445	2	B82954	probable dihydroor
848	26	60.5	446	2	A83355	hypothetical prote
849	26	60.5	448	2	B56558	retinoic acid rece
850	26	60.5	452	2	S77155	UDP-N-acetylmuramo
851	26	60.5	460	2	JL0145	interleukin-6 rece
852	26	60.5	460	2	H87396	conserved hypothet
853	26	60.5	461	2	T06936	photosystem II chl
854	26	60.5	461	2	T14822	probable serine/th
855	26	60.5	462	1	A37986	interleukin-6 rece
856	26	60.5	462	2	C69676	alkaline phosphata
857	26	60.5	463	2	F70627	probable narU prot
858	26	60.5	463	2	AH2025	hypothetical prote
859	26	60.5	464	2	A56558	retinoic acid rece
860	26	60.5	467	1	P2WL33	L2 protein - human
861	26	60.5	468	2	AE2422	hypothetical prote
862	26	60.5	470	2	D87485	glutamyl-tRNA synt
863	26	60.5	473	1	F2SP44	photosystem II chl
864	26	60.5	473	2	T38350	threonine-tRNA lig
865	26	60.5	473	2	JN0346	photosystem II chl
866	26	60.5	473	2	S03436	photosystem II chl
867	26	60.5	473	2	T07548	photosystem II chl
868	26	60.5	474	2	B69470	lipase homolog - A
869	26	60.5	483	2	S76583	hypothetical prote
870	26	60.5	486	2	C96699	hypothetical prote
871	26	60.5	487	2	E70961	hypothetical prote
872	26	60.5	489	2	G64039	hypothetical prote
873	26	60.5	490	1	O4RBP2	laurate omega-minu
874	26	60.5	491	2	T01856	hypothetical prote
875	26	60.5	492	2	C83592	hypothetical prote
876	26	60.5	494	2	B89827	hypothetical prote
877	26	60.5	494	2	A40860	probable protein k
878	26	60.5	495	2	G84675	probable cytochrom
879	26	60.5	497	2	T23563	hypothetical prote
880	26	60.5	498	2	A55622	cytochrome P450 C1
881	26	60.5	500	2	JX0252	aldosterone syntha
882	26	60.5	501	2	S70171	integral membrane
883	26	60.5	509	1	S04346	steroid 17alpha-mo
884	26	60.5	510	2	D86249	hypothetical prote
885	26	60.5	510	2	A35342	steroid 11beta-mon
886	26	60.5	518	2	T05876	cytochrome P450 ho
887	26	60.5	520	2	S47142	mating type A prot
888	26	60.5	524	2	AI0544	probable rtn prote
889	26	60.5	531	2	T16263	hypothetical prote
890	26	60.5	532	2	T39459	repressible alkali
891	26	60.5	533	2	AG2328	2,3-bisphosphoglyc
892	26	60.5	533	2	T00742	ubiquitin-binding
893	26	60.5	535	2	T03260	cytochrome P450 -
894	26	60.5	535	2	T03246	cytochrome p450 -
895	26	60.5	535	2	E87656	hypothetical prote
896	26	60.5	539	2	T27559	hypothetical prote
897	26	60.5	546	2	A61209	hypertension-assoc
898	26	60.5	547	2	T29717	hypothetical prote
899	26	60.5	548	2	T23436	hypothetical prote
900	26	60.5	563	1	C69549	iron (II) transpor
901	26	60.5	565	2	T29718	hypothetical prote
902	26	60.5	565	2	C82280	sensor kinase citA
903	26	60.5	566	2	S62482	serine/threonine p
904	26	60.5	570	2	AF0277	phage hypothetical
905	26	60.5	579	2	AE1855	hypothetical prote
906	26	60.5	580	2	S49308	beta-fructofuranos
907	26	60.5	582	2	S37047	beta-fructofuranos
908	26	60.5	588	2	B65168	probable adenine d
909	26	60.5	588	2	B91204	probable adenine d
910	26	60.5	588	2	D86050	probable adenine d
911	26	60.5	590	2	T02096	probable beta-fruc
912	26	60.5	592	2	S61503	beta-fructofuranos
913	26	60.5	592	2	S56681	beta-fructofuranos
914	26	60.5	592	2	JQ0991	beta-fructofuranos
915	26	60.5	605	2	S74455	ABC-type transport
916	26	60.5	608	2	F83397	probable peptidase
917	26	60.5	611	2	T27013	hypothetical prote
918	26	60.5	617	2	S14278	noradrenaline tran
919	26	60.5	621	2	S70121	signal recognition
920	26	60.5	630	2	S37663	peplomeric polypro
921	26	60.5	633	2	F96652	protein F23N19.13
922	26	60.5	633	2	T17262	hypothetical prote
923	26	60.5	634	2	T36614	hypothetical prote
924	26	60.5	649	2	T05630	hypothetical prote
925	26	60.5	649	2	T01106	hypothetical prote
926	26	60.5	656	2	T23338	hypothetical prote
927	26	60.5	661	2	F83342	probable cation-tr
928	26	60.5	669	2	T28754	hypothetical prote
929	26	60.5	680	2	T42923	infected cell prot
930	26	60.5	685	2	A81246	methionyl-tRNA syn
931	26	60.5	691	2	B71322	probable excinucle
932	26	60.5	715	1	TNBE77	77K alpha trans-in
933	26	60.5	716	2	T47449	hypothetical prote
934	26	60.5	716	2	A86181	hypothetical prote
935	26	60.5	718	1	TNBEF6	77K alpha trans-in
936	26	60.5	725	1	Z2BPA4	rapid lysis protei
937	26	60.5	725	2	H81030	TonB-dependent rec
938	26	60.5	725	2	D81976	probable ferric si
939	26	60.5	727	2	F95422	catalase (EC 1.11.
940	26	60.5	729	2	T46328	probable adenosine
941	26	60.5	735	2	S76425	hypothetical prote
942	26	60.5	740	2	T45091	catalase (EC 1.11.
943	26	60.5	741	2	T20314	hypothetical prote
944	26	60.5	754	2	S71783	ETR1 protein homol
945	26	60.5	754	2	T52288	ethylene receptor
946	26	60.5	758	2	I64084	hemoglobin recepto
947	26	60.5	771	2	C70716	probable DNA helic
948	26	60.5	772	2	D95858	probable aldehyde
949	26	60.5	778	2	A86928	probable ATP-depen
950	26	60.5	779	1	S61571	suppressor protein
951	26	60.5	779	1	S40382	box A-binding fact
952	26	60.5	781	2	F82584	catalase/peroxidas
953	26	60.5	786	2	T08664	Toll protein-like
954	26	60.5	788	2	C70441	lipoate-protein li
955	26	60.5	798	2	JC7500	qik protein - chic
956	26	60.5	808	2	F70747	probable uridylylt
957	26	60.5	817	2	T01866	hypothetical prote
958	26	60.5	821	2	E87503	1,4-beta-D-glucan
959	26	60.5	825	2	S28478	rfbN protein - Vib
960	26	60.5	825	2	B82347	acyl protein synth
961	26	60.5	830	2	AH0477	probable TonB depe
962	26	60.5	835	2	T34770	probable protein p
963	26	60.5	839	2	T21207	hypothetical prote
964	26	60.5	843	1	JQ2229	DNA-directed DNA p
965	26	60.5	846	2	A30889	integrin beta chai
966	26	60.5	853	2	AD0544	outer membrane fim
967	26	60.5	858	2	D83491	probable sensor/re
968	26	60.5	860	2	JC5986	A-kinase anchoring
969	26	60.5	863	2	H84490	hypothetical prote
970	26	60.5	871	2	AE3085	two component sens
971	26	60.5	873	2	T12535	hypothetical prote
972	26	60.5	878	2	H83184	phosphoenolpyruvat
973	26	60.5	880	2	D98201	hypothetical prote
974	26	60.5	899	2	T42976	hypothetical prote
975	26	60.5	900	1	GNNYMV	genome polyprotein
976	26	60.5	905	1	S25564	DNA-directed RNA p
977	26	60.5	907	2	B75182	DNA-directed RNA p
978	26	60.5	907	2	H71031	probable DNA-direc

979	26	60.5	907	2	JE0176	orphan G protein-c
980	26	60.5	909	2	AG3419	phage host specifi
981	26	60.5	919	2	S45298	retinoblastoma-ass
982	26	60.5	921	2	A33718	retinoblastoma pro
983	26	60.5	923	2	T41350	meiotic recombinat
984	26	60.5	925	2	A55748	protein kinase (EC
985	26	60.5	926	2	T16184	hypothetical prote
986	26	60.5	928	1	RBHU	retinoblastoma-ass
987	26	60.5	934	1	S42874	oxoglutarate dehyd
988	26	60.5	939	2	G75481	sensory box/GGDEF
989	26	60.5	940	2	A38149	RNA-directed RNA p
990	26	60.5	949	2	T44577	hypothetical prote
991	26	60.5	952	1	QYMG	phosphoenolpyruvat
992	26	60.5	956	2	S40304	phosphoenolpyruvat
993	26	60.5	960	1	QYIX2	phosphoenolpyruvat
994	26	60.5	960	2	JH0381	phosphoenolpyruvat
995	26	60.5	960	2	S31159	phosphoenolpyruvat
996	26	60.5	960	2	S22507	phosphoenolpyruvat
997	26	60.5	960	2	S18240	phosphoenolpyruvat
998	26	60.5	963	2	S49344	phosphoenolpyruvat
999	26	60.5	964	1	QYNT	phosphoenolpyruvat
1000	26	60.5	964	2	T08138	phosphoenolpyruvat

ALIGNMENTS

RESULT 1
S42466
Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42466
R;Shiyanov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
submitted to the EMBL Data Library, March 1994
A;Reference number: S42466
A;Accession: S42466
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-117 <SHI>
A;Cross-references: UNIPARC:UPI00001161DC; EMBL:X78108; NID:g460824; PIDN:CAA54998.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;26-100/Domain: immunoglobulin homology <IMM>

Query Match 88.4%; Score 38; DB 2; Length 117;
Best Local Similarity 85.7%; Pred. No. 1.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
| |||||
Db 60 WASTRHT 66

RESULT 2
PL0207
anti-idiotypic antibody E225, kappa chain V region precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C;Accession: PL0207
R;Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.
Mol. Immunol. 27, 429-433, 1990
A;Title: Nucleotide sequence of the VH, VL regions of an anti-idiotopic antibody reactin
A;Reference number: PL0207; MUID:90309764; PMID:1973259
A;Accession: PL0207
A;Molecule type: mRNA
A;Residues: 1-131 <SOU>
A;Cross-references: UNIPARC:UPI000017678F
A;Note: This sequence corresponds to subgroup V mouse immunoglobulin light chain
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-20/Domain: signal sequence #status predicted <SIG>
F;36-110/Domain: immunoglobulin homology <IMM>
F;44-54/Region: complementarity-determining 1
F;70-76/Region: complementarity-determining 2
F;109-117/Region: complementarity-determining 3
F;116-127/Region: J region

Query Match 88.4%; Score 38; DB 2; Length 131;
Best Local Similarity 85.7%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
| |||||
Db 70 WASTRHT 76

RESULT 3
S30751
Ig kappa chain precursor V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 21-Jan-2000
C;Accession: S30751
R;Grant, F.J.; Levin, S.D.; Gilbert, T.; Kindsvogel, W.
Nucleic Acids Res. 15, 5496, 1987
A;Title: Improved RNA sequencing method to determine immunoglobulin mRNA sequence.
A;Reference number: S30751; MUID:87260030; PMID:3601683
A;Accession: S30751
A;Molecule type: mRNA
A;Residues: 1-152 <GRA>
A;Cross-references: UNIPARC:UPI0000115D91; EMBL:X05877; NID:g52195; PIDN:CAA29301.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;45-119/Domain: immunoglobulin homology <IMM>
F;138-152/Domain: C region (C-kappa) (fragment) #status predicted <CRE>

Query Match 88.4%; Score 38; DB 2; Length 152;
Best Local Similarity 85.7%; Pred. No. 1.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
| |||||
Db 79 WASTRHT 85

RESULT 4
T01897
ethylene-response protein ETR1 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 05-Oct-2004
C;Accession: T01897
R;Knoester, M.; Hennig, J.; Van Loon, L.C.; Bol, J.F.; Linthorst, H.J.M.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z14452
A;Accession: T01897
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-738 <KNO>
A;Cross-references: UNIPROT:O48929; UNIPARC:UPI000012A264; EMBL:AF022727; NID:g2655060; P
A;Experimental source: cultivar Samsun NN
C;Superfamily: Hybrid-type ethylene sensor histidine kinase; response regulator homology
C;Keywords: phosphoprotein
F;614-726/Domain: response regulator homology <RRH>
F;661/Binding site: phosphate (Asp) (covalent) #status predicted

Query Match 86.0%; Score 37; DB 2; Length 738;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|||| ||
Db 73 WTSTAHT 79

RESULT 5
B69676
alkaline phosphatase (EC 3.1.3.1) IV precursor - Bacillus subtilis

N;Alternate names: alkaline phosphatase A (phoA); alkaline phosphomonoesterase; glycerop
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C;Accession: B69676; A53375; A39096; JQ0808
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: B69676
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-461 <KUN>
A;Cross-references: UNIPROT:P19406; UNIPARC:UPI0000060142; GB:Z99109; GB:AL009126; NID:g
A;Experimental source: strain 168
R;Hulett, F.M.; Lee, J.; Shi, L.; Sun, G.; Chesnut, R.; Sharkova, E.; Duggan, M.F.; Kapp
J. Bacteriol. 176, 1348-1358, 1994
A;Title: Sequential action of two-component genetic switches regulates the PHO regulon i
A;Reference number: A53375; MUID:94156839; PMID:8113174
A;Accession: A53375
A;Molecule type: DNA
A;Residues: 4-84 <HUL1>
A;Cross-references: UNIPARC:UPI000017594C; GB:U02550; NID:g470382
R;Hulett, F.M.; Kim, E.E.; Bookstein, C.; Kapp, N.V.; Edwards, C.W.; Wyckoff, H.W.
J. Biol. Chem. 266, 1077-1084, 1991
A;Title: Bacillus subtilis alkaline phosphatases III and IV. Cloning, sequencing, and co
.
A;Reference number: A39096; MUID:91093215; PMID:1898729
A;Accession: A39096
A;Molecule type: DNA
A;Residues: 39-461 <HUL2>
A;Cross-references: UNIPARC:UPI000017594D; GB:M37165; NID:g470382
R;Kapp, N.V.; Edwards, C.W.; Chesnut, R.S.; Hulett, F.M.
Gene 96, 95-100, 1990
A;Title: The Bacillus subtilis phoAIV gene; effects of in vitro inactivation on total al
A;Reference number: JQ0808; MUID:91092508; PMID:2125017
A;Accession: JQ0808
A;Molecule type: DNA
A;Residues: 39-142 <KAP>
A;Cross-references: UNIPARC:UPI000017594E
C;Genetics:
A;Gene: phoA; phoAIV
A;Map position: 73 min
C;Superfamily: Alkaline phosphatase
C;Keywords: phosphoprotein; phosphoric monoester hydrolase
F;1-41/Domain: signal sequence #status predicted <SIG>
F;42-461/Product: alkaline phosphatase IV #status experimental <MAT>

```
  Query Match             83.7%;  Score 36;  DB 2;  Length 461;
  Best Local Similarity   85.7%;  Pred. No. 15;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||| ||
Db        418 WTSTDHT 424
```

RESULT 6
T06271
probable ethylene-response protein ETR2 - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Oct-2004
C;Accession: T06271; T07847
R;Lashbrook, C.C.; Tieman, D.M.; Klee, H.J.
submitted to the EMBL Data Library, January 1998
A;Description: Differential regulation of the tomato ETR gene family throughout plant dev
A;Reference number: Z15580
A;Accession: T06271
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-736 <LAS>
A;Cross-references: UNIPROT:O49187; UNIPARC:UPI000012A265; EMBL:AF043085; NID:g2852992; P
A;Experimental source: cultivar Rutgers
R;Tucker, M.L.
submitted to the EMBL Data Library, January 1996
A;Reference number: Z16172
A;Accession: T07847
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 31-473,'E',475-736 <TUC>
A;Cross-references: UNIPARC:UPI000016DF79; EMBL:U47279; NID:g1272245; PIDN:AAB39386.1; PI
A;Experimental source: strain UC82-B; clone TFE27
C;Genetics:
A;Gene: ETR2; ETR1
C;Superfamily: Hybrid-type ethylene sensor histidine kinase; response regulator homology
F;614-726/Domain: response regulator homology <RRH>

```
  Query Match             83.7%;  Score 36;  DB 2;  Length 736;
  Best Local Similarity   85.7%;  Pred. No. 24;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||| ||
Db         73 WTSTPHT 79
```

RESULT 7
T32807
hypothetical protein F52C6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32807
R;Wamsley, P.; Gibson, A.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid F52C6.
A;Reference number: Z21226
A;Accession: T32807
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-195 <WAM>
A;Cross-references: UNIPROT:O44821; UNIPARC:UPI0000164080; EMBL:AF040645; PIDN:AAB94971.1
A;Experimental source: strain Bristol N2; clone F52C6
C;Genetics:
A;Gene: CESP:F52C6.2
A;Map position: 2
A;Introns: 38/1; 110/2

```
  Query Match             79.1%;  Score 34;  DB 2;  Length 195;
  Best Local Similarity   83.3%;  Pred. No. 15;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRH 6
              |||:||
Db        185 WTSSRH 190
```

RESULT 8
S64140
hypothetical protein YGL129c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G2856
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: S64140; S31267; S63784; S72397
R;Cerdan, E.; Rodriguez-Torres, A.M.; Rodriguez-Belmonte, E.; Tizon, B.; Cadahia, J.L.; C
submitted to the Protein Sequence Database, May 1996

A;Reference number: S64134
A;Accession: S64140
A;Molecule type: DNA
A;Residues: 1-488 <CER>
A;Cross-references: UNIPROT:Q01163; UNIPARC:UPI0000053097; EMBL:Z72651; NID:g1322694; PI
A;Experimental source: strain S288C
R;Shibagaki, Y.; Itoh, N.; Yamada, H.; Nagata, S.; Mizumoto, K.
J. Biol. Chem. 267, 9521-9528, 1992
A;Title: mRNA capping enzyme. Isolation and characterization of the gene encoding mRNA g
A;Reference number: S31266; MUID:92250598; PMID:1315757
A;Accession: S31267
A;Molecule type: DNA
A;Residues: 39-488 <SHI>
A;Cross-references: UNIPARC:UPI0000168B65; EMBL:D10263; NID:g529646; PIDN:BAA01104.1; PI
R;Rodriguez-Belmonte, E.; Rodriguez-Torres, A.M.; Tizon, B.; Cadahia, J.L.; Gonzalez-Sis
Yeast 12, 145-148, 1996
A;Title: Sequence analysis of a 10 kb DNA fragment from yeast chromosome VII reveals a r
A;Reference number: S63783; MUID:96287651; PMID:8686378
A;Accession: S63784
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-188,'VG',191,'EP',194-488 <ROD>
A;Cross-references: UNIPARC:UPI000017CCFF; EMBL:X87252
R;Cerdan, E.
submitted to the EMBL Data Library, May 1995
A;Reference number: S72397
A;Accession: S72397
A;Molecule type: DNA
A;Residues: 1-488 <CEW>
A;Cross-references: UNIPARC:UPI0000053097; EMBL:X87252; NID:g1246906; PIDN:CAA60702.1; P
C;Genetics:
A;Gene: SGD:RSM23
A;Cross-references: SGD:S0003097
A;Map position: 7L
A;Note: YGL129c

Query Match 79.1%; Score 34; DB 2; Length 488;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
||:| ||
Db 98 WTNTTHT 104

RESULT 9
A69166
5-methylcytosine-specific restriction enzyme McrB related protein - Methanobacterium the
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: A69166
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: A69166
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-546 <MTH>
A;Cross-references: UNIPROT:O26601; UNIPARC:UPI0000066614; GB:AE000833; GB:AE000666; NID
A;Experimental source: strain Delta H
C;Genetics:
A;Gene: MTH501
A;Start codon: GTG

Query Match 79.1%; Score 34; DB 2; Length 546;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRH 6
|| |||
Db 277 WTETRH 282

RESULT 10
T07184
subtilisin-like proteinase (EC 3.4.21.-) precursor P69B, pathogenesis-related - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C;Accession: T07184
R;Tornero, P.; Conejero, V.; Vera, P.
J. Biol. Chem. 272, 14412-14419, 1997
A;Title: Identification of a new pathogen-induced member of the subtilisin-like processir
A;Reference number: Z15980; MUID:97306355; PMID:9162080
A;Accession: T07184
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-745 <TOR>
A;Cross-references: UNIPROT:O04678; UNIPARC:UPI00000ACD2F; EMBL:Y10149; NID:g2230958; PII
A;Experimental source: cultivar Rutgers; leaf
C;Genetics:
A;Gene: P69B
C;Superfamily: subtilisin-like proteinase ag12; subtilisin homology
C;Keywords: hydrolase; serine proteinase
F;1-115/Domain: signal sequence and amino-terminal propeptide #status predicted <PRO>
F;115-745/Product: subtilisin-like proteinase #status predicted <MAT>

Query Match 79.1%; Score 34; DB 2; Length 745;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
||| ||:
Db 729 WTSNRHS 735

RESULT 11
JC6119
subtilisin-like proteinase (EC 3.4.21.-) - tomato
N;Alternate names: calcium-activated andopeptidase; proteinase p69
C;Species: Lycopersicon esculentum (tomato)
C;Date: 23-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C;Accession: JC6119
R;Tornero, P.; Conejero, V.; Vera, P.
Proc. Natl. Acad. Sci. U.S.A. 93, 6332-6337, 1996
A;Title: Primary structure and expression of a pathogen-induced protease (PR-P69) in toma
A;Reference number: JC6119; MUID:96270538; PMID:8692815
A;Accession: JC6119
A;Molecule type: mRNA
A;Residues: 1-745 <TOR>
A;Cross-references: UNIPROT:Q96478; UNIPARC:UPI00000ACE71; EMBL:X95270; NID:g1524114; PII
C;Comment: This enzyme, a secreted calcium-activated endopeptidase, is a plant pathogenes
fense against attacking pathogens.
C;Genetics:
A;Gene: p69
C;Superfamily: subtilisin-like proteinase ag12; subtilisin homology
C;Keywords: hydrolase; serine proteinase
F;137-546/Domain: subtilisin homology #status atypical <SBT>

Query Match 79.1%; Score 34; DB 2; Length 745;
Best Local Similarity 71.4%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
||| ||:
Db 728 WTSNRHS 734

RESULT 12
E82121
peptidase, insulinase family VC2072 [imported] - Vibrio cholerae (strain N16961 serogroup
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 31-Dec-2004
C;Accession: E82121

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: E82121
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-939 <HEI>
A;Cross-references: UNIPROT:Q9KQC8; UNIPARC:UPI00000C31CC; GB:AE004281; GB:AE003852; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2072
A;Map position: 1
C;Superfamily: insulin-degrading enzyme (IDE)/zinc protease

 Query Match 79.1%; Score 34; DB 2; Length 939;
 Best Local Similarity 71.4%; Pred. No. 80;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|| | ||
Db 104 WTGTEHT 110

RESULT 13
G90732
hypothetical protein ECs0831 [imported] - Escherichia coli (strain O157:H7, substrain RI
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: G90732
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G90732
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <HAY>
A;Cross-references: UNIPROT:Q8X863; UNIPARC:UPI00000D0993; GB:BA000007; PIDN:BAB34254.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0831

 Query Match 74.4%; Score 32; DB 2; Length 91;
 Best Local Similarity 83.3%; Pred. No. 16;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRH 6
|| |||
Db 74 WTVTRH 79

RESULT 14
A85583
unknown protein encoded by prophage CP-933K [imported] - Escherichia coli (strain O157:H
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: A85583
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85583
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <STO>
A;Cross-references: UNIPROT:Q8X863; UNIPARC:UPI00000D0993; GB:AE005174; NID:g12513737; P
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z0969

 Query Match 74.4%; Score 32; DB 2; Length 91;
 Best Local Similarity 83.3%; Pred. No. 16;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRH 6
|| |||
Db 74 WTVTRH 79

RESULT 15
E86962
probable oxidoreductase ML0429 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 05-Oct-2004
C;Accession: E86962
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hor R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squ
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: E86962
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-268 <STO>
A;Cross-references: UNIPROT:O07709; UNIPARC:UPI00000D438C; GB:AL450380; NID:g13092684; PI
C;Genetics:
A;Gene: ML0429
C;Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology

 Query Match 74.4%; Score 32; DB 2; Length 268;
 Best Local Similarity 71.4%; Pred. No. 52;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
| || ||
Db 212 WISTEHT 218

RESULT 16
E70551
probable oxidoreductase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 05-Oct-2004
C;Accession: E70551
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S., Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: E70551
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-268 <COL>
A;Cross-references: UNIPROT:O06172; UNIPARC:UPI00000D5E68; GB:Z95556; GB:AL123456; NID:g
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv2509
C;Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology
F;10-188/Domain: short-chain alcohol dehydrogenase homology <SADH>

 Query Match 74.4%; Score 32; DB 2; Length 268;
 Best Local Similarity 71.4%; Pred. No. 52;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
| || ||
Db 212 WISTEHT 218

RESULT 17
AF3187
flavin-dependent oxidoreductase Atu5227 [imported] - Agrobacterium tumefaciens (strain C
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF3187
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF3187
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-358 <KUR>
A;Cross-references: UNIPROT:Q8UK96; UNIPARC:UPI00000D1544; GB:AE008687; PIDN:AAL45916.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu5227
A;Genome: plasmid
C;Superfamily: alkanal monooxygenase [FMN-linked] (bacterial luciferase)

 Query Match 74.4%; Score 32; DB 2; Length 358;
 Best Local Similarity 71.4%; Pred. No. 71;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
||| ||
Db 41 WTSEHHT 47

RESULT 18
S38744
serotonin receptor 5B - rat
N;Alternate names: 5-hydroxytryptamine receptor 5B (5-HTR5B)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S38744; A47472
R;Wisden, W.; Parker, E.M.; Mahle, C.D.; Grisel, D.A.; Nowak, H.P.; Yocca, F.D.; Felder,
FEBS Lett. 333, 25-31, 1993
A;Title: Cloning and characterization of the rat 5-HT(5B) receptor. Evidence that the 5-
A;Reference number: S38744; MUID:94039744; PMID:8224165
A;Accession: S38744
A;Molecule type: mRNA
A;Residues: 1-369 <WIS>
A;Cross-references: UNIPROT:P35365; UNIPARC:UPI000004477D
R;Erlander, M.G.; Lovenberg, T.W.; Baron, B.M.; de Lecea, L.; Danielson, P.E.; Racke, M.
Proc. Natl. Acad. Sci. U.S.A. 90, 3452-3456, 1993
A;Title: Two members of a distinct subfamily of 5-hydroxytryptamine receptors differenti
A;Reference number: A47472; MUID:93234515; PMID:7682702
A;Accession: A47472
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-176,'I',177-369 <ERL>
A;Cross-references: UNIPARC:UPI000004477C; GB:L10073; NID:g310074; PIDN:AAA40616.1; PID:
A;Experimental source: hypothalamus
A;Note: sequence extracted from NCBI backbone (NCBIN:129665, NCBIP:129668)
C;Superfamily: octopamine receptor type I
C;Keywords: G protein-coupled receptor; transmembrane protein

 Query Match 74.4%; Score 32; DB 2; Length 369;
 Best Local Similarity 83.3%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRH 6
|| |||
Db 154 WTITRH 159

RESULT 19
I48231
serotonin receptor 5B - mouse
N;Alternate names: 5-hydroxytryptamine 5B receptor (5HTR-5C)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48231
R;Matthes, H.; Boschert, U.; Amlaiky, N.; Grailhe, R.; Plassat, J.L.; Muscatelli, F.; Mat
Mol. Pharmacol. 43, 313-319, 1993
A;Title: Mouse 5-hydroxytryptamine5A and 5-hydroxytryptamine5B receptors define a new fan
A;Reference number: I48231; MUID:93196607; PMID:8450829
A;Accession: I48231
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-370 <RES>
A;Cross-references: UNIPROT:P31387; UNIPARC:UPI0000029AC0; EMBL:X69867; NID:g288735; PIDN
C;Superfamily: octopamine receptor type I
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmem

 Query Match 74.4%; Score 32; DB 2; Length 370;
 Best Local Similarity 83.3%; Pred. No. 74;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRH 6
|| |||
Db 154 WTITRH 159

RESULT 20
AE1073
phosphopentomutase (EC 5.4.2.7) [imported] - Salmonella enterica subsp. enterica serovar
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AE1073
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AE1073
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-407 <PAR>
A;Cross-references: UNIPARC:UPI000005A9E2; GB:AL513382; PIDN:CAD03404.1; PID:g16505673; C
C;Genetics:
A;Gene: deoB
C;Superfamily: phosphopentomutase
C;Keywords: intramolecular transferase; isomerase

 Query Match 74.4%; Score 32; DB 2; Length 407;
 Best Local Similarity 71.4%; Pred. No. 82;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|| | ||
Db 354 WTGTDHT 360

RESULT 21
F91296
phosphopentomutase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: F91296
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genon
A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: F91296
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-407 <HAY>
A;Cross-references: UNIPROT:P07651; UNIPARC:UPI00000380EF; GB:BA000007; PIDN:BAB38765.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs5342
C;Superfamily: phosphopentomutase

Query Match 74.4%; Score 32; DB 2; Length 407;
Best Local Similarity 71.4%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|| | ||
Db 354 WTGTDHT 360

RESULT 22
H86137
phosphopentomutase [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H86137
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H86137
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-407 <STO>
A;Cross-references: UNIPROT:P07651; UNIPARC:UPI00000380EF; GB:AE005174; NID:g12519410; P
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: deoB
C;Superfamily: phosphopentomutase

Query Match 74.4%; Score 32; DB 2; Length 407;
Best Local Similarity 71.4%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|| | ||
Db 354 WTGTDHT 360

RESULT 23
S56607
phosphopentomutase (EC 5.4.2.7) deoB - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S56607; B22909; F65253
R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
A;Reference number: S56314; MUID:95334362; PMID:7610040
A;Accession: S56607
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-407 <BUR>
A;Cross-references: UNIPROT:P07651; UNIPARC:UPI00000380EF; EMBL:U14003; NID:g1263172; PI
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
R;Valentin-Hansen, P.; Hammer, K.; Larsen, J.E.L.; Svendsen, I.
Nucleic Acids Res. 12, 5211-5224, 1984
A;Title: The internal regulated promoter of the deo operon of Escherichia coli K-12.
A;Reference number: A93525; MUID:84272212; PMID:6087276
A;Accession: B22909
A;Molecule type: DNA
A;Residues: 1-37 <VAL>
A;Cross-references: UNIPARC:UPI000016F0C3; GB:X00742; NID:g41249; PIDN:CAA25325.1; PID:g

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F65253
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-407 <BLAT>
A;Cross-references: UNIPARC:UPI00000380EF; GB:AE000508; GB:U00096; NID:g2367382; PIDN:AAC
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: deoB
A;Map position: 100 min
C;Superfamily: phosphopentomutase
C;Keywords: intramolecular transferase; isomerase

Query Match 74.4%; Score 32; DB 2; Length 407;
Best Local Similarity 71.4%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|| | ||
Db 354 WTGTDHT 360

RESULT 24
AG1697
hypothetical protein homolog lin2121 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Dec-2002
C;Accession: AG1697
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AG1697
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-434 <GLA>
A;Cross-references: UNIPARC:UPI00000CC770; GB:AL592022; PIDN:CAC97351.1; PID:g16414635; C
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2121
C;Superfamily: uncharacterized conserved protein

Query Match 74.4%; Score 32; DB 2; Length 434;
Best Local Similarity 71.4%; Pred. No. 88;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
| || ||
Db 147 WKSTNHT 153

RESULT 25
DEECPC
pyruvate dehydrogenase (cytochrome) (EC 1.2.2.2) - Escherichia coli (strain K-12)
N;Alternate names: pyruvate oxidase
C;Species: Escherichia coli
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 31-Dec-2004
C;Accession: A23648; G64825; I55291; I57856
R;Grabau, C.; Cronan Jr., J.E.
Nucleic Acids Res. 14, 5449-5460, 1986
A;Title: Nucleotide sequence and deduced amino acid sequence of Escherichia coli pyruvate
A;Reference number: A23648; MUID:86286555; PMID:3016647
A;Accession: A23648
A;Molecule type: DNA
A;Residues: 1-572 <GRA>

A;Cross-references: UNIPARC:UPI000004CE7A; GB:X04105; GB:M13947; GB:M13948; NID:g42472;
A;Experimental source: strain K-12
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: G64825
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-572 <BLAT>
A;Cross-references: UNIPARC:UPI000004CE7A; GB:AE000188; GB:U00096; NID:g1787084; PIDN:AA
A;Experimental source: strain K-12, substrain MG1655
R;Grabau, C.; Chang, Y.Y.; Cronan, J.E.
J. Biol. Chem. 264, 12510-12519, 1989
A;Title: Lipid binding by Escherichia coli pyruvate oxidase is disrupted by small altera
A;Reference number: I55291; MUID:89308683; PMID:2663858
A;Accession: I55291
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-363,'HE',366-413,'HGV',417-572 <RES>
A;Cross-references: UNIPARC:UPI000016F3FB; GB:M28208; NID:g1009024; PIDN:AAB59101.1; PID
A;Experimental source: strain K-12
R;Chang, Y.Y.; Wang, A.Y.; Cronan, J.E.
Mol. Microbiol. 11, 1019-1028, 1994
A;Title: Expression of Escherichia coli pyruvate oxidase (PoxB) depends on the sigma fac
A;Reference number: I57856; MUID:94293772; PMID:8022274
A;Accession: I57856
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-22 <RE2>
A;Cross-references: UNIPARC:UPI000016FFDB; GB:S73268; NID:g685127; PIDN:AAB31180.1; PID:
C;Comment: The sequence of this protein was shown to be homologous with those of the lar
ough pyruvate is the end product.
C;Comment: This protein is not to be confused with a similar enzyme, pyruvate (or pyruvi
ion of pyruvate to acetyl phosphate, carbon dioxide, and hydrogen peroxide.
C;Genetics:
A;Gene: poxB
A;Map position: 19 min
C;Complex: homotetramer
C;Function:
A;Description: catalyzes the conversion of pyruvate to acetate and carbon dioxide in the
A;Note: in the presence of pyruvate and cofactor thiamine pyrophosphate, the addition of
C;Superfamily: thiamine diphosphate-dependent enzyme, acetolactate synthase type; thiami
C;Keywords: FAD; flavoprotein; homotetramer; lipid binding; magnesium; membrane protein;
F;422-470/Domain: thiamin pyrophosphate-binding domain homology <TPB>
F;50/Active site: Glu #status predicted

Query Match 74.4%; Score 32; DB 1; Length 572;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRH 6
| ||||
Db 44 WMSTRH 49

RESULT 26
A85599
pyruvate oxidase poxB [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2004
C;Accession: A85599
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85599
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-572 <STO>
A;Cross-references: UNIPROT:Q8X6L4; UNIPARC:UPI00000D0B64; GB:AE005174; NID:g12513898; P
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: poxB
C;Superfamily: thiamine diphosphate-dependent enzyme, acetolactate synthase type; thiamir

Query Match 74.4%; Score 32; DB 2; Length 572;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRH 6
| ||||
Db 44 WMSTRH 49

RESULT 27
E90748
pyruvate oxidase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 31-Dec-2004
C;Accession: E90748
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genon
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E90748
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-572 <HAY>
A;Cross-references: UNIPROT:Q8X6L4; UNIPARC:UPI00000D0B64; GB:BA000007; PIDN:BAB34380.1,
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0957
C;Superfamily: thiamine diphosphate-dependent enzyme, acetolactate synthase type; thiamir

Query Match 74.4%; Score 32; DB 2; Length 572;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRH 6
| ||||
Db 44 WMSTRH 49

RESULT 28
AB0915
probable transferase [imported] - Salmonella enterica subsp. enterica serovar Typhi (stra
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0915
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0915
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-607 <PAR>
A;Cross-references: UNIPARC:UPI000005A555; GB:AL513382; PIDN:CAD07912.1; PID:g16504457; (
C;Genetics:
A;Gene: STY3579

Query Match 74.4%; Score 32; DB 2; Length 607;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|| |:||
Db 458 WTWTQHT 464

```
RESULT 29
T33231
hypothetical protein T10B5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33231
R;Geisel, C.; Bradshaw, H.; O'Brien, D.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid T10B5.
A;Reference number: Z21305
A;Accession: T33231
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-712 <GEI>
A;Cross-references: UNIPROT:O76408; UNIPARC:UPI0000076EB3; EMBL:AF067947; PIDN:AAC19226.
A;Experimental source: strain Bristol N2; clone T10B5
C;Genetics:
A;Gene: CESP:T10B5.2
A;Map position: 5
A;Introns: 12/1; 39/3; 95/3; 123/3; 186/3; 255/1; 500/2; 544/3; 580/3; 621/2

  Query Match             74.4%;  Score 32;  DB 2;  Length 712;
  Best Local Similarity   83.3%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRH 6
              || |||
Db        405 WTLTRH 410


RESULT 30
A88483
protein C05D11.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A88483
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: A88483
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-995 <STO>
A;Cross-references: UNIPROT:P48053; UNIPARC:UPI000013BDA4; GB:chr_III; PIDN:AAB53833.1;
C;Genetics:
A;Gene: C05D11.1
A;Map position: 3

  Query Match             74.4%;  Score 32;  DB 2;  Length 995;
  Best Local Similarity   71.4%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              || | ||
Db         94 WTDTDHT 100


RESULT 31
T38841
probable pre-mRNA splicing factor - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38841
R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1995
A;Reference number: Z21815
A;Accession: T38841
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2363 <GEN>
A;Cross-references: UNIPROT:O14187; UNIPARC:UPI000006A413; EMBL:Z98530; PIDN:CAB11062.1;
A;Experimental source: strain 972h-; cosmid c4F8
C;Genetics:
A;Gene: SPDB:SPAC4F8.12c
A;Map position: 1

  Query Match             74.4%;  Score 32;  DB 2;  Length 2363;
  Best Local Similarity   83.3%;  Pred. No. 5.5e+02;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRH 6
              ||| ||
Db       1479 WTSQRH 1484


RESULT 32
A57096
nudel protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 27-Oct-1995 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C;Accession: A57096
R;Hong, C.C.; Hashimoto, C.
Cell 82, 785-794, 1995
A;Title: An unusual mosaic protein with a protease domain, encoded by the nudel gene, is
A;Reference number: A57096; MUID:95401268; PMID:7671306
A;Accession: A57096
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-2616 <HON>
A;Cross-references: UNIPROT:P98159; UNIPARC:UPI000012FED5; GB:U29153; NID:g984320; PIDN:A
C;Genetics:
A;Gene: FlyBase:ndl
A;Cross-references: FlyBase:FBgn0002926
C;Superfamily: nudel protein; LDL receptor ligand-binding repeat homology; trypsin homolo
C;Keywords: extracellular protein
F;891-929/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;1145-1378/Domain: trypsin homology <TRY>
F;1396-1430/Domain: LDL receptor ligand-binding repeat homology <LDL7>
F;1776-1811/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;2310-2344/Domain: LDL receptor ligand-binding repeat homology <LDL8>
F;2351-2387/Domain: LDL receptor ligand-binding repeat homology <LDL5>
F;2421-2457/Domain: LDL receptor ligand-binding repeat homology <LDL3>

  Query Match             74.4%;  Score 32;  DB 2;  Length 2616;
  Best Local Similarity   57.1%;  Pred. No. 6.1e+02;
  Matches    4;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||:::||
Db       2472 WTNSQHT 2478


RESULT 33
A58955
metalloendoproteinase (EC 3.4.24.-) - honey fungus (fragment)
C;Species: Armillaria mellea (honey fungus)
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: A58955
R;Healy, V.; O'Connell, J.; McCarthy, T.V.; Doonan, S.
Biochem. Biophys. Res. Commun. 262, 60-63, 1999
A;Title: The lysine-specific proteinase from Armillaria mellea is a member of a novel cla
A;Reference number: A59052; MUID:99382241; PMID:10448068
A;Accession: A58955
A;Molecule type: protein
A;Residues: 1-26 <HEA>
A;Cross-references: UNIPROT:Q7M4T2; UNIPARC:UPI000017CAE5
A;Note: submitted to the Protein Sequence Database, April 1999
C;Keywords: hydrolase; metalloproteinase

  Query Match             72.1%;  Score 31;  DB 2;  Length 26;
  Best Local Similarity   71.4%;  Pred. No. 6.7;
```

```
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||:| |
Db          6 WTSSRQT 12


RESULT 34
A30503
Ig gamma-2b chain C region (E5.7A12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: A30503
R;Gilmore, G.L.; Bard, J.A.; Birshtein, B.K.
J. Immunol. 141, 1754-1761, 1988
A;Title: DNA rearrangements affecting both variable and constant regions of Ig H chain g
A;Reference number: A30503; MUID:88315788; PMID:2842402
A;Accession: A30503
A;Molecule type: mRNA
A;Residues: 1-88 <GIL>
A;Cross-references: UNIPARC:UPI0000176F07; GB:M21925
A;Experimental source: myeloma cell line MPC11
A;Note: the authors translated the codon GAG for residue 41 as Ser
C;Genetics:
A;Introns: 46/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-70/Domain: immunoglobulin homology <IMM>

  Query Match             72.1%;  Score 31;  DB 2;  Length 88;
  Best Local Similarity   71.4%;  Pred. No. 25;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||  ||
Db         77 WTSNGHT 83


RESULT 35
JC7376
hardening-inducible protein HIC12 - Chlorella vulgaris
C;Species: Chlorella vulgaris
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 09-Jul-2004
C;Accession: JC7376
R;Honjoh, K.; Matsumoto, H.; Shimizu, H.; Ooyama, K.; Tanaka, K.; Oda, Y.; Takata, R.; J
Biosci. Biotechnol. Biochem. 64, 1656-1663, 2000
A;Title: Cryoprotective activities of group 3 late embryogenesis abundant proteins from
A;Reference number: JC7376
A;Accession: JC7376
A;Molecule type: mRNA
A;Residues: 1-104 <HON>
A;Cross-references: UNIPROT:Q9SLP7; UNIPARC:UPI00000A7366; DDBJ:AB035642
A;Experimental source: strain IAM C-27
C;Comment: This protein, homolog of group 3 late embryogenesis abundant protein, has eff
C;Genetics:
A;Gene: hiC12

  Query Match             72.1%;  Score 31;  DB 2;  Length 104;
  Best Local Similarity   66.7%;  Pred. No. 30;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRH 6
              || |:|
Db         88 WTETKH 93


RESULT 36
B30503
Ig gamma-2a chain C region (E5.7A12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1989 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: B30503
R;Gilmore, G.L.; Bard, J.A.; Birshtein, B.K.
J. Immunol. 141, 1754-1761, 1988
A;Title: DNA rearrangements affecting both variable and constant regions of Ig H chain ge
A;Reference number: A30503; MUID:88315788; PMID:2842402
A;Accession: B30503
A;Molecule type: mRNA
A;Residues: 1-112 <GIL>
A;Cross-references: UNIPARC:UPI0000176F08; GB:M21925
A;Experimental source: myeloma cell line MPC11
A;Note: the authors translated the codon GAG for residue residue 11 as Ser
C;Genetics:
A;Introns: 100/3
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-70/Domain: immunoglobulin homology <IMM>

  Query Match             72.1%;  Score 31;  DB 2;  Length 112;
  Best Local Similarity   71.4%;  Pred. No. 32;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||  ||
Db        101 WTSNGHT 107


RESULT 37
T35320
probable membrane protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35320
R;Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1999
A;Reference number: Z21575
A;Accession: T35320
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-167 <OLI>
A;Cross-references: UNIPROT:Q9X7R2; UNIPARC:UPI00000DB0B7; EMBL:AL049863; PIDN:CAB42929 J
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC5H1.04c
C;Superfamily: Streptomyces coelicolor probable membrane protein SC5H1.04c

  Query Match             72.1%;  Score 31;  DB 2;  Length 167;
  Best Local Similarity   71.4%;  Pred. No. 50;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||  |||
Db        159 WTRHRHT 165


RESULT 38
S30968
major tail protein - Mycobacterium phage L5
C;Species: Mycobacterium phage L5
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S30968
R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.
Mol. Microbiol. 7, 407-417, 1993
A;Title: Superinfection immunity of mycobacteriophage L5: applications for genetic transf
A;Reference number: S30949; MUID:93211283; PMID:8459767
A;Accession: S30968
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-198 <DON>
A;Cross-references: UNIPROT:Q05229; UNIPARC:UPI0000164A91; EMBL:Z18946; NID:g15859; PIDN
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C;Genetics:
A;Gene: 23

  Query Match             72.1%;  Score 31;  DB 2;  Length 198;
  Best Local Similarity   71.4%;  Pred. No. 60;
```

```
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||  ||
Db         48 WTSVGHT 54


RESULT 39
CYBOB
beta-crystallin B2 [validated] - bovine
N;Alternate names: beta-crystallin chain Bp
C;Species: Bos primigenius taurus (cattle)
C;Date: 01-Sep-1981 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: A54730; A02924
R;Hogg, D.; Gorin, M.B.; Heinzmann, C.; Zollman, S.; Mohandas, T.; Klisak, I.; Sparkes,
Curr. Eye Res. 6, 1335-1342, 1987
A;Title: Nucleotide sequence for the cDNA of the bovine betaB2 crystallin and assignment
A;Reference number: A54730; MUID:88110635; PMID:3427982
A;Accession: A54730
A;Molecule type: mRNA
A;Residues: 1-205 <HOG>
A;Cross-references: UNIPROT:P02522; UNIPARC:UPI0000167C42; GB:M22466; NID:g162911; PIDN:
R;Driessen, H.P.C.; Herbrink, P.; Bloemendal, H.; de Jong, W.W.
Eur. J. Biochem. 121, 83-91, 1981
A;Title: Primary structure of the bovine beta-crystallin Bp chain. Internal duplication
A;Reference number: A02924; MUID:82117057; PMID:7035168
A;Accession: A02924
A;Molecule type: protein
A;Residues: 2-3,'N',5,'E',7-27,'H',29-31,'Q',33-34,'BPGB',39,'C',41-205 <DRI>
A;Cross-references: UNIPARC:UPI0000173D41
R;Bax, B.; Lapatto, R.; Nalini, V.; Driessen, H.; Lindley, P.F.; Mahadevan, D.; Blundell
submitted to the Brookhaven Protein Data Bank, September 1992
A;Reference number: A51450; PDB:2BB2
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 15-195
R;Bax, B.; Lapatlo, R.; Nalini, V.; Driessen, H.; Lindley, P.F.; Mahadevan, D.; Blundell
Nature 347, 776-780, 1990
A;Title: X-ray analysis of beta B2-crystallin and evolution of oligomeric lens proteins.
A;Reference number: A58563; MUID:91043031; PMID:2234050
A;Contents: annotation; X-ray crystallography, 2.1 angstroms
C;Superfamily: beta-crystallin
C;Keywords: acetylated amino end; duplication; eye lens
F;2-205/Product: beta-crystallin B2 #status experimental <MAT>
F;17-56/Domain: crystallin repeat <GK1>
F;57-101/Domain: crystallin repeat <GK2>
F;107-148/Domain: crystallin repeat <GK3>
F;149-191/Domain: crystallin repeat <GK4>
F;2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

  Query Match             72.1%;  Score 31;  DB 1;  Length 205;
  Best Local Similarity   71.4%;  Pred. No. 62;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||:| |
Db         85 WTSSRRT 91


RESULT 40
JC2009
beta-crystallin B2 - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C;Accession: JC2009
R;Chambers, C.; Russell, P.
Gene 133, 295-299, 1993
A;Title: Sequence of the human lens betaB2-crystallin-encoding cDNA.
A;Reference number: JC2009; MUID:94040827; PMID:8224918
A;Accession: JC2009
A;Molecule type: mRNA
A;Residues: 1-205 <CHA>
A;Cross-references: UNIPROT:P43320; UNIPARC:UPI000013C6A2; GB:L10035; NID:g401760; PIDN:
C;Superfamily: beta-crystallin
C;Keywords: duplication; eye lens

  Query Match             72.1%;  Score 31;  DB 2;  Length 205;
  Best Local Similarity   71.4%;  Pred. No. 62;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||:| |
Db         85 WTSSRRT 91


RESULT 41
JC4964
beta-B2-crystallin - golden hamster
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 09-Jul-2004
C;Accession: JC4964
R;Zarbalis, K.; Chatterjee, B.; Loester, J.; Werner, T.; Graw, J.
Gene 174, 181-184, 1996
A;Title: Sequence analysis of the beta-B2-crystallin cDNA of hamster containing a domain
A;Reference number: JC4964; MUID:97017145; PMID:8863746
A;Accession: JC4964
A;Molecule type: mRNA
A;Residues: 1-205 <ZAR>
A;Cross-references: UNIPROT:P26775; UNIPARC:UPI0000003F4B; EMBL:X94745; NID:g1154866; PII
C;Superfamily: beta-crystallin
C;Keywords: duplication; phosphoprotein
F;143/Binding site: phosphate (Ser) (covalent) #status predicted

  Query Match             72.1%;  Score 31;  DB 2;  Length 205;
  Best Local Similarity   71.4%;  Pred. No. 62;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||:| |
Db         85 WTSSRRT 91


RESULT 42
A39757
beta-crystallin B2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
C;Accession: A39757
R;Chambers, C.; Russell, P.
J. Biol. Chem. 266, 6742-6746, 1991
A;Title: Deletion mutation in an eye lens beta-crystallin. An animal model for inherited
A;Reference number: A39757; MUID:91201313; PMID:1707874
A;Accession: A39757
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-207 <CHA>
A;Cross-references: UNIPROT:P26775; UNIPARC:UPI0000177480; GB:M60559
C;Superfamily: beta-crystallin
C;Keywords: duplication

  Query Match             72.1%;  Score 31;  DB 2;  Length 207;
  Best Local Similarity   71.4%;  Pred. No. 63;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||:| |
Db         85 WTSSRRT 91


RESULT 43
QQBE26
BZLF2 protein - human herpesvirus 4 (strain B95-8)
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
C;Accession: F43042; A03767; S33016
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus.
```

A;Reference number: A93065; MUID:85035713; PMID:6092825
A;Accession: F43042
A;Molecule type: DNA
A;Residues: 1-223 <BAN>
A;Cross-references: UNIPROT:P03205; UNIPARC:UPI000000CDD8; EMBL:V01555; NID:g59074; PIDN
R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
Nature 310, 207-211, 1984
A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
A;Reference number: A03794; MUID:84270667; PMID:6087149
A;Contents: annotation; protein coding region
C;Superfamily: human herpesvirus 4 BZLF2 protein

Query Match 72.1%; Score 31; DB 1; Length 223;
Best Local Similarity 71.4%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|| | ||
Db 81 WTPTLHT 87

RESULT 44
AI3555
histidine utilization repressor [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AI3555
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AI3555
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-247 <KUR>
A;Cross-references: UNIPROT:Q8YD07; UNIPROT:Q8FVB7; UNIPARC:UPI0000058461; GB:AE008918;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0370
A;Map position: II

Query Match 72.1%; Score 31; DB 2; Length 247;
Best Local Similarity 57.1%; Pred. No. 76;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|:| :||
Db 182 WSSAKHT 188

RESULT 45
H75393
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: H75393
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: H75393
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-273 <WHI>
A;Cross-references: UNIPROT:Q9RUE5; UNIPARC:UPI00000C192D; GB:AE001989; GB:AE000513; NID
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1442
A;Map position: 1

Query Match 72.1%; Score 31; DB 2; Length 273;
Best Local Similarity 83.3%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WTSTRH 6
|||| |
Db 82 WTSTYH 87

RESULT 46
A36051
H+/K+-exchanging ATPase (EC 3.6.3.10) beta chain - rabbit
N;Alternate names: H+/K+-transporting ATPase beta chain
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 31-Dec-2004
C;Accession: A36051
R;Reuben, M.A.; Lasater, L.S.; Sachs, G.
Proc. Natl. Acad. Sci. U.S.A. 87, 6767-6771, 1990
A;Title: Characterization of a beta subunit of the gastric H+/K+-transporting ATPase.
A;Reference number: A36051; MUID:90370865; PMID:2168558
A;Accession: A36051
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-291 <REU>
A;Cross-references: UNIPROT:P18597; UNIPARC:UPI000012623C; GB:M35544; NID:g165031; PIDN
C;Superfamily: Na(+)/K(+)-exchanging ATPase beta-3 chain
C;Keywords: hydrolase; transmembrane protein

Query Match 72.1%; Score 31; DB 2; Length 291;
Best Local Similarity 71.4%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
||| ||
Db 106 WTSLTHT 112

RESULT 47
T24736
hypothetical protein T09E11.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24736
R;McLay, K.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19930
A;Accession: T24736
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-305 <WIL>
A;Cross-references: UNIPROT:Q9XVF9; UNIPARC:UPI000007AA66; EMBL:Z81147; PIDN:CAB03530.1;
A;Experimental source: clone T09E11
C;Genetics:
A;Gene: CESP:T09E11.3
A;Map position: 1
A;Introns: 32/1; 47/3; 95/2; 137/2; 237/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F49D11.3

Query Match 72.1%; Score 31; DB 2; Length 305;
Best Local Similarity 83.3%; Pred. No. 96;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRH 6
|||||:
Db 91 WTSTRN 96

RESULT 48
T17340
hypothetical protein DKFZp586D0624.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T17340

R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18727
A;Accession: T17340
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-315 <DUE>
A;Cross-references: UNIPROT:Q9UFI9; UNIPARC:UPI0000073768; EMBL:AL117654
A;Experimental source: adult uterus; clone DKFZp586D0624
C;Genetics:
A;Note: DKFZp586D0624.1

Query Match 72.1%; Score 31; DB 2; Length 315;
Best Local Similarity 71.4%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|| || |
Db 42 WTDTRET 48

RESULT 49
G2MSBM
Ig gamma-2b chain C region, membrane-bound form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Dec-1982 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: C02154; A02158; B02157
R;Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.
Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982
A;Title: Nucleotide sequences of gene segments encoding membrane domains of immunoglobul
A;Reference number: A02154; MUID:82222190; PMID:6283537
A;Accession: C02154
A;Molecule type: DNA
A;Residues: 335-405 <YAM>
A;Cross-references: UNIPROT:P01867; UNIPARC:UPI00001737A7; GB:J00462
R;Rogers, J.; Choi, E.; Souza, L.; Carter, C.; Word, C.; Kuehl, M.; Eisenberg, D.; Wall,
Cell 26, 19-27, 1981
A;Title: Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma c
A;Reference number: A02158; MUID:82115295; PMID:6799207
A;Accession: A02158
A;Molecule type: DNA
A;Residues: 335-378 <ROG>
A;Cross-references: UNIPARC:UPI00001737A8
A;Note: the translation of the first exon of the membrane-bound segment is given
R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from r
A;Reference number: A02157; MUID:80120716; PMID:6766534
A;Contents: a allele
A;Accession: B02157
A;Molecule type: DNA
A;Residues: 1-335,'K' <YA2>
A;Cross-references: UNIPARC:UPI00000272D2
C;Comment: The sequence of residues 1-334 was assumed to be identical with the corresponding
C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The ma
hat it contains an alternative 3' end, encoded in separate exons, that is homologous wit
C;Genetics:
A;Introns: 1/1; 98/1; 120/1; 230/1; 335/1; 378/3
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu
F;143-212/Domain: immunoglobulin homology <IMM>
F;352-369/Domain: transmembrane #status predicted <TMM>
F;370-405/Domain: intracellular #status predicted <INT>
F;186/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.1%; Score 31; DB 1; Length 405;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
||| ||
Db 270 WTSNGHT 276

RESULT 50
A47041
probable transposase - Alcaligenes eutrophus insertion sequence ISAE1
C;Species: Alcaligenes eutrophus
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 05-Oct-2004
C;Accession: A47041
R;Kung, S.S.; Chen, J.; Chow, W.Y.
J. Bacteriol. 174, 8023-8029, 1992
A;Title: Molecular and genetic characterization of an Alcaligenes eutrophus insertion ele
A;Reference number: A47041; MUID:93094133; PMID:1334068
A;Accession: A47041
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-408 <KUN>
A;Cross-references: UNIPROT:Q48349; UNIPARC:UPI00000B1BDB
A;Experimental source: strain H1, ATCC 17698
A;Note: sequence extracted from NCBI backbone (NCBIN:119957, NCBIP:119958)
C;Genetics:
A;Mobile element: insertion sequence ISAE1
C;Superfamily: transposase for insertion sequence element IS1557
C;Keywords: DNA binding

Query Match 72.1%; Score 31; DB 2; Length 408;
Best Local Similarity 71.4%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|| || |
Db 354 WTQTRQT 360

Search completed: March 23, 2006, 02:04:16
Job time : 28.6849 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:40:40 ; Search time 60.2192 Seconds
(without alignments)
82.012 Million cell updates/sec

Title: US-10-755-382-21
Perfect score: 43
Sequence: 1 WTSTRHT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	39	90.7	743	2	Q9LWA4_LYCES	Q9lwa4 lycopersico
2	39	90.7	746	2	Q9LWA3_LYCES	Q9lwa3 lycopersico
3	39	90.7	865	2	Q6TXF5_RAT	Q6txf5 rattus norv
4	38	88.4	238	2	Q58EU4_MOUSE	Q58eu4 mus musculu
5	38	88.4	434	2	Q4QHI3_LEIMA	Q4qhi3 leishmania
6	37	86.0	354	2	Q8W2M6_PETHY	Q8w2m6 petunia hyb
7	37	86.0	738	1	ETR1_TOBAC	O48929 nicotiana t
8	37	86.0	738	2	Q8W2M8_PETHY	Q8w2m8 petunia hyb
9	37	86.0	738	2	Q8W2M9_PETHY	Q8w2m9 petunia hyb
10	36	83.7	443	2	Q8CUS8_OCEIH	Q8cus8 oceanobacil
11	36	83.7	461	1	PPB4_BACSU	P19406 bacillus su
12	36	83.7	736	1	ETR2_LYCES	O49187 lycopersico
13	36	83.7	736	2	Q5QG25_LYCES	Q5qg25 lycopersico
14	36	83.7	761	2	Q4QFE8_LEIMA	Q4qfe8 leishmania
15	36	83.7	771	2	Q4N7R8_THEPA	Q4n7r8 theileria p
16	35	81.4	118	2	O77171_PLAFA	O77171 plasmodium
17	35	81.4	118	2	Q8CA09_MOUSE	Q8ca09 mus musculu
18	35	81.4	120	2	Q8T4Z9_PLAFA	Q8t4z9 plasmodium
19	35	81.4	121	2	Q868X3_PLAFA	Q868x3 plasmodium
20	35	81.4	121	2	Q868X5_PLAFA	Q868x5 plasmodium
21	35	81.4	121	2	Q8T533_PLAFA	Q8t533 plasmodium
22	35	81.4	121	2	Q9XZ76_PLAFA	Q9xz76 plasmodium
23	35	81.4	122	2	O77193_PLAFA	O77193 plasmodium
24	35	81.4	122	2	Q8T4X5_PLAFA	Q8t4x5 plasmodium
25	35	81.4	122	2	Q9XZ75_PLAFA	Q9xz75 plasmodium
26	35	81.4	123	2	Q8T332_PLAFA	Q8t332 plasmodium
27	35	81.4	124	2	O77190_PLAFA	O77190 plasmodium
28	35	81.4	124	2	Q6E2M4_9CAUD	Q6e2m4 uncultured
29	35	81.4	125	2	Q868Y7_PLAFA	Q868y7 plasmodium
30	35	81.4	125	2	Q86RR8_PLAFA	Q86rr8 plasmodium
31	35	81.4	125	2	Q8T506_PLAFA	Q8t506 plasmodium
32	35	81.4	126	2	Q868W0_PLAFA	Q868w0 plasmodium
33	35	81.4	126	2	Q86RR6_PLAFA	Q86rr6 plasmodium
34	35	81.4	127	2	Q8T345_PLAFA	Q8t345 plasmodium
35	35	81.4	127	2	Q8T4Z0_PLAFA	Q8t4z0 plasmodium
36	35	81.4	128	2	Q9XZA5_PLAFA	Q9xza5 plasmodium
37	35	81.4	129	2	Q95Z31_PLAFA	Q95z31 plasmodium
38	35	81.4	129	2	Q9NHL3_PLAFA	Q9nhl3 plasmodium
39	35	81.4	130	2	O77184_PLAFA	O77184 plasmodium
40	35	81.4	130	2	Q8T4V6_PLAFA	Q8t4v6 plasmodium
41	35	81.4	130	2	Q9XZ84_PLAFA	Q9xz84 plasmodium
42	35	81.4	131	2	Q868Z2_PLAFA	Q868z2 plasmodium
43	35	81.4	131	2	Q8STF4_PLAFA	Q8stf4 plasmodium
44	35	81.4	131	2	Q8T4U7_PLAFA	Q8t4u7 plasmodium
45	35	81.4	131	2	Q8T4X9_PLAFA	Q8t4x9 plasmodium
46	35	81.4	131	2	Q8T577_PLAFA	Q8t577 plasmodium
47	35	81.4	132	2	Q8T355_PLAFA	Q8t355 plasmodium
48	35	81.4	133	2	Q86RR3_PLAFA	Q86rr3 plasmodium
49	35	81.4	133	2	Q86RR4_PLAFA	Q86rr4 plasmodium
50	35	81.4	133	2	Q964S4_PLAFA	Q964s4 plasmodium
51	35	81.4	134	2	Q95Z49_PLAFA	Q95z49 plasmodium
52	35	81.4	135	2	Q8T4Y0_PLAFA	Q8t4y0 plasmodium
53	35	81.4	135	2	Q9GT85_PLAFA	Q9gt85 plasmodium
54	35	81.4	136	2	Q6S8Q6_PLAFA	Q6s8q6 plasmodium
55	35	81.4	137	2	Q8T4Z6_PLAFA	Q8t4z6 plasmodium
56	35	81.4	137	2	Q8T513_PLAFA	Q8t513 plasmodium
57	35	81.4	138	2	Q95Z26_PLAFA	Q95z26 plasmodium
58	35	81.4	139	2	Q9NHM4_PLAFA	Q9nhm4 plasmodium
59	35	81.4	140	2	Q86RR7_PLAFA	Q86rr7 plasmodium
60	35	81.4	141	2	Q6S8Q7_PLAFA	Q6s8q7 plasmodium
61	35	81.4	141	2	Q86RR5_PLAFA	Q86rr5 plasmodium
62	35	81.4	142	2	Q6S8T7_PLAFA	Q6s8t7 plasmodium
63	35	81.4	144	2	Q6S8R6_PLAFA	Q6s8r6 plasmodium
64	35	81.4	144	2	Q7Z235_PLAFA	Q7z235 plasmodium
65	35	81.4	145	2	Q6S8P5_PLAFA	Q6s8p5 plasmodium
66	35	81.4	146	2	Q6S8Z5_PLAFA	Q6s8z5 plasmodium
67	35	81.4	151	2	Q6S8Q9_PLAFA	Q6s8q9 plasmodium
68	35	81.4	152	2	Q6S8T6_PLAFA	Q6s8t6 plasmodium
69	35	81.4	153	2	Q6S8P9_PLAFA	Q6s8p9 plasmodium
70	35	81.4	156	2	Q6S8P4_PLAFA	Q6s8p4 plasmodium
71	35	81.4	165	2	O96406_PLAFA	O96406 plasmodium
72	35	81.4	190	2	Q8WTD8_PLAFA	Q8wtd8 plasmodium
73	35	81.4	193	2	O96736_PLAFA	O96736 plasmodium
74	35	81.4	205	2	Q8WTE2_PLAFA	Q8wte2 plasmodium
75	35	81.4	210	2	Q6E2K4_9CAUD	Q6e2k4 uncultured
76	35	81.4	210	2	Q6E2L3_9CAUD	Q6e2l3 uncultured
77	35	81.4	210	2	Q6E2M3_9CAUD	Q6e2m3 uncultured
78	35	81.4	211	2	Q6E2M6_9CAUD	Q6e2m6 uncultured
79	35	81.4	258	2	Q9U7I2_PLAFA	Q9u7i2 plasmodium
80	35	81.4	267	2	O61076_PLAFA	O61076 plasmodium
81	35	81.4	273	2	Q4JV54_CORJK	Q4jv54 corynebacte
82	35	81.4	764	2	Q6PRG6_PLAFA	Q6prg6 plasmodium
83	35	81.4	2265	2	Q8IAS3_PLAF7	Q8ias3 plasmodium
84	35	81.4	2268	2	Q8I4N5_PLAF7	Q8i4n5 plasmodium
85	35	81.4	2275	2	Q8IBX2_PLAF7	Q8ibx2 plasmodium
86	35	81.4	2326	2	Q8I1V6_PLAF7	Q8i1v6 plasmodium
87	34	79.1	119	2	O77186_PLAFA	O77186 plasmodium
88	34	79.1	193	2	Q8WTE3_PLAFA	Q8wte3 plasmodium
89	34	79.1	199	2	Q9LVF8_ARATH	Q9lvf8 arabidopsis
90	34	79.1	225	2	Q4J0E7_AZOVI	Q4j0e7 azotobacter
91	34	79.1	229	2	Q69S30_ORYSA	Q69s30 oryza sativ
92	34	79.1	435	1	ZFNL5_ARATH	Q5rjc5 arabidopsis
93	34	79.1	488	1	YGM9_YEAST	Q01163 saccharomyc
94	34	79.1	496	2	Q8KU77_ENTFA	Q8ku77 enterococcu
95	34	79.1	508	2	Q6UDI8_9HERP	Q6udi8 psittacid h
96	34	79.1	533	2	Q5GVK0_XANOR	Q5gvk0 xanthomonas
97	34	79.1	546	2	O26601_METTH	O26601 methanobact
98	34	79.1	585	2	Q4WCQ9_ASPFU	Q4wcq9 aspergillus
99	34	79.1	727	2	Q6A0E8_MOUSE	Q6a0e8 mus musculu
100	34	79.1	745	2	O04678_LYCES	O04678 lycopersico
101	34	79.1	745	2	Q96478_LYCES	Q96478 lycopersico
102	34	79.1	747	2	O82007_LYCES	O82007 lycopersico
103	34	79.1	758	2	Q9LRH8_PEA	Q9lrh8 pisum sativ
104	34	79.1	795	1	TLR1_MOUSE	Q9epq1 mus musculu

105	34	79.1	795	1	TLR6_MOUSE	Q9epw9 mus musculu
106	34	79.1	806	2	Q6P690_RAT	Q6p690 rattus norv
107	34	79.1	806	2	Q7TPC5_MOUSE	Q7tpc5 mus musculu
108	34	79.1	925	2	Q8DB46_VIBVU	Q8db46 vibrio vuln
109	34	79.1	925	2	Q87MM5_VIBPA	Q87mm5 vibrio para
110	34	79.1	925	2	Q7MIS6_VIBVY	Q7mis6 vibrio vuln
111	34	79.1	929	2	Q8ECQ2_SHEON	Q8ecq2 shewanella
112	34	79.1	939	2	Q9KQC8_VIBCH	Q9kqc8 vibrio chol
113	34	79.1	1367	2	Q5BAN9_EMENI	Q5ban9 aspergillus
114	33	76.7	66	2	Q8P9W6_XANCP	Q8p9w6 xanthomonas
115	33	76.7	161	2	Q57QB0_SALCH	Q57qb0 salmonella
116	33	76.7	190	2	Q8GE21_HELMO	Q8ge21 heliobacill
117	33	76.7	219	2	Q4SV49_TETNG	Q4sv49 tetraodon n
118	33	76.7	222	2	Q4HVP0_GIBZE	Q4hvp0 gibberella
119	33	76.7	233	2	Q5GYN4_XANOR	Q5gyn4 xanthomonas
120	33	76.7	233	2	Q4UTS0_XANCP	Q4uts0 xanthomonas
121	33	76.7	233	2	Q8P9W7_XANCP	Q8p9w7 xanthomonas
122	33	76.7	233	2	Q8PLP6_XANAC	Q8plp6 xanthomonas
123	33	76.7	234	2	Q4NYE5_9DELT	Q4nye5 anaeromyxob
124	33	76.7	241	2	Q4LUI7_9BURK	Q4lui7 burkholderi
125	33	76.7	241	2	Q63N64_BURPS	Q63n64 burkholderi
126	33	76.7	242	2	Q29153_VULVU	Q29153 vulpes vulp
127	33	76.7	268	2	Q6NGN6_CORDI	Q6ngn6 corynebacte
128	33	76.7	268	2	Q8NP44_CORGL	Q8np44 corynebacte
129	33	76.7	274	2	Q8FPB1_COREF	Q8fpb1 corynebacte
130	33	76.7	368	2	O90726_HPV67	O90726 human papil
131	33	76.7	378	2	Q9CLC0_PASMU	Q9clc0 pasteurella
132	33	76.7	380	2	Q861S1_PIG	Q861s1 sus scrofa
133	33	76.7	387	2	Q9R6M6_9RHIZ	Q9r6m6 agrobacteri
134	33	76.7	400	2	O68995_MYCAV	O68995 mycobacteri
135	33	76.7	407	2	Q740Q5_MYCPA	Q740q5 mycobacteri
136	33	76.7	420	2	Q7WFW3_BORBR	Q7wfw3 bordetella
137	33	76.7	420	2	Q7W4F3_BORPA	Q7w4f3 bordetella
138	33	76.7	426	2	Q5KWF0_GEOKA	Q5kwf0 geobacillus
139	33	76.7	432	2	Q4NWS2_9DELT	Q4nws2 anaeromyxob
140	33	76.7	461	2	Q852L2_ORYSA	Q852l2 oryza sativ
141	33	76.7	470	2	Q8L8I0_ORYSA	Q8l8i0 oryza sativ
142	33	76.7	490	2	Q4FKI6_9TRYP	Q4fki6 trypanosoma
143	33	76.7	620	2	Q4QGF5_LEIMA	Q4qgf5 leishmania
144	33	76.7	756	2	Q5E2U2_VIBF1	Q5e2u2 vibrio fisc
145	33	76.7	767	2	Q4P8K8_USTMA	Q4p8k8 ustilago ma
146	33	76.7	798	2	Q8C7A1_MOUSE	Q8c7a1 mus musculu
147	33	76.7	846	2	Q4RGP6_TETNG	Q4rgp6 tetraodon n
148	33	76.7	996	2	Q4UHT9_THEAN	Q4uht9 theileria a
149	33	76.7	1045	2	Q5AQJ6_EMENI	Q5aqj6 aspergillus
150	33	76.7	1046	2	Q4IA58_GIBZE	Q4ia58 gibberella
151	33	76.7	1058	2	Q4WP08_ASPFU	Q4wp08 aspergillus
152	33	76.7	1293	2	Q8IWF1_HUMAN	Q8iwf1 homo sapien
153	33	76.7	1639	2	Q7Z3K8_HUMAN	Q7z3k8 homo sapien
154	33	76.7	1745	2	Q14675_HUMAN	Q14675 homo sapien
155	33	76.7	1749	2	Q5SRE5_HUMAN	Q5sre5 homo sapien
156	33	76.7	1759	2	Q4VA15_MOUSE	Q4va15 mus musculu
157	33	76.7	1761	2	Q6ZQH8_MOUSE	Q6zqh8 mus musculu
158	33	76.7	3201	2	Q5D6D4_COCHE	Q5d6d4 cochliobolu
159	33	76.7	5609	2	Q4Q1T2_LEIMA	Q4q1t2 leishmania
160	32	74.4	62	2	Q4VMG7_9EURO	Q4vmg7 aspergillus
161	32	74.4	73	2	Q91SF1_9NUCL	Q91sf1 trichoplusi
162	32	74.4	91	2	Q8X863_ECO57	Q8x863 escherichia
163	32	74.4	95	2	Q4GZD8_9TRYP	Q4gzd8 trypanosoma
164	32	74.4	99	2	Q4KT60_9NUCL	Q4kt60 chrysodeixi
165	32	74.4	122	2	Q7WLR0_BORBR	Q7wlr0 bordetella
166	32	74.4	158	2	Q9RFA1_SALPU	Q9rfa1 salmonella
167	32	74.4	160	2	Q7PLR3_DROME	Q7plr3 drosophila
168	32	74.4	168	2	Q8XQG1_RALSO	Q8xqg1 ralstonia s
169	32	74.4	175	2	Q4F9L8_9EUCA	Q4f918 orconectes
170	32	74.4	216	1	SRY_MESST	Q864q4 mesoplodon
171	32	74.4	217	2	Q4VMH4_9EURO	Q4vmh4 neosartorya
172	32	74.4	227	2	Q4VMG9_9EURO	Q4vmg9 aspergillus
173	32	74.4	228	2	Q8JY05_9HEPC	Q8jy05 hepatitis c
174	32	74.4	231	2	Q4VMG8_ASPVI	Q4vmg8 aspergillus
175	32	74.4	231	2	Q4VMH2_9EURO	Q4vmh2 neosartorya
176	32	74.4	231	2	Q4VMH3_9EURO	Q4vmh3 neosartorya
177	32	74.4	231	2	Q4VMH5_9EURO	Q4vmh5 neosartorya
178	32	74.4	236	1	MTGA_RHIME	Q92123 rhizobium m
179	32	74.4	249	2	Q65DD3_BACLD	Q65dd3 bacillus li
180	32	74.4	251	2	Q72F50_DESVH	Q72f50 desulfovibr
181	32	74.4	257	2	Q93TU6_9NOCA	Q93tu6 rhodococcus
182	32	74.4	263	2	O84989_RHOOP	O84989 rhodococcus
183	32	74.4	268	2	O07709_MYCLE	O07709 mycobacteri
184	32	74.4	268	2	O06172_MYCTU	O06172 mycobacteri
185	32	74.4	268	2	Q73XJ1_MYCPA	Q73xj1 mycobacteri
186	32	74.4	268	2	Q7TYF1_MYCBO	Q7tyf1 mycobacteri
187	32	74.4	280	2	Q5ZHQ7_CHICK	Q5zhq7 gallus gall
188	32	74.4	304	2	Q9L6L7_SALTY	Q91617 salmonella
189	32	74.4	314	2	Q6RWH6_9ZZZZ	Q6rwh6 uncultured
190	32	74.4	331	2	Q5CNU8_CRYHO	Q5cnu8 cryptospori
191	32	74.4	333	2	Q48538_9LACO	Q48538 lactobacill
192	32	74.4	343	2	Q9IET0_9VIRU	Q9iet0 citrus leaf
193	32	74.4	351	2	Q4WK42_ASPFU	Q4wk42 aspergillus
194	32	74.4	352	2	Q8ZKV1_SALTY	Q8zkv1 salmonella
195	32	74.4	356	2	Q4Q372_LEIMA	Q4q372 leishmania
196	32	74.4	358	2	Q8UK96_AGRT5	Q8uk96 agrobacteri
197	32	74.4	370	1	5HT5B_MOUSE	P31387 mus musculu
198	32	74.4	370	1	5HT5B_RAT	P35365 rattus norv
199	32	74.4	380	2	O76408_CAEEL	O76408 caenorhabdi
200	32	74.4	390	2	Q4S8T4_TETNG	Q4s8t4 tetraodon n
201	32	74.4	407	1	DEOB_ECO57	P0a6k8 escherichia
202	32	74.4	407	1	DEOB_ECOL6	P0a6k7 escherichia
203	32	74.4	407	1	DEOB_ECOLI	P0a6k6 escherichia
204	32	74.4	407	1	DEOB_SALTI	P63924 salmonella
205	32	74.4	407	1	DEOB_SALTY	P63923 salmonella
206	32	74.4	407	1	DEOB_SHIFL	P0a6k9 shigella fl
207	32	74.4	407	2	Q57G39_SALCH	Q57g39 salmonella
208	32	74.4	407	2	Q5PK21_SALPA	Q5pk21 salmonella
209	32	74.4	420	2	Q5I3L9_ECOLI	Q5i3l9 escherichia
210	32	74.4	423	2	Q4V6T8_DROME	Q4v6t8 drosophila
211	32	74.4	425	2	Q4V4W4_DROME	Q4v4w4 drosophila
212	32	74.4	427	2	Q9VJN0_DROME	Q9vjn0 drosophila
213	32	74.4	431	2	Q7EZU1_ORYSA	Q7ezu1 oryza sativ
214	32	74.4	434	2	Q92A01_LISIN	Q92a01 listeria in
215	32	74.4	445	2	Q753D6_ASHGO	Q753d6 ashbya goss
216	32	74.4	448	2	Q71TS8_PASMU	Q71ts8 pasteurella
217	32	74.4	448	2	Q9CMC5_PASMU	Q9cmc5 pasteurella
218	32	74.4	462	2	Q9FB15_9ACTO	Q9fb15 streptomyce
219	32	74.4	464	2	Q7W700_BORPA	Q7w700 bordetella
220	32	74.4	464	2	Q7WIV4_BORBR	Q7wiv4 bordetella
221	32	74.4	476	2	Q6BX67_DEBHA	Q6bx67 debaryomyce
222	32	74.4	518	2	Q8EC58_SHEON	Q8ec58 shewanella
223	32	74.4	542	2	Q60SJ0_CAEBR	Q60sj0 caenorhabdi
224	32	74.4	545	2	Q4NHR2_9MICC	Q4nhr2 arthrobacte
225	32	74.4	572	1	POXB_ECOLI	P07003 escherichia
226	32	74.4	572	2	Q8FJE2_ECOL6	Q8fje2 escherichia
227	32	74.4	572	2	Q83S07_SHIFL	Q83s07 shigella fl
228	32	74.4	572	2	Q8X6L4_ECO57	Q8x614 escherichia
229	32	74.4	588	2	Q6FRZ8_CANGA	Q6frz8 candida gla
230	32	74.4	590	2	Q4T7L2_TETNG	Q4t7l2 tetraodon n
231	32	74.4	596	2	Q57HB7_SALCH	Q57hb7 salmonella
232	32	74.4	596	2	Q5PK49_SALPA	Q5pk49 salmonella
233	32	74.4	596	2	Q8ZKN6_SALTY	Q8zkn6 salmonella
234	32	74.4	607	2	Q57HM8_SALCH	Q57hm8 salmonella
235	32	74.4	607	2	Q8Z3C5_SALTI	Q8z3c5 salmonella
236	32	74.4	610	2	Q4IL56_GIBZE	Q4il56 gibberella
237	32	74.4	610	2	Q4Q558_LEIMA	Q4q558 leishmania
238	32	74.4	644	2	Q8WTN3_CAEEL	Q8wtn3 caenorhabdi
239	32	74.4	645	2	Q48839_LACSK	Q48839 lactobacill
240	32	74.4	660	2	Q55I29_CRYNE	Q55i29 cryptococcu
241	32	74.4	660	2	Q5K7L5_CRYNE	Q5k7l5 cryptococcu
242	32	74.4	663	2	Q4HVF7_GIBZE	Q4hvf7 gibberella
243	32	74.4	672	2	Q9NK74_DROME	Q9nk74 drosophila
244	32	74.4	746	2	Q6U5X1_KLEPN	Q6u5x1 klebsiella
245	32	74.4	786	2	Q8HQ84_SCHOT	Q8hq84 schizosacch
246	32	74.4	876	2	Q6C5C2_YARLI	Q6c5c2 yarrowia li
247	32	74.4	995	1	YPD1_CAEEL	P48053 caenorhabdi
248	32	74.4	996	2	Q60V74_CAEBR	Q60v74 caenorhabdi
249	32	74.4	1019	2	Q6FTA7_CANGA	Q6fta7 candida gla
250	32	74.4	1086	2	Q7Q342_ANOGA	Q7q342 anopheles g

251	32	74.4	1299	2	Q9AXC5_ANTHI	Q9axc5	antirrhinum
252	32	74.4	1315	2	Q57W46_9TRYP	Q57w46	trypanosoma
253	32	74.4	1524	2	Q9V854_DROME	Q9v854	drosophila
254	32	74.4	1616	2	Q4QGH9_LEIMA	Q4qgh9	leishmania
255	32	74.4	1623	2	Q518Y3_ENTHI	Q518y3	entamoeba h
256	32	74.4	1962	2	Q91QZ3_9VIRU	Q91qz3	citrus leaf
257	32	74.4	2266	2	Q5CYJ4_CRYPV	Q5cyj4	cryptospori
258	32	74.4	2334	1	POLG_EBHSG	Q96725	e genome po
259	32	74.4	2356	2	Q6CCC5_YARLI	Q6ccc5	yarrowia li
260	32	74.4	2363	2	O14187_SCHPO	O14187	schizosacch
261	32	74.4	2369	2	Q520V6_MAGGR	Q520v6	magnaporthe
262	32	74.4	2370	2	Q4IJS2_GIBZE	Q4ijs2	gibberella
263	32	74.4	2374	2	Q7SBD3_NEUCR	Q7sbd3	neurospora
264	32	74.4	2440	2	Q4QCT8_LEIMA	Q4qct8	leishmania
265	32	74.4	2616	1	NUDEL_DROME	P98159	drosophila
266	32	74.4	2868	2	Q4QDV7_LEIMA	Q4qdv7	leishmania
267	32	74.4	2945	2	Q5B4K7_EMENI	Q5b4k7	aspergillus
268	32	74.4	3170	2	Q4WI55_ASPFU	Q4wi55	aspergillus
269	31	72.1	26	2	Q7M4T2_ARMME	Q7m4t2	armillaria
270	31	72.1	55	2	Q5GV43_XANOR	Q5gv43	xanthomonas
271	31	72.1	79	2	Q4V279_BACCZ	Q4v279	bacillus ce
272	31	72.1	104	2	Q9SLP7_CHLVU	Q9slp7	chlorella v
273	31	72.1	107	2	Q5R3X7_MOUSE	Q5r3x7	mus musculu
274	31	72.1	119	2	Q5RB62_PONPY	Q5rb62	pongo pygma
275	31	72.1	121	2	Q688Y0_ORYSA	Q688y0	oryza sativ
276	31	72.1	124	2	Q4Q0H6_LEIMA	Q4q0h6	leishmania
277	31	72.1	124	2	Q848K0_9BACT	Q848k0	uncultured
278	31	72.1	143	2	Q9N000_MACFA	Q9n000	macaca fasc
279	31	72.1	150	2	Q8N7V8_HUMAN	Q8n7v8	homo sapien
280	31	72.1	152	2	Q5W197_HUMAN	Q5w197	homo sapien
281	31	72.1	167	2	Q9X7R2_STRCO	Q9x7r2	streptomyce
282	31	72.1	171	2	Q6A901_PROAC	Q6a901	propionibac
283	31	72.1	172	2	Q8KAV3_CHLTE	Q8kav3	chlorobium
284	31	72.1	173	2	Q82KH8_STRAW	Q82kh8	streptomyce
285	31	72.1	182	2	Q8KY04_BRAJA	Q8ky04	bradyrhizob
286	31	72.1	195	2	Q5YT02_NOCFA	Q5yt02	nocardia fa
287	31	72.1	197	1	VG23_BPML5	Q05229	mycobacteri
288	31	72.1	204	1	CRBB2_BOVIN	P02522	bos taurus
289	31	72.1	204	1	CRBB2_HUMAN	P43320	homo sapien
290	31	72.1	204	1	CRBB2_MESAU	P62698	mesocricetu
291	31	72.1	204	1	CRBB2_MOUSE	P62696	mus musculu
292	31	72.1	204	1	CRBB2_RAT	P62697	rattus norv
293	31	72.1	204	2	Q7ZNA5_9HIV1	Q7zna5	human immun
294	31	72.1	217	2	Q7NLW0_GLOVI	Q7nlw0	gloeobacter
295	31	72.1	222	2	Q8JZY3_MOUSE	Q8jzy3	mus musculu
296	31	72.1	223	1	YZL2_EBV	P03205	epstein-bar
297	31	72.1	223	2	Q777E6_9GAMA	Q777e6	human herpe
298	31	72.1	224	2	Q4LX44_9BURK	Q4lx44	burkholderi
299	31	72.1	247	2	Q579E5_BRUAB	Q579e5	brucella ab
300	31	72.1	247	2	Q8FVB7_BRUSU	Q8fvb7	brucella su
301	31	72.1	247	2	Q8YD07_BRUME	Q8yd07	brucella me
302	31	72.1	248	2	Q9RLW6_KLEPN	Q9rlw6	klebsiella
303	31	72.1	256	2	Q9D7C1_MOUSE	Q9d7c1	mus musculu
304	31	72.1	256	2	Q8C3X2_MOUSE	Q8c3x2	mus musculu
305	31	72.1	273	2	Q9RUE5_DEIRA	Q9rue5	deinococcus
306	31	72.1	276	2	Q9FJV5_ARATH	Q9fjv5	arabidopsis
307	31	72.1	277	2	Q4TGT0_TETNG	Q4tgt0	tetraodon n
308	31	72.1	287	2	Q7ZVB8_BRARE	Q7zvb8	brachydanio
309	31	72.1	291	1	ATP4B_RABIT	P18597	oryctolagus
310	31	72.1	292	2	Q4Q077_LEIMA	Q4q077	leishmania
311	31	72.1	293	2	Q4TDH1_TETNG	Q4tdh1	tetraodon n
312	31	72.1	296	2	Q8LA68_ARATH	Q8la68	arabidopsis
313	31	72.1	305	2	Q4WTZ3_ASPFU	Q4wtz3	aspergillus
314	31	72.1	305	2	Q9XVF9_CAEEL	Q9xvf9	caenorhabdi
315	31	72.1	308	1	ARH_HUMAN	Q5sw96	homo sapien
316	31	72.1	308	1	ARH_MOUSE	Q8c142	mus musculu
317	31	72.1	309	1	ARHA_XENLA	Q801g1	xenopus lae
318	31	72.1	309	1	ARHB_XENLA	Q67fq3	xenopus lae
319	31	72.1	313	2	Q95QL5_CAEEL	Q95ql5	caenorhabdi
320	31	72.1	314	2	Q4XVB5_PLACH	Q4xvb5	plasmodium
321	31	72.1	317	2	Q4RNV8_TETNG	Q4rnv8	tetraodon n
322	31	72.1	322	2	Q84UP8_ORYSA	Q84up8	oryza sativ
323	31	72.1	335	2	Q4X098_ASPFU	Q4x098	aspergillus
324	31	72.1	336	1	GCB_MOUSE	P01866	mus musculu
325	31	72.1	345	2	Q6NUL8_HUMAN	Q6nul8	homo sapien
326	31	72.1	346	2	O75525_HUMAN	O75525	homo sapien
327	31	72.1	346	2	O88624_MOUSE	O88624	mus musculu
328	31	72.1	346	2	Q9JLP1_RAT	Q9jlp1	rattus norv
329	31	72.1	346	2	Q9R226_MOUSE	Q9r226	mus musculu
330	31	72.1	353	2	Q7ZP08_9HIV1	Q7zp08	human immun
331	31	72.1	356	1	CMO_PYRFU	Q51741	pyrococcus
332	31	72.1	394	2	Q9L4X0_9ACTO	Q9l4x0	streptomyce
333	31	72.1	399	2	Q4TGS9_TETNG	Q4tgs9	tetraodon n
334	31	72.1	404	1	GCBM_MOUSE	P01867	mus musculu
335	31	72.1	408	2	Q79IP4_ALCEU	Q79ip4	alcaligenes
336	31	72.1	415	2	Q6C937_YARLI	Q6c937	yarrowia li
337	31	72.1	432	2	Q6FQ32_CANGA	Q6fq32	candida gla
338	31	72.1	432	2	Q82LF1_STRAW	Q82lf1	streptomyce
339	31	72.1	432	2	Q53IM5_FUGRU	Q53im5	fugu rubrip
340	31	72.1	437	2	Q6BW66_DEBHA	Q6bw66	debaryomyce
341	31	72.1	450	2	Q55NL4_CRYNE	Q55nl4	cryptococcu
342	31	72.1	450	2	Q5KC02_CRYNE	Q5kc02	cryptococcu
343	31	72.1	454	2	O65425_ARATH	O65425	arabidopsis
344	31	72.1	466	2	Q895F5_CLOTE	Q895f5	clostridium
345	31	72.1	473	2	Q4WL08_ASPFU	Q4wl08	aspergillus
346	31	72.1	473	2	Q91Z05_MOUSE	Q91z05	mus musculu
347	31	72.1	474	2	Q8R3H6_MOUSE	Q8r3h6	mus musculu
348	31	72.1	476	2	Q569X1_MOUSE	Q569x1	mus musculu
349	31	72.1	502	2	Q4HUM2_GIBZE	Q4hum2	gibberella
350	31	72.1	517	2	Q974W1_SULTO	Q974w1	sulfolobus
351	31	72.1	543	2	Q6DEM6_BRARE	Q6dem6	brachydanio
352	31	72.1	548	2	Q989T8_RHILO	Q989t8	rhizobium l
353	31	72.1	559	2	Q5LWI5_SILPO	Q5lwi5	silicibacte
354	31	72.1	561	2	Q89EN1_BRAJA	Q89en1	bradyrhizob
355	31	72.1	569	2	Q82LA5_STRAW	Q82la5	streptomyce
356	31	72.1	630	2	O24608_DIACA	O24608	dianthus ca
357	31	72.1	634	2	Q6JN51_MAIZE	Q6jn51	zea mays (m
358	31	72.1	634	2	Q6JN52_MAIZE	Q6jn52	zea mays (m
359	31	72.1	636	2	O24176_ORYSA	O24176	oryza sativ
360	31	72.1	636	2	Q7EWE2_ORYSA	Q7ewe2	oryza sativ
361	31	72.1	636	2	Q53RH0_ORYSA	Q53rh0	oryza sativ
362	31	72.1	669	2	Q8H8J8_ORYSA	Q8h8j8	oryza sativ
363	31	72.1	677	2	Q7YTW6_TRYBB	Q7ytw6	trypanosoma
364	31	72.1	677	2	Q8I7C1_ECHMU	Q8i7c1	echinococcu
365	31	72.1	686	2	Q583K1_9TRYP	Q583k1	trypanosoma
366	31	72.1	694	1	FRE5_YEAST	Q08908	saccharomyc
367	31	72.1	696	2	Q7UXC6_RHOBA	Q7uxc6	rhodopirell
368	31	72.1	726	2	Q9SUD9_ARATH	Q9sud9	arabidopsis
369	31	72.1	739	2	Q8JVD0_9PICO	Q8jvd0	foot-and-mo
370	31	72.1	750	2	O64983_SPIOL	O64983	spinacia ol
371	31	72.1	803	2	Q80ZF5_RAT	Q80zf5	rattus norv
372	31	72.1	829	2	Q5YU92_NOCFA	Q5yu92	nocardia fa
373	31	72.1	846	2	O93920_MAGGR	O93920	magnaporthe
374	31	72.1	846	2	Q6AM73_DESPS	Q6am73	desulfotale
375	31	72.1	847	2	Q529E0_MAGGR	Q529e0	magnaporthe
376	31	72.1	850	2	Q6FJ59_CANGA	Q6fj59	candida gla
377	31	72.1	929	2	Q5VRT1_ORYSA	Q5vrt1	oryza sativ
378	31	72.1	932	2	Q6RCI9_9CHLR	Q6rci9	thermomicro
379	31	72.1	941	2	Q6JBD8_TOBAC	Q6jbd8	nicotiana t
380	31	72.1	1021	2	Q4WW05_ASPFU	Q4ww05	aspergillus
381	31	72.1	1067	2	Q17517_CAEEL	Q17517	caenorhabdi
382	31	72.1	1067	2	Q7JMF9_CAEEL	Q7jmf9	caenorhabdi
383	31	72.1	1071	2	Q4TBC6_TETNG	Q4tbc6	tetraodon n
384	31	72.1	1108	2	Q4P9N9_USTMA	Q4p9n9	ustilago ma
385	31	72.1	1128	2	Q75WV4_TOBAC	Q75wv4	nicotiana t
386	31	72.1	1130	2	O45624_CAEEL	O45624	caenorhabdi
387	31	72.1	1132	2	Q4V967_BRARE	Q4v967	brachydanio
388	31	72.1	1133	2	O45623_CAEEL	O45623	caenorhabdi
389	31	72.1	1135	2	Q7JKC3_CAEEL	Q7jkc3	caenorhabdi
390	31	72.1	1144	1	TMVRN_NICGU	Q40392	nicotiana g
391	31	72.1	1228	1	CR1BA_BACTE	P0a374	bacillus th
392	31	72.1	1228	1	CR1BA_BACTK	P0a373	bacillus th
393	31	72.1	1228	2	Q93NM5_BACTU	Q93nm5	bacillus th
394	31	72.1	1228	2	Q93T75_BACTE	Q93t75	bacillus th
395	31	72.1	1231	2	Q4PB15_USTMA	Q4pb15	ustilago ma
396	31	72.1	1237	2	Q5B1F6_EMENI	Q5b1f6	aspergillus

397	31	72.1	1536	1	Y984_THEMA	Q9x079 thermotoga
398	31	72.1	1826	2	Q4Q9F5_LEIMA	Q4q9f5 leishmania
399	31	72.1	1844	1	POLR_TYMV	P10358 turnip yell
400	31	72.1	1844	1	POLR_TYMVA	P20128 turnip yell
401	31	72.1	1844	1	POLR_TYMVC	P28477 turnip yell
402	31	72.1	1844	2	O56254_TYMV	O56254 turnip yell
403	31	72.1	2322	2	O01510_CAEEL	O01510 caenorhabdi
404	31	72.1	2599	2	Q98PE9_MYCPU	Q98pe9 mycoplasma
405	31	72.1	2768	2	Q751J3_ASHGO	Q751j3 ashbya goss
406	31	72.1	3198	2	Q9U8G8_MANSE	Q9u8g8 manduca sex
407	30.5	70.9	371	2	Q9EZH2_STRPN	Q9ezh2 streptococc
408	30	69.8	73	2	Q6Z594_ORYSA	Q6z594 oryza sativ
409	30	69.8	87	2	Q8XGB4_RALSO	Q8xgb4 ralstonia s
410	30	69.8	88	2	Q6CG84_YARLI	Q6cg84 yarrowia li
411	30	69.8	94	2	Q7UW87_RHOBA	Q7uw87 rhodopirell
412	30	69.8	112	2	Q5ZA18_ORYSA	Q5za18 oryza sativ
413	30	69.8	124	2	Q4V2P3_BURMA	Q4v2p3 burkholderi
414	30	69.8	127	2	Q9NHL0_PLAFA	Q9nhl0 plasmodium
415	30	69.8	129	2	Q868Y2_PLAFA	Q868y2 plasmodium
416	30	69.8	130	2	Q9ETS1_NEIME	Q9ets1 neisseria m
417	30	69.8	134	2	Q52DN5_MAGGR	Q52dn5 magnaporthe
418	30	69.8	135	2	Q7UW32_RHOBA	Q7uw32 rhodopirell
419	30	69.8	143	2	Q4V4G9_DROME	Q4v4g9 drosophila
420	30	69.8	148	2	Q655D8_ORYSA	Q655d8 oryza sativ
421	30	69.8	149	1	RECX_AMYMD	Q9rev5 amycolatops
422	30	69.8	150	2	Q9LKM0_LOLPR	Q9lkm0 lolium pere
423	30	69.8	153	2	Q5NWB3_AZOSE	Q5nwb3 azoarcus sp
424	30	69.8	156	2	Q9B8A9_TRISP	Q9b8a9 trichinella
425	30	69.8	161	2	Q653H0_ORYSA	Q653h0 oryza sativ
426	30	69.8	161	2	Q7F7E3_ORYSA	Q7f7e3 oryza sativ
427	30	69.8	174	2	Q6II10_DROME	Q6ii10 drosophila
428	30	69.8	178	2	Q4NBC6_9MICC	Q4nbc6 arthrobacte
429	30	69.8	181	2	Q4LIG6_9BURK	Q4lig6 burkholderi
430	30	69.8	192	2	Q5GW65_XANOR	Q5gw65 xanthomonas
431	30	69.8	195	2	Q9BPS9_DROME	Q9bps9 drosophila
432	30	69.8	197	1	T4S5_HUMAN	O14894 homo sapien
433	30	69.8	197	2	Q6FHF6_HUMAN	Q6fhf6 homo sapien
434	30	69.8	205	2	Q4UQZ6_XANCP	Q4uqz6 xanthomonas
435	30	69.8	205	2	Q8PCH7_XANCP	Q8pch7 xanthomonas
436	30	69.8	206	2	Q5YSH9_NOCFA	Q5ysh9 nocardia fa
437	30	69.8	207	2	Q9JB47_9HIV1	Q9jb47 human immun
438	30	69.8	210	1	MTRR_NEIGO	P39897 neisseria g
439	30	69.8	210	2	Q59608_NEIGO	Q59608 neisseria g
440	30	69.8	210	2	Q5F723_NEIG1	Q5f723 neisseria g
441	30	69.8	212	2	O62508_CAEEL	O62508 caenorhabdi
442	30	69.8	214	2	Q7XF15_ORYSA	Q7xf15 oryza sativ
443	30	69.8	214	2	Q94HB6_ORYSA	Q94hb6 oryza sativ
444	30	69.8	219	2	Q61X77_CAEBR	Q61x77 caenorhabdi
445	30	69.8	220	2	Q93966_CAEEL	Q93966 caenorhabdi
446	30	69.8	221	2	Q8PP88_XANAC	Q8pp88 xanthomonas
447	30	69.8	223	1	YGCF_ECO57	P64555 escherichia
448	30	69.8	223	1	YGCF_ECOLI	P64554 escherichia
449	30	69.8	223	1	YGCF_SHIFL	P64556 shigella fl
450	30	69.8	223	2	Q6EVL6_ECOLI	Q6ev16 escherichia
451	30	69.8	223	2	Q57KH2_SALCH	Q57kh2 salmonella
452	30	69.8	223	2	Q4MQQ5_BACCE	Q4mqq5 bacillus ce
453	30	69.8	223	2	Q5PEH5_SALPA	Q5peh5 salmonella
454	30	69.8	223	2	Q7CPW4_SALTY	Q7cpw4 salmonella
455	30	69.8	223	2	Q7N8L8_PHOLL	Q7n8l8 photorhabdu
456	30	69.8	223	2	Q8FEH6_ECOL6	Q8feh6 escherichia
457	30	69.8	223	2	Q8XEY5_SALTI	Q8xey5 salmonella
458	30	69.8	223	2	Q8ZBN4_YERPE	Q8zbn4 yersinia pe
459	30	69.8	223	2	Q66ED6_YERPS	Q66ed6 yersinia ps
460	30	69.8	223	2	Q6D194_ERWCT	Q6d194 erwinia car
461	30	69.8	223	2	Q63G57_BACCZ	Q63g57 bacillus ce
462	30	69.8	223	2	Q6HNM7_BACHK	Q6hnm7 bacillus th
463	30	69.8	223	2	Q73DR2_BACC1	Q73dr2 bacillus ce
464	30	69.8	223	2	Q81I36_BACCR	Q81i36 bacillus ce
465	30	69.8	223	2	Q81VB2_BACAN	Q81vb2 bacillus an
466	30	69.8	226	2	Q6A7U6_PROAC	Q6a7u6 propionibac
467	30	69.8	237	2	Q8G6Y9_BIFLO	Q8g6y9 bifidobacte
468	30	69.8	245	2	O14644_HUMAN	O14644 homo sapien
469	30	69.8	246	1	YEBC_ECO57	P67176 escherichia
470	30	69.8	246	1	YEBC_ECOL6	P67175 escherichia
471	30	69.8	246	1	YEBC_ECOLI	P0a8a0 escherichia
472	30	69.8	246	1	YEBC_SALPA	Q5pmz4 salmonella
473	30	69.8	246	1	YEBC_SALTI	P67180 salmonella
474	30	69.8	246	1	YEBC_SALTY	P67179 salmonella
475	30	69.8	246	1	YEBC_SHIFL	P0a8a1 shigella fl
476	30	69.8	246	2	Q57N98_SALCH	Q57n98 salmonella
477	30	69.8	250	2	Q75EF9_ASHGO	Q75ef9 ashbya goss
478	30	69.8	251	2	Q5PG50_SALPA	Q5pg50 salmonella
479	30	69.8	251	2	Q8Z891_SALTI	Q8z891 salmonella
480	30	69.8	255	2	Q82F26_STRAW	Q82f26 streptomyce
481	30	69.8	262	2	Q652Z0_ORYSA	Q652z0 oryza sativ
482	30	69.8	263	2	Q9AVH5_PEA	Q9avh5 pisum sativ
483	30	69.8	271	2	Q615D8_CAEBR	Q615d8 caenorhabdi
484	30	69.8	274	2	Q56TP8_WHEAT	Q56tp8 triticum ae
485	30	69.8	293	2	Q7QCJ9_ANOGA	Q7qcj9 anopheles g
486	30	69.8	299	2	Q60KB9_CAEBR	Q60kb9 caenorhabdi
487	30	69.8	304	2	Q9N120_RABIT	Q9n120 oryctolagus
488	30	69.8	304	2	Q4T3D0_TETNG	Q4t3d0 tetraodon n
489	30	69.8	311	2	Q61AF2_CAEBR	Q61af2 caenorhabdi
490	30	69.8	317	2	Q92NV3_RHIME	Q92nv3 rhizobium m
491	30	69.8	341	2	Q9HXE8_PSEAE	Q9hxe8 pseudomonas
492	30	69.8	342	2	Q5W706_ORYSA	Q5w706 oryza sativ
493	30	69.8	344	2	Q6AA03_PROAC	Q6aa03 propionibac
494	30	69.8	350	2	Q7PHG0_ANOGA	Q7phg0 anopheles g
495	30	69.8	353	2	Q75B06_ASHGO	Q75b06 ashbya goss
496	30	69.8	354	2	Q4FVZ4_LEIMA	Q4fvz4 leishmania
497	30	69.8	355	1	CM4T_STRPE	Q06528 streptomyce
498	30	69.8	355	2	Q8FN44_COREF	Q8fn44 corynebacte
499	30	69.8	356	2	Q55216_STRSQ	Q55216 streptomyce
500	30	69.8	360	2	Q4YSG6_PLABE	Q4ysg6 plasmodium
501	30	69.8	366	2	Q8X099_NEUCR	Q8x099 neurospora
502	30	69.8	378	1	MUTY_HAEIN	P44320 haemophilus
503	30	69.8	378	2	Q4QME0_HAEI8	Q4qme0 haemophilus
504	30	69.8	379	2	Q6FWU2_CANGA	Q6fwu2 candida gla
505	30	69.8	382	2	Q7PQ88_ANOGA	Q7pq88 anopheles g
506	30	69.8	382	2	Q82GT9_STRAW	Q82gt9 streptomyce
507	30	69.8	383	2	Q4WFT7_ASPFU	Q4wft7 aspergillus
508	30	69.8	383	2	O25370_HELPY	O25370 helicobacte
509	30	69.8	390	2	Q4TT05_9SPHN	Q4tt05 erythrobact
510	30	69.8	397	2	Q5B189_EMENI	Q5b189 aspergillus
511	30	69.8	397	2	Q4IE25_GIBZE	Q4ie25 gibberella
512	30	69.8	399	2	Q60R44_CAEBR	Q60r44 caenorhabdi
513	30	69.8	402	2	Q7V4M1_PROMM	Q7v4m1 prochloroco
514	30	69.8	405	2	Q4VDF0_CRYGA	Q4vdf0 cryptococcu
515	30	69.8	405	2	Q4VDE9_CRYGA	Q4vde9 cryptococcu
516	30	69.8	405	2	Q4VDE8_CRYGA	Q4vde8 cryptococcu
517	30	69.8	405	2	Q4VDE7_CRYGA	Q4vde7 cryptococcu
518	30	69.8	405	2	Q4VDE6_CRYGA	Q4vde6 cryptococcu
519	30	69.8	406	2	Q4VDF4_CRYGA	Q4vdf4 cryptococcu
520	30	69.8	406	2	Q4VDF3_CRYGA	Q4vdf3 cryptococcu
521	30	69.8	406	2	Q4VDF2_CRYGA	Q4vdf2 cryptococcu
522	30	69.8	406	2	Q4VDF1_CRYGA	Q4vdf1 cryptococcu
523	30	69.8	406	2	Q5Y237_CRYGA	Q5y237 cryptococcu
524	30	69.8	408	2	Q6WB77_ALCFA	Q6wb77 alcaligenes
525	30	69.8	410	2	Q4JY12_CORJK	Q4jy12 corynebacte
526	30	69.8	411	2	Q5NAC0_ORYSA	Q5nac0 oryza sativ
527	30	69.8	419	2	Q45111_BURCE	Q45111 burkholderi
528	30	69.8	419	2	Q9ZFQ7_BURCE	Q9zfq7 burkholderi
529	30	69.8	419	2	Q4LKA9_9BURK	Q4lka9 burkholderi
530	30	69.8	420	2	Q7ZA28_9BASI	Q7za28 puccinia tr
531	30	69.8	425	2	Q97IF1_CLOAB	Q97if1 clostridium
532	30	69.8	432	2	Q6Z2C7_ORYSA	Q6z2c7 oryza sativ
533	30	69.8	432	2	Q7F8T9_ORYSA	Q7f8t9 oryza sativ
534	30	69.8	433	2	Q4KRH8_THENE	Q4krh8 thermotoga
535	30	69.8	434	2	Q55W81_CRYNE	Q55w81 cryptococcu
536	30	69.8	434	2	Q5KK15_CRYNE	Q5kk15 cryptococcu
537	30	69.8	434	2	Q5CB85_9THEM	Q5cb85 thermotoga
538	30	69.8	434	2	Q5CBN1_9THEM	Q5cbn1 thermotoga
539	30	69.8	434	2	Q9WY03_THEMA	Q9wy03 thermotoga
540	30	69.8	436	2	Q6AED1_LEIXX	Q6aed1 leifsonia x
541	30	69.8	449	2	Q53QP5_HUMAN	Q53qp5 homo sapien
542	30	69.8	458	2	Q8XG08_RALSO	Q8xg08 ralstonia s

543	30	69.8	462	2	Q5GAQ5_MAIZE	Q5gaq5 zea mays (m	616	30	69.8	729	2	Q9XUD2_CAEEL	Q9xud2 caenorhabdi				
544	30	69.8	462	2	Q7X6I6_ORYSA	Q7x6i6 oryza sativ	617	30	69.8	729	2	Q4SHY3_TETNG	Q4shy3 tetraodon n				
545	30	69.8	465	2	Q5AQE0_EMENI	Q5aqe0 aspergillus	618	30	69.8	747	2	Q5JZ84_HUMAN	Q5jz84 homo sapien				
546	30	69.8	474	2	Q6G648_STAAS	Q6g648 staphylococ	619	30	69.8	748	2	Q4HV20_GIBZE	Q4hv20 gibberella				
547	30	69.8	474	2	Q5HCS1_STAAC	Q5hcs1 staphylococ	620	30	69.8	750	2	Q7QQF9_GIALA	Q7qqf9 giardia lam				
548	30	69.8	474	2	Q7A385_STAAN	Q7a385 staphylococ	621	30	69.8	750	2	Q8UD18_AGRT5	Q8ud18 agrobacteri				
549	30	69.8	474	2	Q8NUL2_STAAW	Q8nul2 staphylococ	622	30	69.8	751	2	Q6C0Z1_YARLI	Q6c0z1 yarrowia li				
550	30	69.8	474	2	Q99R10_STAAM	Q99r10 staphylococ	623	30	69.8	762	2	Q84PE3_MEDTR	Q84pe3 medicago tr				
551	30	69.8	477	2	Q5WI75_BACSK	Q5wi75 bacillus cl	624	30	69.8	762	2	Q8GSL7_MEDTR	Q8gsl7 medicago tr				
552	30	69.8	490	2	Q4I628_GIBZE	Q4i628 gibberella	625	30	69.8	771	2	Q5FT66_GLUOX	Q5ft66 gluconobact				
553	30	69.8	492	2	Q5PQS9_RAT	Q5pqs9 rattus norv	626	30	69.8	773	2	Q66IN9_XENLA	Q66in9 xenopus lae				
554	30	69.8	497	2	Q6Z4J7_ORYSA	Q6z4j7 oryza sativ	627	30	69.8	778	2	Q7TZE9_MYCBO	Q7tze9 mycobacteri				
555	30	69.8	497	2	Q4S753_TETNG	Q4s753 tetraodon n	628	30	69.8	778	2	P95149_MYCTU	P95149 mycobacteri				
556	30	69.8	499	1	C11B1_RAT	P15393 rattus norv	629	30	69.8	779	2	Q7CXD3_AGRT5	Q7cxd3 agrobacteri				
557	30	69.8	500	1	C11B2_MESAU	Q64658 mesocricetu	630	30	69.8	779	2	Q9A546_CAUCR	Q9a546 caulobacter				
558	30	69.8	500	1	C11B2_MOUSE	P15539 mus musculu	631	30	69.8	781	2	Q8C0N7_MOUSE	Q8c0n7 mus musculu				
559	30	69.8	500	2	Q9QW69_9MURI	Q9qw69 mus sp. 11	632	30	69.8	789	2	Q8X0N2_NEUCR	Q8x0n2 neurospora				
560	30	69.8	501	1	VGLC_GAHVB	P22650 gallid herp	633	30	69.8	798	1	K1683_MACFA	Q8wnu4 macaca fasc				
561	30	69.8	501	1	VGLC_GAHVM	P22651 gallid herp	634	30	69.8	804	2	Q8VJV5_MYCTU	Q8vjv5 mycobacteri				
562	30	69.8	501	1	VGLC_GAHVR	P33500 gallid herp	635	30	69.8	834	2	Q6D0N0_ERWCT	Q6d0n0 erwinia car				
563	30	69.8	501	2	Q6YL27_MEHV1	Q6yl27 meleagrid h	636	30	69.8	841	2	Q4P1G3_USTMA	Q4p1g3 ustilago ma				
564	30	69.8	501	2	Q77MR8_MEHV1	Q77mr8 meleagrid h	637	30	69.8	846	2	Q894T5_CLOTE	Q894t5 clostridium				
565	30	69.8	501	2	Q8JLV7_MEHV1	Q8jlv7 meleagrid h	638	30	69.8	857	1	M2GD_RAT	Q63342 rattus norv				
566	30	69.8	501	2	Q8JLV8_MEHV1	Q8jlv8 meleagrid h	639	30	69.8	857	2	Q5RKL4_RAT	Q5rkl4 rattus norv				
567	30	69.8	505	1	VGLC_GAHVG	P10681 gallid herp	640	30	69.8	866	1	M2GD_HUMAN	Q9ui17 homo sapien				
568	30	69.8	505	2	Q9L037_STRCO	Q9l037 streptomyce	641	30	69.8	869	1	M2GD_MOUSE	Q9dbt9 mus musculu				
569	30	69.8	511	2	Q7S800_NEUCR	Q7s800 neurospora	642	30	69.8	869	2	Q5EBH4_MOUSE	Q5ebh4 mus musculu				
570	30	69.8	514	2	Q8LII7_ORYSA	Q8lii7 oryza sativ	643	30	69.8	871	2	Q58DC8_BOVIN	Q58dc8 bos taurus				
571	30	69.8	518	2	Q8C0V2_MOUSE	Q8c0v2 mus musculu	644	30	69.8	886	2	Q68XX5_RICTY	Q68xx5 rickettsia				
572	30	69.8	521	2	Q4UF28_THEAN	Q4uf28 theileria a	645	30	69.8	888	2	Q9ZE41_RICPR	Q9ze41 rickettsia				
573	30	69.8	528	2	Q8X0M5_NEUCR	Q8x0m5 neurospora	646	30	69.8	892	2	Q4P344_USTMA	Q4p344 ustilago ma				
574	30	69.8	539	2	Q4WDK9_ASPFU	Q4wdk9 aspergillus	647	30	69.8	909	2	Q5U5L9_MOUSE	Q5u5l9 mus musculu				
575	30	69.8	544	2	Q7XVA7_ORYSA	Q7xva7 oryza sativ	648	30	69.8	911	1	DSG1C_MOUSE	Q7tsf0 mus musculu				
576	30	69.8	552	1	YGXB_BACSU	P37874 bacillus su	649	30	69.8	935	2	Q6ZQM5_MOUSE	Q6zqm5 mus musculu				
577	30	69.8	557	2	Q4WAB7_ASPFU	Q4wab7 aspergillus	650	30	69.8	968	2	Q4I554_GIBZE	Q4i554 gibberella				
578	30	69.8	564	2	Q5LA53_BACFN	Q5la53 bacteroides	651	30	69.8	977	2	Q52EM1_MAGGR	Q52em1 magnaporthe				
579	30	69.8	580	2	Q64QH1_BACFR	Q64qh1 bacteroides	652	30	69.8	998	2	Q75I84_ORYSA	Q75i84 oryza sativ				
580	30	69.8	591	2	Q80MI8_9HEPC	Q80mi8 hepatitis c	653	30	69.8	1017	2	Q5FJC2_LACAC	Q5fjc2 lactobacill				
581	30	69.8	592	2	Q5KYG2_GEOKA	Q5kyg2 geobacillus	654	30	69.8	1048	2	Q9VYW5_DROME	Q9vyw5 drosophila				
582	30	69.8	598	2	Q9JS52_CHLPN	Q9js52 chlamydia p	655	30	69.8	1063	1	DHE2_ACHKL	P41755 achlya kleb				
583	30	69.8	598	2	Q9Z9C5_CHLPN	Q9z9c5 chlamydia p	656	30	69.8	1067	1	TRI1_STRCO	Q9rde2 streptomyce				
584	30	69.8	600	2	Q51TG2_MAGGR	Q51tg2 magnaporthe	657	30	69.8	1067	2	Q7SCG9_NEUCR	Q7scg9 neurospora				
585	30	69.8	605	2	Q9P564_NEUCR	Q9p564 neurospora	658	30	69.8	1073	2	Q82BY0_STRAW	Q82by0 streptomyce				
586	30	69.8	606	1	ABCD4_HUMAN	O14678 homo sapien	659	30	69.8	1093	2	Q8RQV0_BACGO	Q8rqv0 bacillus gl				
587	30	69.8	606	2	Q6IAQ0_HUMAN	Q6iaq0 homo sapien	660	30	69.8	1097	2	Q7UFE6_RHOBA	Q7ufe6 rhodopirell				
588	30	69.8	606	2	Q96E75_HUMAN	Q96e75 homo sapien	661	30	69.8	1122	2	Q60Q16_CAEBR	Q60q16 caenorhabdi				
589	30	69.8	608	2	Q4ZMC0_PSESY	Q4zmc0 pseudomonas	662	30	69.8	1140	2	Q8G9W1_ECOLI	Q8g9w1 escherichia				
590	30	69.8	609	2	Q989R7_RHILO	Q989r7 rhizobium l	663	30	69.8	1217	2	Q4XPF6_PLACH	Q4xpf6 plasmodium				
591	30	69.8	610	2	Q4K4U7_PSEF5	Q4k4u7 pseudomonas	664	30	69.8	1229	1	CR1BB_BACTU	Q45739 bacillus th				
592	30	69.8	613	2	Q8TCC6_HUMAN	Q8tcc6 homo sapien	665	30	69.8	1231	1	CR1BD_BACTZ	Q9zaz5 bacillus th				
593	30	69.8	622	2	O07653_9GAMM	O07653 cellvibrio	666	30	69.8	1231	2	Q8KNY2_BACTU	Q8kny2 bacillus th				
594	30	69.8	630	2	Q61JN2_CAEBR	Q61jn2 caenorhabdi	667	30	69.8	1233	1	CR1BC_BACTM	Q45774 bacillus th				
595	30	69.8	638	2	Q9XJ24_LUPAL	Q9xj24 lupinus alb	668	30	69.8	1266	2	Q9YGM1_CHICK	Q9ygm1 gallus gall				
596	30	69.8	641	2	Q7Y0Y5_GOSHI	Q7y0y5 gossypium h	669	30	69.8	1269	2	Q7RGW4_PLAYO	Q7rgw4 plasmodium				
597	30	69.8	641	2	Q65K31_BACLD	Q65k31 bacillus li	670	30	69.8	1270	1	RPOB_BACTN	Q8a469 bacteroides				
598	30	69.8	643	2	Q18290_CAEEL	Q18290 caenorhabdi	671	30	69.8	1297	2	Q4P954_USTMA	Q4p954 ustilago ma				
599	30	69.8	651	2	Q4QEV6_LEIMA	Q4qev6 leishmania	672	30	69.8	1301	2	Q4P2K7_USTMA	Q4p2k7 ustilago ma				
600	30	69.8	674	2	Q4IDP2_GIBZE	Q4idp2 gibberella	673	30	69.8	1322	2	Q6PB63_MOUSE	Q6pb63 mus musculu				
601	30	69.8	675	1	PROS_BOVIN	P07224 bos taurus	674	30	69.8	1440	2	Q5AYW9_EMENI	Q5ayw9 aspergillus				
602	30	69.8	696	2	O61834_CAEEL	O61834 caenorhabdi	675	30	69.8	1508	2	Q6A0D6_MOUSE	Q6a0d6 mus musculu				
603	30	69.8	699	2	Q7URK0_RHOBA	Q7urk0 rhodopirell	676	30	69.8	1638	2	Q7KPP4_CAEEL	Q7kpp4 caenorhabdi				
604	30	69.8	704	2	Q72WK8_DESVH	Q72wk8 desulfovibr	677	30	69.8	1649	2	Q6J655_9VIRU	Q6j655 dendrolimus				
605	30	69.8	706	2	Q6IA69_HUMAN	Q6ia69 homo sapien	678	30	69.8	1742	2	Q24463_DROME	Q24463 drosophila				
606	30	69.8	706	2	Q86SN2_HUMAN	Q86sn2 homo sapien	679	30	69.8	1756	2	Q4X0H7_ASPFU	Q4x0h7 aspergillus				
607	30	69.8	706	2	Q9HA25_HUMAN	Q9ha25 homo sapien	680	30	69.8	1894	2	Q51VF8_MAGGR	Q51vf8 magnaporthe				
608	30	69.8	706	2	Q9NVM8_HUMAN	Q9nvm8 homo sapien	681	30	69.8	1926	2	Q4T3C9_TETNG	Q4t3c9 tetraodon n				
609	30	69.8	706	2	Q4R5Y2_MACFA	Q4r5y2 macaca fasc	682	30	69.8	2051	2	Q4SLV2_TETNG	Q4slv2 tetraodon n				
610	30	69.8	711	1	PO22_POPJA	Q03274 popillia ja	683	30	69.8	2140	2	Q6BEW2_CAEEL	Q6bew2 caenorhabdi				
611	30	69.8	719	2	Q4I480_GIBZE	Q4i480 gibberella	684	30	69.8	2182	2	Q26034_PLAFA	Q26034 plasmodium				
612	30	69.8	722	2	Q4HC70_9DEIO	Q4hc70 deinococcus	685	30	69.8	2236	1	PYR1_DROME	P05990 drosophila				
613	30	69.8	723	2	Q527L2_MAGGR	Q52712 magnaporthe	686	30	69.8	2303	2	Q4RXZ9_TETNG	Q4rxz9 tetraodon n				
614	30	69.8	726	2	Q8SRX5_ENCCU	Q8srx5 encephalito	687	30	69.8	2359	2	Q59FG2_HUMAN	Q59fg2 homo sapien				
615	30	69.8	727	2	Q91W76_MOUSE	Q91w76 mus musculu	688	30	69.8	2378	2	Q4RW31_TETNG	Q4rw31 tetraodon n				

689	30	69.8	2383	2	Q5DTT3_MOUSE	Q5dtt3 mus musculu
690	30	69.8	2411	2	Q6CXV6_KLULA	Q6cxv6 kluyveromyc
691	30	69.8	2414	2	Q72BT9_DESVH	Q72bt9 desulfovibr
692	30	69.8	2488	2	O61528_CAEEL	O61528 caenorhabdi
693	30	69.8	3009	1	POLG_HCVTW	P29846 h genome po
694	30	69.8	3866	1	HRX_MOUSE	P55200 mus musculu
695	30	69.8	3969	1	HRX_HUMAN	Q03164 homo sapien
696	30	69.8	4543	1	LRP1_CHICK	P98157 gallus gall
697	30	69.8	4544	1	LRP1_HUMAN	Q07954 homo sapien
698	30	69.8	4545	2	Q61291_MOUSE	Q61291 mus musculu
699	30	69.8	4545	2	Q91ZX7_MOUSE	Q91zx7 mus musculu
700	30	69.8	4545	2	Q920Y4_MOUSE	Q920y4 mus musculu
701	30	69.8	4599	1	LRP1B_HUMAN	Q9nzr2 homo sapien
702	30	69.8	4599	1	LRP1B_MOUSE	Q9ji18 mus musculu
703	30	69.8	6658	2	O76281_DROME	O76281 drosophila
704	30	69.8	8647	2	Q7KQP5_DROME	Q7kqp5 drosophila
705	30	69.8	8648	2	Q7KQP6_DROME	Q7kqp6 drosophila
706	30	69.8	8930	2	Q7KQP7_DROME	Q7kqp7 drosophila
707	30	69.8	8943	2	Q9V4F7_DROME	Q9v4f7 drosophila
708	29	67.4	30	2	Q5BRL2_SCHJA	Q5brl2 schistosoma
709	29	67.4	51	2	Q8N5G3_HUMAN	Q8n5g3 homo sapien
710	29	67.4	61	2	Q52PN0_9CAUD	Q52pn0 xanthomonas
711	29	67.4	69	2	Q7UEB9_RHOBA	Q7ueb9 rhodopirell
712	29	67.4	74	2	Q4N1Z5_THEPA	Q4n1z5 theileria p
713	29	67.4	78	1	YO09_BPL2	P42544 bacteriopha
714	29	67.4	78	2	O40608_9HEPC	O40608 hepatitis c
715	29	67.4	78	2	O40609_9HEPC	O40609 hepatitis c
716	29	67.4	88	2	Q5U9L3_9ACTO	Q5u9l3 nocardioide
717	29	67.4	94	2	Q6H4Q3_ORYSA	Q6h4q3 oryza sativ
718	29	67.4	95	2	Q7Y470_9CAUD	Q7y470 enterobacte
719	29	67.4	108	2	Q7UNR9_RHOBA	Q7unr9 rhodopirell
720	29	67.4	109	2	Q4RGR4_TETNG	Q4rgr4 tetraodon n
721	29	67.4	117	2	Q7NTH7_CHRVO	Q7nth7 chromobacte
722	29	67.4	118	2	Q8TJV2_METAC	Q8tjv2 methanosarc
723	29	67.4	118	2	Q6YKV7_9HEPC	Q6ykv7 hepatitis c
724	29	67.4	121	2	Q6YKW7_9HEPC	Q6ykw7 hepatitis c
725	29	67.4	122	2	Q6AV27_ORYSA	Q6av27 oryza sativ
726	29	67.4	123	2	Q95Z50_PLAFA	Q95z50 plasmodium
727	29	67.4	126	2	Q6RXU0_HPBV0	Q6rxu0 hepatitis b
728	29	67.4	128	2	Q8ST76_PLAFA	Q8st76 plasmodium
729	29	67.4	129	2	Q6N6T5_RHOPA	Q6n6t5 rhodopseudo
730	29	67.4	130	2	Q9XZ88_PLAFA	Q9xz88 plasmodium
731	29	67.4	130	2	Q6YL16_9HEPC	Q6yl16 hepatitis c
732	29	67.4	131	2	Q9NHJ8_PLAFA	Q9nhj8 plasmodium
733	29	67.4	131	2	Q9D1L2_MOUSE	Q9d1l2 mus musculu
734	29	67.4	131	2	Q6YKS6_9HEPC	Q6yks6 hepatitis c
735	29	67.4	132	2	Q9XZ92_PLAFA	Q9xz92 plasmodium
736	29	67.4	132	2	Q6YKY1_9HEPC	Q6yky1 hepatitis c
737	29	67.4	133	2	Q7V9B6_PROMM	Q7v9b6 prochloroco
738	29	67.4	133	2	Q6YKX7_9HEPC	Q6ykx7 hepatitis c
739	29	67.4	133	2	Q6YKY0_9HEPC	Q6yky0 hepatitis c
740	29	67.4	134	2	Q56434_THETH	Q56434 thermus the
741	29	67.4	134	2	Q5M8V1_XENTR	Q5m8v1 xenopus tro
742	29	67.4	136	2	Q95W67_PLAFA	Q95w67 plasmodium
743	29	67.4	136	2	Q6YKY5_9HEPC	Q6yky5 hepatitis c
744	29	67.4	136	2	Q6YKY8_9HEPC	Q6yky8 hepatitis c
745	29	67.4	137	2	Q6S8Q5_PLAFA	Q6s8q5 plasmodium
746	29	67.4	137	2	Q6YKY4_9HEPC	Q6yky4 hepatitis c
747	29	67.4	137	2	Q6YKZ4_9HEPC	Q6ykz4 hepatitis c
748	29	67.4	138	2	Q6YKU0_9HEPC	Q6yku0 hepatitis c
749	29	67.4	138	2	Q6YKZ0_9HEPC	Q6ykz0 hepatitis c
750	29	67.4	138	2	Q6YL10_9HEPC	Q6yl10 hepatitis c
751	29	67.4	139	2	Q6YKS9_9HEPC	Q6yks9 hepatitis c
752	29	67.4	139	2	Q6YKW9_9HEPC	Q6ykw9 hepatitis c
753	29	67.4	139	2	Q6YKY9_9HEPC	Q6yky9 hepatitis c
754	29	67.4	139	2	Q6YL15_9HEPC	Q6yl15 hepatitis c
755	29	67.4	140	2	Q6YKX3_9HEPC	Q6ykx3 hepatitis c
756	29	67.4	141	2	Q6YKS0_9HEPC	Q6yks0 hepatitis c
757	29	67.4	141	2	Q6YKS2_9HEPC	Q6yks2 hepatitis c
758	29	67.4	141	2	Q6YKS3_9HEPC	Q6yks3 hepatitis c
759	29	67.4	141	2	Q6YKS5_9HEPC	Q6yks5 hepatitis c
760	29	67.4	141	2	Q6YKS8_9HEPC	Q6yks8 hepatitis c
761	29	67.4	141	2	Q6YKT4_9HEPC	Q6ykt4 hepatitis c
762	29	67.4	141	2	Q6YKT5_9HEPC	Q6ykt5 hepatitis c
763	29	67.4	141	2	Q6YKT6_9HEPC	Q6ykt6 hepatitis c
764	29	67.4	141	2	Q6YKT7_9HEPC	Q6ykt7 hepatitis c
765	29	67.4	141	2	Q6YKT8_9HEPC	Q6ykt8 hepatitis c
766	29	67.4	141	2	Q6YKU3_9HEPC	Q6yku3 hepatitis c
767	29	67.4	141	2	Q6YKU4_9HEPC	Q6yku4 hepatitis c
768	29	67.4	141	2	Q6YKU5_9HEPC	Q6yku5 hepatitis c
769	29	67.4	141	2	Q6YKU8_9HEPC	Q6yku8 hepatitis c
770	29	67.4	141	2	Q6YKU9_9HEPC	Q6yku9 hepatitis c
771	29	67.4	141	2	Q6YKV0_9HEPC	Q6ykv0 hepatitis c
772	29	67.4	141	2	Q6YKV2_9HEPC	Q6ykv2 hepatitis c
773	29	67.4	141	2	Q6YKV3_9HEPC	Q6ykv3 hepatitis c
774	29	67.4	141	2	Q6YKV5_9HEPC	Q6ykv5 hepatitis c
775	29	67.4	141	2	Q6YKV8_9HEPC	Q6ykv8 hepatitis c
776	29	67.4	141	2	Q6YKV9_9HEPC	Q6ykv9 hepatitis c
777	29	67.4	141	2	Q6YKW3_9HEPC	Q6ykw3 hepatitis c
778	29	67.4	141	2	Q6YKW8_9HEPC	Q6ykw8 hepatitis c
779	29	67.4	141	2	Q6YKX2_9HEPC	Q6ykx2 hepatitis c
780	29	67.4	141	2	Q6YKX4_9HEPC	Q6ykx4 hepatitis c
781	29	67.4	141	2	Q6YKX5_9HEPC	Q6ykx5 hepatitis c
782	29	67.4	141	2	Q6YKX8_9HEPC	Q6ykx8 hepatitis c
783	29	67.4	141	2	Q6YKY7_9HEPC	Q6yky7 hepatitis c
784	29	67.4	141	2	Q6YKZ3_9HEPC	Q6ykz3 hepatitis c
785	29	67.4	141	2	Q6YKZ6_9HEPC	Q6ykz6 hepatitis c
786	29	67.4	141	2	Q6YL01_9HEPC	Q6yl01 hepatitis c
787	29	67.4	141	2	Q6YL05_9HEPC	Q6yl05 hepatitis c
788	29	67.4	141	2	Q6YL09_9HEPC	Q6yl09 hepatitis c
789	29	67.4	141	2	Q6YL13_9HEPC	Q6yl13 hepatitis c
790	29	67.4	142	2	Q6YKS1_9HEPC	Q6yks1 hepatitis c
791	29	67.4	142	2	Q6YKS4_9HEPC	Q6yks4 hepatitis c
792	29	67.4	142	2	Q6YKS7_9HEPC	Q6yks7 hepatitis c
793	29	67.4	142	2	Q6YKT1_9HEPC	Q6ykt1 hepatitis c
794	29	67.4	142	2	Q6YKT2_9HEPC	Q6ykt2 hepatitis c
795	29	67.4	142	2	Q6YKT3_9HEPC	Q6ykt3 hepatitis c
796	29	67.4	142	2	Q6YKU1_9HEPC	Q6yku1 hepatitis c
797	29	67.4	142	2	Q6YKU2_9HEPC	Q6yku2 hepatitis c
798	29	67.4	142	2	Q6YKU6_9HEPC	Q6yku6 hepatitis c
799	29	67.4	142	2	Q6YKU7_9HEPC	Q6yku7 hepatitis c
800	29	67.4	142	2	Q6YKV1_9HEPC	Q6ykv1 hepatitis c
801	29	67.4	142	2	Q6YKV4_9HEPC	Q6ykv4 hepatitis c
802	29	67.4	142	2	Q6YKV6_9HEPC	Q6ykv6 hepatitis c
803	29	67.4	142	2	Q6YKW0_9HEPC	Q6ykw0 hepatitis c
804	29	67.4	142	2	Q6YKW1_9HEPC	Q6ykw1 hepatitis c
805	29	67.4	142	2	Q6YKW2_9HEPC	Q6ykw2 hepatitis c
806	29	67.4	142	2	Q6YKW4_9HEPC	Q6ykw4 hepatitis c
807	29	67.4	142	2	Q6YKW5_9HEPC	Q6ykw5 hepatitis c
808	29	67.4	142	2	Q6YKW6_9HEPC	Q6ykw6 hepatitis c
809	29	67.4	142	2	Q6YKX0_9HEPC	Q6ykx0 hepatitis c
810	29	67.4	142	2	Q6YKX1_9HEPC	Q6ykx1 hepatitis c
811	29	67.4	142	2	Q6YKX6_9HEPC	Q6ykx6 hepatitis c
812	29	67.4	142	2	Q6YKY2_9HEPC	Q6yky2 hepatitis c
813	29	67.4	142	2	Q6YKY3_9HEPC	Q6yky3 hepatitis c
814	29	67.4	142	2	Q6YKY6_9HEPC	Q6yky6 hepatitis c
815	29	67.4	142	2	Q6YKZ1_9HEPC	Q6ykz1 hepatitis c
816	29	67.4	142	2	Q6YKZ2_9HEPC	Q6ykz2 hepatitis c
817	29	67.4	142	2	Q6YKZ7_9HEPC	Q6ykz7 hepatitis c
818	29	67.4	142	2	Q6YKZ8_9HEPC	Q6ykz8 hepatitis c
819	29	67.4	142	2	Q6YKZ9_9HEPC	Q6ykz9 hepatitis c
820	29	67.4	142	2	Q6YL00_9HEPC	Q6yl00 hepatitis c
821	29	67.4	142	2	Q6YL02_9HEPC	Q6yl02 hepatitis c
822	29	67.4	142	2	Q6YL03_9HEPC	Q6yl03 hepatitis c
823	29	67.4	142	2	Q6YL04_9HEPC	Q6yl04 hepatitis c
824	29	67.4	142	2	Q6YL06_9HEPC	Q6yl06 hepatitis c
825	29	67.4	142	2	Q6YL07_9HEPC	Q6yl07 hepatitis c
826	29	67.4	142	2	Q6YL08_9HEPC	Q6yl08 hepatitis c
827	29	67.4	142	2	Q6YL11_9HEPC	Q6yl11 hepatitis c
828	29	67.4	142	2	Q6YL12_9HEPC	Q6yl12 hepatitis c
829	29	67.4	142	2	Q6YL14_9HEPC	Q6yl14 hepatitis c
830	29	67.4	142	2	Q6YL17_9HEPC	Q6yl17 hepatitis c
831	29	67.4	142	2	Q81617_9HEPC	Q81617 hepatitis c
832	29	67.4	149	2	O10377_9VIRU	O10377 pineapple b
833	29	67.4	155	2	Q8C3D3_MOUSE	Q8c3d3 mus musculu
834	29	67.4	156	2	Q75Q04_9HEPC	Q75q04 hepatitis c

835	29	67.4	156	2	Q75Q05_9HEPC	Q75q05	hepatitis c
836	29	67.4	156	2	Q75Q06_9HEPC	Q75q06	hepatitis c
837	29	67.4	156	2	Q75Q07_9HEPC	Q75q07	hepatitis c
838	29	67.4	156	2	Q75Q08_9HEPC	Q75q08	hepatitis c
839	29	67.4	156	2	Q75Q09_9HEPC	Q75q09	hepatitis c
840	29	67.4	156	2	Q75Q10_9HEPC	Q75q10	hepatitis c
841	29	67.4	156	2	Q75Q11_9HEPC	Q75q11	hepatitis c
842	29	67.4	156	2	Q75Q12_9HEPC	Q75q12	hepatitis c
843	29	67.4	156	2	Q75Q13_9HEPC	Q75q13	hepatitis c
844	29	67.4	156	2	Q75Q14_9HEPC	Q75q14	hepatitis c
845	29	67.4	156	2	Q75Q15_9HEPC	Q75q15	hepatitis c
846	29	67.4	156	2	Q75Q16_9HEPC	Q75q16	hepatitis c
847	29	67.4	156	2	Q75Q17_9HEPC	Q75q17	hepatitis c
848	29	67.4	156	2	Q75Q18_9HEPC	Q75q18	hepatitis c
849	29	67.4	156	2	Q75Q19_9HEPC	Q75q19	hepatitis c
850	29	67.4	156	2	Q75Q20_9HEPC	Q75q20	hepatitis c
851	29	67.4	156	2	Q81633_9HEPC	Q81633	hepatitis c
852	29	67.4	158	2	Q58PQ3_9PROT	Q58pq3	uncultured
853	29	67.4	158	2	Q5YNM5_NOCFA	Q5ynm5	nocardia fa
854	29	67.4	158	2	Q80MD2_9HEPC	Q80md2	hepatitis c
855	29	67.4	158	2	Q80MD3_9HEPC	Q80md3	hepatitis c
856	29	67.4	158	2	Q80MD4_9HEPC	Q80md4	hepatitis c
857	29	67.4	158	2	Q80MD5_9HEPC	Q80md5	hepatitis c
858	29	67.4	158	2	Q80MD6_9HEPC	Q80md6	hepatitis c
859	29	67.4	158	2	Q80MD7_9HEPC	Q80md7	hepatitis c
860	29	67.4	158	2	Q80MD8_9HEPC	Q80md8	hepatitis c
861	29	67.4	158	2	Q80MD9_9HEPC	Q80md9	hepatitis c
862	29	67.4	158	2	Q80ME0_9HEPC	Q80me0	hepatitis c
863	29	67.4	158	2	Q80ME1_9HEPC	Q80me1	hepatitis c
864	29	67.4	158	2	Q80ME2_9HEPC	Q80me2	hepatitis c
865	29	67.4	158	2	Q80ME3_9HEPC	Q80me3	hepatitis c
866	29	67.4	158	2	Q80ME4_9HEPC	Q80me4	hepatitis c
867	29	67.4	158	2	Q80ME5_9HEPC	Q80me5	hepatitis c
868	29	67.4	158	2	Q80ME6_9HEPC	Q80me6	hepatitis c
869	29	67.4	158	2	Q80ME7_9HEPC	Q80me7	hepatitis c
870	29	67.4	158	2	Q80ME8_9HEPC	Q80me8	hepatitis c
871	29	67.4	158	2	Q80ME9_9HEPC	Q80me9	hepatitis c
872	29	67.4	158	2	Q80MF0_9HEPC	Q80mf0	hepatitis c
873	29	67.4	158	2	Q80MF1_9HEPC	Q80mf1	hepatitis c
874	29	67.4	158	2	Q80MF2_9HEPC	Q80mf2	hepatitis c
875	29	67.4	158	2	Q80MF3_9HEPC	Q80mf3	hepatitis c
876	29	67.4	158	2	Q80MF4_9HEPC	Q80mf4	hepatitis c
877	29	67.4	158	2	Q80MF5_9HEPC	Q80mf5	hepatitis c
878	29	67.4	158	2	Q80MF6_9HEPC	Q80mf6	hepatitis c
879	29	67.4	158	2	Q80MF7_9HEPC	Q80mf7	hepatitis c
880	29	67.4	158	2	Q80MG0_9HEPC	Q80mg0	hepatitis c
881	29	67.4	166	1	PFPI_PYRFU	Q51732	pyrococcus
882	29	67.4	166	2	Q5JGM7_PYRKO	Q5jgm7	pyrococcus
883	29	67.4	173	2	Q8B6A9_9PICO	Q8b6a9	aichi virus
884	29	67.4	176	2	Q5Z1Z6_NOCFA	Q5z1z6	nocardia fa
885	29	67.4	186	2	Q9N2X1_CAEEL	Q9n2x1	caenorhabdi
886	29	67.4	187	2	Q8WPX5_PLAFA	Q8wpx5	plasmodium
887	29	67.4	191	2	Q9C741_ARATH	Q9c741	arabidopsis
888	29	67.4	191	2	Q6FDD5_ACIAD	Q6fdd5	acinetobact
889	29	67.4	194	2	Q5L4P6_CHLAB	Q5l4p6	chlamydophi
890	29	67.4	194	2	Q4W816_9HEPC	Q4w816	hepatitis c
891	29	67.4	194	2	Q4W817_9HEPC	Q4w817	hepatitis c
892	29	67.4	194	2	Q4W818_9HEPC	Q4w818	hepatitis c
893	29	67.4	194	2	Q4W819_9HEPC	Q4w819	hepatitis c
894	29	67.4	194	2	Q4W820_9HEPC	Q4w820	hepatitis c
895	29	67.4	194	2	Q4W821_9HEPC	Q4w821	hepatitis c
896	29	67.4	194	2	Q4W822_9HEPC	Q4w822	hepatitis c
897	29	67.4	194	2	Q4W823_9HEPC	Q4w823	hepatitis c
898	29	67.4	194	2	Q4W824_9HEPC	Q4w824	hepatitis c
899	29	67.4	194	2	Q4W825_9HEPC	Q4w825	hepatitis c
900	29	67.4	194	2	Q4W826_9HEPC	Q4w826	hepatitis c
901	29	67.4	197	2	Q52SS4_SIVCZ	Q52ss4	chimpanzee
902	29	67.4	200	2	Q53SC7_HUMAN	Q53sc7	homo sapien
903	29	67.4	201	2	Q93VU9_ORYSA	Q93vu9	oryza sativ
904	29	67.4	202	2	Q52SR8_SIVCZ	Q52sr8	chimpanzee
905	29	67.4	202	2	Q52SR9_SIVCZ	Q52sr9	chimpanzee
906	29	67.4	202	2	Q52SS1_SIVCZ	Q52ss1	chimpanzee
907	29	67.4	202	2	Q52SS2_SIVCZ	Q52ss2	chimpanzee
908	29	67.4	202	2	Q52SS3_SIVCZ	Q52ss3	chimpanzee
909	29	67.4	203	2	Q5E565_VIBF1	Q5e565	vibrio fisc
910	29	67.4	204	1	PTH_PROMA	Q7vdt7	prochloroco
911	29	67.4	204	2	Q8U6D2_AGRT5	Q8u6d2	agrobacteri
912	29	67.4	205	2	Q8JXR1_9HEPC	Q8jxr1	hepatitis c
913	29	67.4	206	2	Q4KDN1_PSEF5	Q4kdn1	pseudomonas
914	29	67.4	206	2	Q9I681_PSEAE	Q9i681	pseudomonas
915	29	67.4	206	2	Q7T7Z0_9HEPC	Q7t7z0	hepatitis c
916	29	67.4	207	2	Q4K6R4_PSEF5	Q4k6r4	pseudomonas
917	29	67.4	207	2	Q7T7Y7_9HEPC	Q7t7y7	hepatitis c
918	29	67.4	210	2	Q8JQ72_9HEPC	Q8jq72	hepatitis c
919	29	67.4	210	2	Q8JY00_9HEPC	Q8jy00	hepatitis c
920	29	67.4	211	2	Q7T7Y6_9HEPC	Q7t7y6	hepatitis c
921	29	67.4	211	2	Q7T7Y8_9HEPC	Q7t7y8	hepatitis c
922	29	67.4	211	2	Q7T7Z1_9HEPC	Q7t7z1	hepatitis c
923	29	67.4	211	2	Q7T7Z2_9HEPC	Q7t7z2	hepatitis c
924	29	67.4	211	2	Q7T7Z3_9HEPC	Q7t7z3	hepatitis c
925	29	67.4	211	2	Q7T7Z4_9HEPC	Q7t7z4	hepatitis c
926	29	67.4	211	2	Q7T7Z5_9HEPC	Q7t7z5	hepatitis c
927	29	67.4	211	2	Q7T7Z6_9HEPC	Q7t7z6	hepatitis c
928	29	67.4	211	2	Q7T7Z7_9HEPC	Q7t7z7	hepatitis c
929	29	67.4	211	2	Q7T7Z8_9HEPC	Q7t7z8	hepatitis c
930	29	67.4	211	2	Q7T7Z9_9HEPC	Q7t7z9	hepatitis c
931	29	67.4	211	2	Q8JXZ7_9HEPC	Q8jxz7	hepatitis c
932	29	67.4	212	1	YCDC_ECOLI	P75899	escherichia
933	29	67.4	212	2	Q6NP39_DROME	Q6np39	drosophila
934	29	67.4	212	2	Q8X4Z7_ECO57	Q8x4z7	escherichia
935	29	67.4	212	2	Q8JXZ8_9HEPC	Q8jxz8	hepatitis c
936	29	67.4	212	2	Q8JXZ9_9HEPC	Q8jxz9	hepatitis c
937	29	67.4	213	2	Q8JY49_9HEPC	Q8jy49	hepatitis c
938	29	67.4	214	2	Q8JXZ2_9HEPC	Q8jxz2	hepatitis c
939	29	67.4	215	2	Q836F8_ENTFA	Q836f8	enterococcu
940	29	67.4	216	1	ALKB_SALTY	P37462	salmonella
941	29	67.4	216	2	Q57M88_SALCH	Q57m88	salmonella
942	29	67.4	216	2	Q5PI38_SALPA	Q5pi38	salmonella
943	29	67.4	216	2	Q8JXR5_9HEPC	Q8jxr5	hepatitis c
944	29	67.4	216	2	Q80JX9_9PICO	Q80jx9	foot-and-mo
945	29	67.4	217	2	Q82ND0_STRAW	Q82nd0	streptomyce
946	29	67.4	217	2	Q8JXR0_9HEPC	Q8jxr0	hepatitis c
947	29	67.4	217	2	Q8JXR2_9HEPC	Q8jxr2	hepatitis c
948	29	67.4	217	2	Q8JXR3_9HEPC	Q8jxr3	hepatitis c
949	29	67.4	217	2	Q8JXR4_9HEPC	Q8jxr4	hepatitis c
950	29	67.4	217	2	Q8JXS1_9HEPC	Q8jxs1	hepatitis c
951	29	67.4	217	2	Q8JY10_9HEPC	Q8jy10	hepatitis c
952	29	67.4	218	2	Q8JXZ1_9HEPC	Q8jxz1	hepatitis c
953	29	67.4	219	2	Q8JXZ0_9HEPC	Q8jxz0	hepatitis c
954	29	67.4	220	2	Q6CBD8_YARLI	Q6cbd8	yarrowia li
955	29	67.4	220	2	Q8JY55_9HEPC	Q8jy55	hepatitis c
956	29	67.4	221	2	Q8JXS6_9HEPC	Q8jxs6	hepatitis c
957	29	67.4	223	2	Q8JXZ3_9HEPC	Q8jxz3	hepatitis c
958	29	67.4	223	2	Q8JXZ4_9HEPC	Q8jxz4	hepatitis c
959	29	67.4	223	2	Q8JXZ5_9HEPC	Q8jxz5	hepatitis c
960	29	67.4	224	2	Q8JXZ6_9HEPC	Q8jxz6	hepatitis c
961	29	67.4	225	2	Q6NFH6_CORDI	Q6nfh6	corynebacte
962	29	67.4	225	2	Q8JY01_9HEPC	Q8jy01	hepatitis c
963	29	67.4	225	2	Q8JY22_9HEPC	Q8jy22	hepatitis c
964	29	67.4	225	2	Q8JY29_9HEPC	Q8jy29	hepatitis c
965	29	67.4	225	2	Q8JY48_9HEPC	Q8jy48	hepatitis c
966	29	67.4	225	2	Q8JY50_9HEPC	Q8jy50	hepatitis c
967	29	67.4	225	2	Q8JY53_9HEPC	Q8jy53	hepatitis c
968	29	67.4	226	2	Q8JXR7_9HEPC	Q8jxr7	hepatitis c
969	29	67.4	226	2	Q8JXR8_9HEPC	Q8jxr8	hepatitis c
970	29	67.4	226	2	Q8JXT5_9HEPC	Q8jxt5	hepatitis c
971	29	67.4	227	2	Q82QL7_STRAW	Q82ql7	streptomyce
972	29	67.4	227	2	Q8JQ76_9HEPC	Q8jq76	hepatitis c
973	29	67.4	227	2	Q8JQ77_9HEPC	Q8jq77	hepatitis c
974	29	67.4	227	2	Q8JQ78_9HEPC	Q8jq78	hepatitis c
975	29	67.4	227	2	Q8JQ79_9HEPC	Q8jq79	hepatitis c
976	29	67.4	227	2	Q8JQ80_9HEPC	Q8jq80	hepatitis c
977	29	67.4	227	2	Q8JQ82_9HEPC	Q8jq82	hepatitis c
978	29	67.4	227	2	Q8JQ83_9HEPC	Q8jq83	hepatitis c
979	29	67.4	227	2	Q8JQ84_9HEPC	Q8jq84	hepatitis c
980	29	67.4	227	2	Q8JQ85_9HEPC	Q8jq85	hepatitis c

981	29	67.4	227	2	Q8JQ86_9HEPC	Q8jq86 hepatitis c
982	29	67.4	227	2	Q8JQ87_9HEPC	Q8jq87 hepatitis c
983	29	67.4	227	2	Q8JQ88_9HEPC	Q8jq88 hepatitis c
984	29	67.4	227	2	Q8JQ89_9HEPC	Q8jq89 hepatitis c
985	29	67.4	227	2	Q8JXR9_9HEPC	Q8jxr9 hepatitis c
986	29	67.4	227	2	Q8JXV9_9HEPC	Q8jxv9 hepatitis c
987	29	67.4	227	2	Q8JXW6_9HEPC	Q8jxw6 hepatitis c
988	29	67.4	227	2	Q8JY02_9HEPC	Q8jy02 hepatitis c
989	29	67.4	227	2	Q8JY03_9HEPC	Q8jy03 hepatitis c
990	29	67.4	227	2	Q8JY04_9HEPC	Q8jy04 hepatitis c
991	29	67.4	227	2	Q8JY06_9HEPC	Q8jy06 hepatitis c
992	29	67.4	227	2	Q8JY08_9HEPC	Q8jy08 hepatitis c
993	29	67.4	227	2	Q8JY09_9HEPC	Q8jy09 hepatitis c
994	29	67.4	227	2	Q8JY11_9HEPC	Q8jy11 hepatitis c
995	29	67.4	227	2	Q8JY12_9HEPC	Q8jy12 hepatitis c
996	29	67.4	227	2	Q8JY13_9HEPC	Q8jy13 hepatitis c
997	29	67.4	227	2	Q8JY14_9HEPC	Q8jy14 hepatitis c
998	29	67.4	227	2	Q8JY15_9HEPC	Q8jy15 hepatitis c
999	29	67.4	227	2	Q8JY16_9HEPC	Q8jy16 hepatitis c
1000	29	67.4	227	2	Q8JY20_9HEPC	Q8jy20 hepatitis c

ALIGNMENTS

```
RESULT 1
Q9LWA4_LYCES
ID   Q9LWA4_LYCES PRELIMINARY;      PRT;   743 AA.
AC   Q9LWA4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Subtilisin-like protease.
GN   Name=P69E;
OS   Lycopersicon esculentum (Tomato).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
OX   NCBI_TaxID=4081;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Leaf;
RX   MEDLINE=20098714; PubMed=10631250; DOI=10.1104/pp.122.1.67;
RA   Jorda L., Conejero V., Vera P.;
RT   "Characterization of two differentially regulated genes (P69E and
RT   P69F) encoding new members of the subtilisin-like protease clan from
RT   tomato plants.";
RL   Plant Physiol. 122:67-76(2000).
DR   EMBL; Y18931; CAB67119.1; -; Genomic_DNA.
DR   HSSP; Q99405; 1MPT.
DR   MEROPS; S08.006; -.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0042802; F:protein self binding; IEA.
DR   GO; GO:0004289; F:subtilase activity; IEA.
DR   GO; GO:0043086; P:negative regulation of enzyme activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR003137; PA.
DR   InterPro; IPR000209; Pept_S8_S53.
DR   InterPro; IPR010259; Prot_inh_S8A.
DR   Pfam; PF02225; PA; 1.
DR   Pfam; PF00082; Peptidase_S8; 1.
DR   Pfam; PF05922; Subtilisin_N; 1.
DR   PRINTS; PR00723; SUBTILISIN.
DR   PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
DR   PROSITE; PS00138; SUBTILASE_SER; UNKNOWN_1.
KW   Protease.
SQ   SEQUENCE   743 AA;  79133 MW;  63EE2F92B2510BCA CRC64;

  Query Match             90.7%;  Score 39;  DB 2;  Length 743;
  Best Local Similarity   85.7%;  Pred. No. 73;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||||||:
Db        727 WTSTRHS 733


RESULT 2
Q9LWA3_LYCES
ID   Q9LWA3_LYCES PRELIMINARY;      PRT;   746 AA.
AC   Q9LWA3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Subtilisin-like protease.
GN   Name=P69F;
OS   Lycopersicon esculentum (Tomato).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
OX   NCBI_TaxID=4081;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Leaf;
RX   MEDLINE=20098714; PubMed=10631250; DOI=10.1104/pp.122.1.67;
RA   Jorda L., Conejero V., Vera P.;
RT   "Characterization of two differentially regulated genes (P69E and
RT   P69F) encoding new members of the subtilisin-like protease clan from
RT   tomato plants.";
RL   Plant Physiol. 122:67-76(2000).
DR   EMBL; Y18932; CAB67120.1; -; Genomic_DNA.
DR   HSSP; P29599; 1ST3.
DR   MEROPS; S08.006; -.
DR   GO; GO:0008233; F:peptidase activity; IEA.
DR   GO; GO:0042802; F:protein self binding; IEA.
DR   GO; GO:0004289; F:subtilase activity; IEA.
DR   GO; GO:0043086; P:negative regulation of enzyme activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR003137; PA.
DR   InterPro; IPR000209; Pept_S8_S53.
DR   InterPro; IPR010259; Prot_inh_S8A.
DR   Pfam; PF02225; PA; 1.
DR   Pfam; PF00082; Peptidase_S8; 1.
DR   Pfam; PF05922; Subtilisin_N; 1.
DR   PRINTS; PR00723; SUBTILISIN.
DR   PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1.
DR   PROSITE; PS00138; SUBTILASE_SER; UNKNOWN_1.
KW   Protease.
SQ   SEQUENCE   746 AA;  79062 MW;  F2B9D6B7EA0EA4AB CRC64;

  Query Match             90.7%;  Score 39;  DB 2;  Length 746;
  Best Local Similarity   85.7%;  Pred. No. 73;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||||||:
Db        730 WTSTRHS 736


RESULT 3
Q6TXF5_RAT
ID   Q6TXF5_RAT  PRELIMINARY;      PRT;   865 AA.
AC   Q6TXF5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   LRRGT00044.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RA   Xu C.S., Chang C.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
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RA   Yang K.J., Zhao L.F., Ma H., Wang L., Wang S.F., Xing X.K., Shen G.M.,
RA   Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY383699; AAQ96257.1; -; mRNA.
DR   Ensembl; ENSRNOG00000026585; Rattus norvegicus.
DR   InterPro; IPR001611; LRR.
DR   Pfam; PF00560; LRR_1; 2.
DR   PRINTS; PR00019; LEURICHRPT.
KW   Leucine-rich repeat; Repeat.
SQ   SEQUENCE   865 AA;  95988 MW;  43BE96C199460485 CRC64;

  Query Match            90.7%;  Score 39;  DB 2;  Length 865;
  Best Local Similarity   85.7%;  Pred. No. 85;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db         43 WSSTRHT 49


RESULT 4
Q58EU4_MOUSE
ID   Q58EU4_MOUSE PRELIMINARY;      PRT;   238 AA.
AC   Q58EU4;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Igk-C protein.
GN   Name=Igk-C;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RG   NIH MGC Project;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC091754; AAH91754.1; -; mRNA.
DR   SMR; Q58EU4; 25-238.
DR   GO; GO:0003823; F:antigen binding; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   238 AA;  26440 MW;  AE2B2BA90B9F7D5D CRC64;

  Query Match            88.4%;  Score 38;  DB 2;  Length 238;
  Best Local Similarity   85.7%;  Pred. No. 34;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         74 WASTRHT 80


RESULT 5
Q4QHI3_LEIMA
ID   Q4QHI3_LEIMA PRELIMINARY;      PRT;   434 AA.
AC   Q4QHI3;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=LmjF10.0330;
OS   Leishmania major.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX   NCBI_TaxID=5664;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Friedlin;
RA   Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA   Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S.,
RA   Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CT005249; CAJ02505.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   434 AA;  45591 MW;  9FB29C30E11BDAE5 CRC64;

  Query Match            88.4%;  Score 38;  DB 2;  Length 434;
  Best Local Similarity   100.0%;  Pred. No. 64;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRH 6
              ||||||
Db         98 WTSTRH 103


RESULT 6
Q8W2M6_PETHY
ID   Q8W2M6_PETHY PRELIMINARY;      PRT;   354 AA.
AC   Q8W2M6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ethylene receptor.
GN   Name=ETR3;
OS   Petunia hybrida (Petunia).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Solanales; Solanaceae; Petunia.
OX   NCBI_TaxID=4102;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lai J.P., Shaw J.F.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF145975; AAL40904.1; -; mRNA.
DR   HSSP; P49333; 1DCF.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0000156; F:two-component response regulator activity; IEA.
DR   GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR   InterPro; IPR003018; GAF.
DR   InterPro; IPR001789; Response_reg.
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DR   Pfam; PF01590; GAF; 1.
DR   Pfam; PF00072; Response_reg; 1.
DR   ProDom; PD000039; Response_reg; 1.
DR   SMART; SM00448; REC; 1.
DR   PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW   Receptor.
SQ   SEQUENCE   354 AA;  39927 MW;  A663EB1F10D2D1ED CRC64;

  Query Match             86.0%;  Score 37;  DB 2;  Length 354;
  Best Local Similarity   85.7%;  Pred. No. 80;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||| ||
Db         73 WTSTAHT 79


RESULT 7
ETR1_TOBAC
ID   ETR1_TOBAC     STANDARD;      PRT;   738 AA.
AC   O48929;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Ethylene receptor (EC 2.7.3.-) (NT-ETR1).
GN   Name=ETR1;
OS   Nicotiana tabacum (Common tobacco).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   asterids; lamiids; Solanales; Solanaceae; Nicotiana.
OX   NCBI_TaxID=4097;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=cv. Samsun NN; TISSUE=Leaf;
RA   Knoester M., Hennig J., van Loon L.C., Bol J.F., Linthorst H.J.M.;
RT   "Isolation and characterization of a tobacco cDNA encoding an ETR1
RT   homolog.";
RL   (er) Plant Gene Register PGR97-188.
CC   -!- FUNCTION: May act early in the ethylene signal transduction
CC       pathway, possibly as an ethylene receptor, or as a regulator of
CC       the pathway (By similarity).
CC   -!- COFACTOR: Binds 1 copper ion per dimer (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: Endoplasmic reticulum (By similarity).
CC   -!- INDUCTION: Constitutive expression. Not induced by senescence,
CC       wounding, application of ethephon or infection with virus.
CC   -!- PTM: Activation probably requires a transfer of a phosphate group
CC       between a His in the transmitter domain and an Asp of the receiver
CC       domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ethylene receptor family.
CC   -!- SIMILARITY: Contains 1 histidine kinase domain.
CC   -!- SIMILARITY: Contains 1 response regulatory domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; AF022727; AAB97160.1; -; mRNA.
DR   PIR; T01897; T01897.
DR   HSSP; P49333; 1DCF.
DR   InterPro; IPR003594; ATP_bd_ATPase.
DR   InterPro; IPR003018; GAF.
DR   InterPro; IPR004358; His_kin_like_C.
DR   InterPro; IPR003661; His_kinA_N.
DR   InterPro; IPR005467; His_kinase.
DR   InterPro; IPR001789; Response_reg.
DR   Pfam; PF01590; GAF; 1.
DR   Pfam; PF02518; HATPase_c; 1.
DR   Pfam; PF00512; HisKA; 1.
DR   Pfam; PF00072; Response_reg; 1.
DR   PRINTS; PR00344; BCTRLSENSOR.
DR   ProDom; PD000039; Response_reg; 1.
DR   SMART; SM00065; GAF; 1.
DR   SMART; SM00387; HATPase_c; 1.
DR   SMART; SM00388; HisKA; 1.
DR   SMART; SM00448; REC; 1.
DR   PROSITE; PS50109; HIS_KIN; 1.
DR   PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW   Copper; Endoplasmic reticulum; Kinase; Metal-binding; Phosphorylation;
KW   Receptor; Sensory transduction; Transferase; Transmembrane;
KW   Two-component regulatory system.
FT   TRANSMEM     22     42       Potential.
FT   TRANSMEM     53     73       Potential.
FT   TRANSMEM     91    111       Potential.
FT   DOMAIN      348    585       Histidine kinase.
FT   DOMAIN      613    730       Response regulatory.
FT   METAL        64     64       Copper (By similarity).
FT   METAL        68     68       Copper (By similarity).
FT   MOD_RES     351    351       Phosphohistidine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     661    661       4-aspartylphosphate (By similarity).
FT   DISULFID      3      3       Interchain (By similarity).
FT   DISULFID      5      5       Interchain (By similarity).
SQ   SEQUENCE   738 AA;  82294 MW;  D6C5F7B16F16A7DE CRC64;

  Query Match             86.0%;  Score 37;  DB 1;  Length 738;
  Best Local Similarity   85.7%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||| ||
Db         73 WTSTAHT 79


RESULT 8
Q8W2M8_PETHY
ID   Q8W2M8_PETHY PRELIMINARY;      PRT;   738 AA.
AC   Q8W2M8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ethylene receptor.
GN   Name=ETR1-2;
OS   Petunia hybrida (Petunia).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Solanales; Solanaceae; Petunia.
OX   NCBI_TaxID=4102;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lai J.P., Shaw J.F.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF145973; AAL40902.1; -; mRNA.
DR   HSSP; P49333; 1DCF.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0000156; F:two-component response regulator activity; IEA.
DR   GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR   InterPro; IPR003594; ATPbind_ATPase.
DR   InterPro; IPR003018; GAF.
DR   InterPro; IPR005467; His_kinase.
DR   InterPro; IPR003661; His_kinA_N.
DR   InterPro; IPR004358; His_kin_like_C.
DR   InterPro; IPR001789; Response_reg.
DR   Pfam; PF01590; GAF; 1.
DR   Pfam; PF02518; HATPase_c; 1.
DR   Pfam; PF00512; HisKA; 1.
DR   Pfam; PF00072; Response_reg; 1.
DR   PRINTS; PR00344; BCTRLSENSOR.
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DR   ProDom; PD000039; Response_reg; 1.
DR   SMART; SM00065; GAF; 1.
DR   SMART; SM00387; HATPase_c; 1.
DR   SMART; SM00388; HisKA; 1.
DR   SMART; SM00448; REC; 1.
DR   PROSITE; PS50109; HIS_KIN; 1.
DR   PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW   Receptor.
SQ   SEQUENCE   738 AA;  82267 MW;  39617ECEA265F821 CRC64;

  Query Match             86.0%;  Score 37;  DB 2;  Length 738;
  Best Local Similarity   85.7%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||| ||
Db         73 WTSTAHT 79


RESULT 9
Q8W2M9_PETHY
ID   Q8W2M9_PETHY PRELIMINARY;      PRT;   738 AA.
AC   Q8W2M9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ethylene receptor.
GN   Name=ETR1-1;
OS   Petunia hybrida (Petunia).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Solanales; Solanaceae; Petunia.
OX   NCBI_TaxID=4102;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Lai J.P., Shaw J.F.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF145972; AAL40901.1; -; mRNA.
DR   HSSP; P49333; 1DCF.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0000156; F:two-component response regulator activity; IEA.
DR   GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   GO; GO:0000160; P:two-component signal transduction system (p. . .; IEA.
DR   InterPro; IPR003594; ATPbind_ATPase.
DR   InterPro; IPR003018; GAF.
DR   InterPro; IPR005467; His_kinase.
DR   InterPro; IPR003661; His_kinA_N.
DR   InterPro; IPR004358; His_kin_like_C.
DR   InterPro; IPR001789; Response_reg.
DR   Pfam; PF01590; GAF; 1.
DR   Pfam; PF02518; HATPase_c; 1.
DR   Pfam; PF00512; HisKA; 1.
DR   Pfam; PF00072; Response_reg; 1.
DR   PRINTS; PR00344; BCTRLSENSOR.
DR   ProDom; PD000039; Response_reg; 1.
DR   SMART; SM00065; GAF; 1.
DR   SMART; SM00387; HATPase_c; 1.
DR   SMART; SM00388; HisKA; 1.
DR   SMART; SM00448; REC; 1.
DR   PROSITE; PS50109; HIS_KIN; 1.
DR   PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW   Receptor.
SQ   SEQUENCE   738 AA;  82407 MW;  96E12975A89ED710 CRC64;

  Query Match             86.0%;  Score 37;  DB 2;  Length 738;
  Best Local Similarity   85.7%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||| ||
Db         73 WTSTAHT 79


RESULT 10
Q8CUS8_OCEIH
ID   Q8CUS8_OCEIH PRELIMINARY;      PRT;   443 AA.
AC   Q8CUS8;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Alkaline phosphatase (EC 3.1.3.1).
GN   OrderedLocusNames=OB1029;
OS   Oceanobacillus iheyensis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
OX   NCBI_TaxID=182710;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=HTE831 / DSM 14371 / JCM 11309;
RX   MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;
RA   Takami H., Takaki Y., Uchiyama I.;
RT   "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya
RT   Ridge and its unexpected adaptive capabilities to extreme
RT   environments.";
RL   Nucleic Acids Res. 30:3927-3935(2002).
DR   EMBL; BA000028; BAC12985.1; -; Genomic_DNA.
DR   HSSP; P00634; 1AJA.
DR   GO; GO:0004035; F:alkaline phosphatase activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR001952; Alk_phosphtse.
DR   Pfam; PF00245; Alk_phosphatase; 1.
DR   PRINTS; PR00113; ALKPHPHTASE.
DR   SMART; SM00098; alkPPc; 1.
DR   PROSITE; PS00123; ALKALINE_PHOSPHATASE; UNKNOWN_1.
KW   Complete proteome; Hydrolase.
SQ   SEQUENCE   443 AA;  48148 MW;  B1C5B600116F4500 CRC64;

  Query Match             83.7%;  Score 36;  DB 2;  Length 443;
  Best Local Similarity   85.7%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||| ||
Db        401 WTSTGHT 407


RESULT 11
PPB4_BACSU
ID   PPB4_BACSU     STANDARD;      PRT;   461 AA.
AC   P19406;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Alkaline phosphatase IV precursor (EC 3.1.3.1) (APase IV).
GN   Name=phoA; Synonyms=phoAIV; OrderedLocusNames=BSU09410;
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=168 / JH642;
RX   MEDLINE=94156839; PubMed=8113174;
RA   Hulett F.M., Lee J., Shi L., Sun G., Chesnut R., Sharkova E.,
RA   Duggan M.F., Kapp N.;
RT   "Sequential action of two-component genetic switches regulates the PHO
RT   regulon in Bacillus subtilis.";
RL   J. Bacteriol. 176:1348-1358(1994).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=168;
RX   MEDLINE=98240224; PubMed=9579061;
```

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RA   Noback M.A., Holsappel S., Kiewiet R., Terpstra P., Wambutt R.,
RA   Wedler H., Venema G., Bron S.;
RT   "The 172 kb prkA-addAB region from 83 degrees to 97 degrees of the
RT   Bacillus subtilis chromosome contains several dysfunctional genes, the
RT   glyB marker, many genes encoding transporter proteins, and the
RT   ubiquitous hit gene.";
RL   Microbiology 144:859-875(1998).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=168;
RX   MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA   Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA   Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA   Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA   Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA   Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA   Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T.,
RA   Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA   Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA   Ghim S.-Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA   Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA   Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,
RA   Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA   Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
RA   Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA   Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C.,
RA   Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA   Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA   Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA   Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA   Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA   Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA   Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
RA   Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA   Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA   Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA   Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA   Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA   Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,
RA   Yoshikawa H., Danchin A.;
RT   "The complete genome sequence of the Gram-positive bacterium Bacillus
RT   subtilis.";
RL   Nature 390:249-256(1997).
RN   [4]
RP   NUCLEOTIDE SEQUENCE OF 39-461.
RC   STRAIN=168 / JH642;
RX   MEDLINE=91093215; PubMed=1898729;
RA   Hulett F.M., Kim M.E., Bookstein C., Kapp N.V., Edwards C.W.,
RA   Wyckoff H.W.;
RT   "Bacillus subtilis alkaline phosphatases III and IV. Cloning,
RT   sequencing, and comparisons of deduced amino acid sequence with
RT   Escherichia coli alkaline phosphatase three-dimensional structure.";
RL   J. Biol. Chem. 266:1077-1084(1991).
RN   [5]
RP   NUCLEOTIDE SEQUENCE OF 39-142.
RC   STRAIN=168 / JH642;
RX   MEDLINE=91092508; PubMed=2125017; DOI=10.1016/0378-1119(90)90346-S;
RA   Kapp N.V., Edwards C.W., Chesnut R.S., Hulett F.M.;
RT   "The Bacillus subtilis phoAIV gene: effects of in vitro inactivation
RT   on total alkaline phosphatase production.";
RL   Gene 96:95-100(1990).
RN   [6]
RP   PROTEIN SEQUENCE OF 42-63.
RX   MEDLINE=90130309; PubMed=2105301;
RA   Hulett F.M., Bookstein C., Jensen K.;
RT   "Evidence for two structural genes for alkaline phosphatase in
RT   Bacillus subtilis.";
RL   J. Bacteriol. 172:735-740(1990).
RN   [7]
RP   NUCLEOTIDE SEQUENCE OF 433-461.
RC   STRAIN=168 / Marburg;
RX   MEDLINE=94193548; PubMed=8144469;
RA   Beall B.W., Moran C.P. Jr.;
RT   "Cloning and characterization of spoVR, a gene from Bacillus subtilis
RT   involved in spore cortex formation.";
RL   J. Bacteriol. 176:2003-2012(1994).
CC   -!- CATALYTIC ACTIVITY: A phosphate monoester + H(2)O = an alcohol +
CC       phosphate.
CC   -!- COFACTOR: Binds 1 magnesium ion.
CC   -!- COFACTOR: Binds 2 zinc ions.
CC   -!- SUBUNIT: Monomer.
CC   -!- SIMILARITY: Belongs to the alkaline phosphatase family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U02550; AAA18323.1; -; Unassigned_DNA.
DR   EMBL; Y14082; CAA74486.1; -; Genomic_DNA.
DR   EMBL; Z99109; CAB12780.1; -; Genomic_DNA.
DR   EMBL; L26337; AAA22812.1; -; Genomic_DNA.
DR   PIR; B69676; B69676.
DR   HSSP; P00634; 1AJA.
DR   SubtiList; BG10183; phoA.
DR   InterPro; IPR001952; Alk_phosphtse.
DR   Pfam; PF00245; Alk_phosphatase; 1.
DR   PRINTS; PR00113; ALKPHPHTASE.
DR   SMART; SM00098; alkPPc; 1.
DR   PROSITE; PS00123; ALKALINE_PHOSPHATASE; 1.
KW   Complete proteome; Direct protein sequencing; Hydrolase; Magnesium;
KW   Multigene family; Phosphorylation; Signal; Zinc.
FT   SIGNAL        1     41
FT   CHAIN        42    461       Alkaline phosphatase IV.
FT   ACT_SITE    108    108       Phosphoserine intermediate (By
FT                                similarity).
FT   CONFLICT     50     50       R -> K (in Ref. 6).
SQ   SEQUENCE   461 AA;  50273 MW;  A2ABD109026A2BFE CRC64;

  Query Match             83.7%;  Score 36;  DB 1;  Length 461;
  Best Local Similarity   85.7%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||| ||
Db        418 WTSTDHT 424


RESULT 12
ETR2_LYCES
ID   ETR2_LYCES     STANDARD;      PRT;   736 AA.
AC   O49187; Q41343;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Ethylene receptor 2 (EC 2.7.3.-) (LeETR2).
GN   Name=ETR2;
OS   Lycopersicon esculentum (Tomato).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
OX   NCBI_TaxID=4081;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=cv. Rutgers; TISSUE=Root;
RX   MEDLINE=98388654; PubMed=9721682;
RA   Lashbrook C.C., Tieman D.M., Klee H.J.;
RT   "Differential regulation of the tomato ETR gene family throughout
RT   plant development.";
RL   Plant J. 15:243-252(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 31-736.
RC   STRAIN=cv. UC82B;
RA   Zhou D., Mattoo A.K., Tucker M.L.;
RT   "Molecular cloning of a tomato cDNA encoding an ethylene receptor.";
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RL   (er) Plant Gene Register PGR96-015.
CC   -!- FUNCTION: May act early in the ethylene signal transduction
CC       pathway, possibly as an ethylene receptor, or as a regulator of
CC       the pathway (By similarity).
CC   -!- COFACTOR: Binds 1 copper ion per dimer (By similarity).
CC   -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC   -!- SUBCELLULAR LOCATION: Endoplasmic reticulum (By similarity).
CC   -!- TISSUE SPECIFICITY: Leaves, flowers and fruits.
CC   -!- DEVELOPMENTAL STAGE: Induced in imbibing seeds prior to
CC       germination and down-regulated in elongating seedlings and
CC       senescing leaf petioles.
CC   -!- INDUCTION: Not induced by ethylene.
CC   -!- PTM: Activation probably requires a transfer of a phosphate group
CC       between a His in the transmitter domain and an Asp of the receiver
CC       domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ethylene receptor family.
CC   -!- SIMILARITY: Contains 1 histidine kinase domain.
CC   -!- SIMILARITY: Contains 1 response regulatory domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF043085; AAC02214.1; -; mRNA.
DR   EMBL; U47279; AAB39386.1; -; mRNA.
DR   PIR; T06271; T06271.
DR   HSSP; P49333; 1DCF.
DR   InterPro; IPR003594; ATP_bd_ATPase.
DR   InterPro; IPR003018; GAF.
DR   InterPro; IPR004358; His_kin_like_C.
DR   InterPro; IPR003661; His_kinA_N.
DR   InterPro; IPR005467; His_kinase.
DR   InterPro; IPR001789; Response_reg.
DR   Pfam; PF01590; GAF; 1.
DR   Pfam; PF02518; HATPase_c; 1.
DR   Pfam; PF00512; HisKA; 1.
DR   Pfam; PF00072; Response_reg; 1.
DR   PRINTS; PR00344; BCTRLSENSOR.
DR   ProDom; PD000039; Response_reg; 1.
DR   SMART; SM00065; GAF; 1.
DR   SMART; SM00387; HATPase_c; 1.
DR   SMART; SM00388; HisKA; 1.
DR   SMART; SM00448; REC; 1.
DR   PROSITE; PS50109; HIS_KIN; 1.
DR   PROSITE; PS50110; RESPONSE_REGULATORY; 1.
KW   Copper; Endoplasmic reticulum; Kinase; Metal-binding;
KW   Multigene family; Phosphorylation; Receptor; Sensory transduction;
KW   Transferase; Transmembrane; Two-component regulatory system.
FT   TRANSMEM     22     42       Potential.
FT   TRANSMEM     53     73       Potential.
FT   TRANSMEM     94    114       Potential.
FT   DOMAIN      348    585       Histidine kinase.
FT   DOMAIN      613    730       Response regulatory.
FT   METAL        64     64       Copper (By similarity).
FT   METAL        68     68       Copper (By similarity).
FT   MOD_RES     351    351       Phosphohistidine (by autocatalysis) (By
FT                                similarity).
FT   MOD_RES     661    661       4-aspartylphosphate (By similarity).
FT   DISULFID      3      3       Interchain (By similarity).
FT   DISULFID      5      5       Interchain (By similarity).
FT   CONFLICT    474    474       K -> E (in Ref. 2).
SQ   SEQUENCE   736 AA;  81701 MW;  A804C61EBC190320 CRC64;

  Query Match             83.7%;  Score 36;  DB 1;  Length 736;
  Best Local Similarity   85.7%;  Pred. No. 2.7e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||| ||
Db         73 WTSTPHT 79
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RESULT 13
Q5QG25_LYCES
ID   Q5QG25_LYCES PRELIMINARY;      PRT;   736 AA.
AC   Q5QG25;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Ethylene receptor.
GN   Name=ETR2;
OS   Lycopersicon esculentum (Tomato).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
OX   NCBI_TaxID=4081;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Moussatche P., Klee H.J.;
RT   "Tomato ethylene receptors.";
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY600436; AAU34074.1; -; Genomic_DNA.
KW   Receptor.
SQ   SEQUENCE   736 AA;  81702 MW;  4604C1A81C190100 CRC64;

  Query Match             83.7%;  Score 36;  DB 2;  Length 736;
  Best Local Similarity   85.7%;  Pred. No. 2.7e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||| ||
Db         73 WTSTPHT 79
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RESULT 14
Q4QFE8_LEIMA
ID   Q4QFE8_LEIMA PRELIMINARY;      PRT;   761 AA.
AC   Q4QFE8;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=LmjF15.0320;
OS   Leishmania major.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX   NCBI_TaxID=5664;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Friedlin;
RA   Peacock C.S., Murphy L., Ivens A.C., Berriman M., Blackwell J.,
RA   Smith D., Collins M., Fosker N., Harris D., Oliver K., O'Neil S.,
RA   Saunders D., Seeger K., Warren T., Rajandream M., and Barrell B.G.;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CT005254; CAJ03260.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   761 AA;  83857 MW;  247450737ACA5A19 CRC64;

  Query Match             83.7%;  Score 36;  DB 2;  Length 761;
  Best Local Similarity   71.4%;  Pred. No. 2.8e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||::|||
Db        210 WTASRHT 216
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RESULT 15
Q4N7R8_THEPA
ID   Q4N7R8_THEPA PRELIMINARY;      PRT;   771 AA.
AC   Q4N7R8;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
```

```
GN   ORFNames=TP01_0752;
OS   Theileria parva.
OC   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileriidae;
OC   Theileria.
OX   NCBI_TaxID=5875;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Muguga;
RA   Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
RA   Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
RA   Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
RA   Jiang L., Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J.,
RA   Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,
RA   Silva J.C., Utterback T.R., Feldblyum T.V., Pertea M., Allen J.,
RA   Taracha E.L.N., Salzberg S.L., White O.R., Fitzhugh H.A., Morzaria S.,
RA   Venter J.C., Fraser C.M., Nene V.;
RT   "Genome sequence of Theileria parva, a bovine pathogen that transforms
RT   lymphocytes.";
RL   Science 309:134-137(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Muguga;
RA   Gardner M., Bishop R., Shah T., de Villiers E., Carlton J.M., Hall N.,
RA   Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
RA   Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
RA   Lynn J., Weaver B., Shoaibi A., Wasawo D., Crabtree J., Wortman J.R.,
RA   Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
RA   Utterback T., Feldblyum T., Pertea M., Allen J., Taracha E.L.,
RA   Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
RA   Fraser C.M., Nene V.;
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAGK01000001; EAN33990.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   771 AA;  89793 MW;  2D4510B0D277E14F CRC64;

  Query Match             83.7%;  Score 36;  DB 2;  Length 771;
  Best Local Similarity   85.7%;  Pred. No. 2.8e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||| ||
Db         99 WTSTDHT 105


RESULT 16
O77171_PLAFA
ID   O77171_PLAFA PRELIMINARY;      PRT;   118 AA.
AC   O77171;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Erythrocyte membrane protein 1 type c (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tiwari B.;
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF084579; AAC62721.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13883 MW;  8203D952A1F7FAE5 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 118;
  Best Local Similarity   71.4%;  Pred. No. 60;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||: |||
Db         57 WTANRHT 63


RESULT 17
Q8CA09_MOUSE
ID   Q8CA09_MOUSE PRELIMINARY;      PRT;   118 AA.
AC   Q8CA09;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Mus musculus 0 day neonate thymus cDNA, RIKEN full-length enriched
DE   library, clone:A430041E03 product:hypothetical protein, full insert
DE   sequence.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
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RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK039996; BAC30494.1; -; mRNA.
DR   Ensembl; ENSMUSG00000054156; Mus musculus.
KW   Hypothetical protein.
SQ   SEQUENCE   118 AA;  13454 MW;  B41AF4CF0C512250 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 118;
  Best Local Similarity   83.3%;  Pred. No. 60;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRH 6
              ||:|||
Db          4 WTATRH 9


RESULT 18
Q8T4Z9_PLAFA
ID   Q8T4Z9_PLAFA PRELIMINARY;      PRT;   120 AA.
AC   Q8T4Z9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Erythrocyte membrane protein 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21839615; PubMed=11849711; DOI=10.1016/S0166-6851(01)00443-1;
RA   Fowler E.V., Peters J.M., Gatton M.L., Chen N., Cheng Q.;
RT   "Genetic diversity of the DBLalpha region in Plasmodium falciparum var
RT   genes among Asia-Pacific isolates.";
RL   Mol. Biochem. Parasitol. 120:117-126(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Fowler E., Peters J., Gatton M., Chen N., Cheng Q.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY054911; AAL11275.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     120    120
SQ   SEQUENCE   120 AA;  13669 MW;  1E456B7DC7CEAA62 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 120;
  Best Local Similarity   71.4%;  Pred. No. 61;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         60 WTANRHT 66


RESULT 19
Q868X3_PLAFA
ID   Q868X3_PLAFA PRELIMINARY;      PRT;   121 AA.
AC   Q868X3;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Erythrocyte membrane protein 1 variant 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22561043; PubMed=12672527; DOI=10.1016/S0166-6851(03)00004-5;
RA   Winter G., Chen Q., Flick K., Kremsner P., Fernandez V., Wahlgren M.;
RT   "The 3D7var5.2 (var COMMON) type var gene family is commonly expressed
RT   in non-placental Plasmodium falciparum malaria.";
RL   Mol. Biochem. Parasitol. 127:179-191(2003).
DR   EMBL; AF528130; AAO85747.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  14337 MW;  A24E932DB2218740 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 121;
  Best Local Similarity   71.4%;  Pred. No. 62;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         65 WTANRHT 71


RESULT 20
Q868X5_PLAFA
ID   Q868X5_PLAFA PRELIMINARY;      PRT;   121 AA.
AC   Q868X5;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Erythrocyte membrane protein 1 variant 3 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22561043; PubMed=12672527; DOI=10.1016/S0166-6851(03)00004-5;
RA   Winter G., Chen Q., Flick K., Kremsner P., Fernandez V., Wahlgren M.;
RT   "The 3D7var5.2 (var COMMON) type var gene family is commonly expressed
RT   in non-placental Plasmodium falciparum malaria.";
RL   Mol. Biochem. Parasitol. 127:179-191(2003).
DR   EMBL; AF528128; AAO85745.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  14097 MW;  B54AF6D14BAC1351 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 121;
  Best Local Similarity   71.4%;  Pred. No. 62;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         57 WTANRHT 63


RESULT 21
Q8T533_PLAFA
ID   Q8T533_PLAFA PRELIMINARY;      PRT;   121 AA.
AC   Q8T533;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
```

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DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Erythrocyte membrane protein 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21839615; PubMed=11849711; DOI=10.1016/S0166-6851(01)00443-1;
RA   Fowler E.V., Peters J.M., Gatton M.L., Chen N., Cheng Q.;
RT   "Genetic diversity of the DBLalpha region in Plasmodium falciparum var
RT   genes among Asia-Pacific isolates.";
RL   Mol. Biochem. Parasitol. 120:117-126(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Fowler E., Peters J., Gatton M., Chen N., Cheng Q.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY054869; AAL11233.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  14168 MW;  AB8A9D52E6BE8D40 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 121;
  Best Local Similarity   71.4%;  Pred. No. 62;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         60 WTANRHT 66


RESULT 22
Q9XZ76_PLAFA
ID   Q9XZ76_PLAFA PRELIMINARY;      PRT;   121 AA.
AC   Q9XZ76;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   DBL alpha protein (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=3D7;
RX   MEDLINE=20078856; PubMed=10613695; DOI=10.1016/S0166-6851(99)00159-0;
RA   Taylor H.M., Kyes S.A., Harris D., Kriek N., Newbold C.I.;
RT   "A study of var gene transcription in vitro using universal var gene
RT   primers.";
RL   Mol. Biochem. Parasitol. 105:13-23(2000).
DR   EMBL; AF133848; AAD33609.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     121    121
SQ   SEQUENCE   121 AA;  14125 MW;  4DD69A1163FDDEBA CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 121;
  Best Local Similarity   71.4%;  Pred. No. 62;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         63 WTANRHT 69


RESULT 23
O77193_PLAFA
ID   O77193_PLAFA PRELIMINARY;      PRT;   122 AA.
AC   O77193;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Erythrocyte membrane protein 1 type af (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tiwari B.;
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF084601; AAC62743.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  14334 MW;  42BBE40F71CC29DE CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 122;
  Best Local Similarity   71.4%;  Pred. No. 62;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         62 WTANRHT 68


RESULT 24
Q8T4X5_PLAFA
ID   Q8T4X5_PLAFA PRELIMINARY;      PRT;   122 AA.
AC   Q8T4X5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Erythrocyte membrane protein 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21839615; PubMed=11849711; DOI=10.1016/S0166-6851(01)00443-1;
RA   Fowler E.V., Peters J.M., Gatton M.L., Chen N., Cheng Q.;
RT   "Genetic diversity of the DBLalpha region in Plasmodium falciparum var
RT   genes among Asia-Pacific isolates.";
RL   Mol. Biochem. Parasitol. 120:117-126(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Fowler E., Peters J., Gatton M., Chen N., Cheng Q.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY054937; AAL11301.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  14419 MW;  E924FE3B64D4701F CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 122;
  Best Local Similarity   71.4%;  Pred. No. 62;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         63 WTANRHT 69


RESULT 25
Q9XZ75_PLAFA
ID   Q9XZ75_PLAFA PRELIMINARY;      PRT;   122 AA.
AC   Q9XZ75;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   DBL alpha protein (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
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RC   STRAIN=3D7;
RX   MEDLINE=20078856; PubMed=10613695; DOI=10.1016/S0166-6851(99)00159-0;
RA   Taylor H.M., Kyes S.A., Harris D., Kriek N., Newbold C.I.;
RT   "A study of var gene transcription in vitro using universal var gene
RT   primers.";
RL   Mol. Biochem. Parasitol. 105:13-23(2000).
DR   EMBL; AF133847; AAD33608.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  14218 MW;  B5EDC05DB8C9E535 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 122;
  Best Local Similarity   71.4%;  Pred. No. 62;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         64 WTANRHT 70


RESULT 26
Q8T332_PLAFA
ID   Q8T332_PLAFA PRELIMINARY;      PRT;   123 AA.
AC   Q8T332;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   PfEMP1 (Fragment).
GN   Name=P154var5;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21927235; PubMed=11930336; DOI=10.1086/339684;
RA   Rowe J.A., Kyes S.A., Rogerson S.J., Babiker H.A., Raza A.;
RT   "Identification of a conserved Plasmodium falciparum var gene
RT   implicated in malaria in pregnancy.";
RL   J. Infect. Dis. 185:1207-1211(2002).
DR   EMBL; AJ420404; CAD20860.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER     123    123
SQ   SEQUENCE   123 AA;  14543 MW;  0D1E62440067B188 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 123;
  Best Local Similarity   71.4%;  Pred. No. 63;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         65 WTANRHT 71


RESULT 27
O77190_PLAFA
ID   O77190_PLAFA PRELIMINARY;      PRT;   124 AA.
AC   O77190;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Erythrocyte membrane protein 1 type ac (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tiwari B.;
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF084598; AAC62740.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     124    124
SQ   SEQUENCE   124 AA;  14766 MW;  8B00B7A62DE2B334 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 124;
  Best Local Similarity   71.4%;  Pred. No. 63;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         62 WTANRHT 68


RESULT 28
Q6E2M4_9CAUD
ID   Q6E2M4_9CAUD PRELIMINARY;      PRT;   124 AA.
AC   Q6E2M4;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   DNA polymerase (Fragment).
OS   Uncultured T7-like podovirus.
OC   Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC   environmental samples.
OX   NCBI_TaxID=271647;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15251204; DOI=10.1016/j.femsle.2004.05.042;
RA   Breitbart M., Miyake J.H., Rohwer F.;
RT   "Global distribution of nearly identical phage-encoded DNA
RT   sequences.";
RL   FEMS Microbiol. Lett. 236:249-256(2004).
DR   EMBL; AY599952; AAT39748.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     124    124
SQ   SEQUENCE   124 AA;  14121 MW;  1C9E0ADE72DC363B CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 124;
  Best Local Similarity   71.4%;  Pred. No. 63;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              || |:||
Db         74 WTPTKHT 80


RESULT 29
Q868Y7_PLAFA
ID   Q868Y7_PLAFA PRELIMINARY;      PRT;   125 AA.
AC   Q868Y7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Erythrocyte membrane protein 1 variant 4 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22561043; PubMed=12672527; DOI=10.1016/S0166-6851(03)00004-5;
RA   Winter G., Chen Q., Flick K., Kremsner P., Fernandez V., Wahlgren M.;
RT   "The 3D7var5.2 (var COMMON) type var gene family is commonly expressed
RT   in non-placental Plasmodium falciparum malaria.";
RL   Mol. Biochem. Parasitol. 127:179-191(2003).
DR   EMBL; AF528116; AAO85733.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER     125    125
SQ   SEQUENCE   125 AA;  14715 MW;  A9CED3695931A7DE CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 125;
  Best Local Similarity   71.4%;  Pred. No. 64;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
```

```
Db         65 WTANRHT 71


RESULT 30
Q86RR8_PLAFA
ID   Q86RR8_PLAFA PRELIMINARY;      PRT;   125 AA.
AC   Q86RR8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Erythrocyte membrane protein 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kirchgatter K., del Portillo H.A.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF416575; AAN39145.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER     125    125
SQ   SEQUENCE   125 AA;  14646 MW;  FD26B5B6E3A060DA CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 125;
  Best Local Similarity   71.4%;  Pred. No. 64;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         65 WTANRHT 71


RESULT 31
Q8T506_PLAFA
ID   Q8T506_PLAFA PRELIMINARY;      PRT;   125 AA.
AC   Q8T506;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Erythrocyte membrane protein 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21839615; PubMed=11849711; DOI=10.1016/S0166-6851(01)00443-1;
RA   Fowler E.V., Peters J.M., Gatton M.L., Chen N., Cheng Q.;
RT   "Genetic diversity of the DBLalpha region in Plasmodium falciparum var
RT   genes among Asia-Pacific isolates.";
RL   Mol. Biochem. Parasitol. 120:117-126(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Fowler E., Peters J., Gatton M., Chen N., Cheng Q.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY054902; AAL11266.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     125    125
SQ   SEQUENCE   125 AA;  14493 MW;  F24AD8A35CA542BA CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 125;
  Best Local Similarity   71.4%;  Pred. No. 64;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         59 WTANRHT 65


RESULT 32
Q868W0_PLAFA
ID   Q868W0_PLAFA PRELIMINARY;      PRT;   126 AA.
AC   Q868W0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Erythrocyte membrane protein 1 variant 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22561043; PubMed=12672527; DOI=10.1016/S0166-6851(03)00004-5;
RA   Winter G., Chen Q., Flick K., Kremsner P., Fernandez V., Wahlgren M.;
RT   "The 3D7var5.2 (var COMMON) type var gene family is commonly expressed
RT   in non-placental Plasmodium falciparum malaria.";
RL   Mol. Biochem. Parasitol. 127:179-191(2003).
DR   EMBL; AF528144; AAO85761.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER     126    126
SQ   SEQUENCE   126 AA;  14819 MW;  1D06ED9D7A3360FB CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 126;
  Best Local Similarity   71.4%;  Pred. No. 64;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         64 WTANRHT 70


RESULT 33
Q86RR6_PLAFA
ID   Q86RR6_PLAFA PRELIMINARY;      PRT;   126 AA.
AC   Q86RR6;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Erythrocyte membrane protein 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kirchgatter K., del Portillo H.A.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF416577; AAN39147.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER     126    126
SQ   SEQUENCE   126 AA;  14690 MW;  2ACB919B9869DD9F CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 126;
  Best Local Similarity   71.4%;  Pred. No. 64;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         66 WTANRHT 72


RESULT 34
Q8T345_PLAFA
ID   Q8T345_PLAFA PRELIMINARY;      PRT;   127 AA.
AC   Q8T345;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   PfEMP1 (Fragment).
GN   Name=P136var4;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
```

```
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21927235; PubMed=11930336; DOI=10.1086/339684;
RA   Rowe J.A., Kyes S.A., Rogerson S.J., Babiker H.A., Raza A.;
RT   "Identification of a conserved Plasmodium falciparum var gene
RT   implicated in malaria in pregnancy.";
RL   J. Infect. Dis. 185:1207-1211(2002).
DR   EMBL; AJ420390; CAD20846.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER     127    127
SQ   SEQUENCE   127 AA;  14545 MW;  9F3CA4B7A00F9171 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 127;
  Best Local Similarity   71.4%;  Pred. No. 65;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         67 WTANRHT 73


RESULT 35
Q8T4Z0_PLAFA
ID   Q8T4Z0_PLAFA PRELIMINARY;      PRT;   127 AA.
AC   Q8T4Z0;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Erythrocyte membrane protein 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21839615; PubMed=11849711; DOI=10.1016/S0166-6851(01)00443-1;
RA   Fowler E.V., Peters J.M., Gatton M.L., Chen N., Cheng Q.;
RT   "Genetic diversity of the DBLalpha region in Plasmodium falciparum var
RT   genes among Asia-Pacific isolates.";
RL   Mol. Biochem. Parasitol. 120:117-126(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Fowler E., Peters J., Gatton M., Chen N., Cheng Q.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY054920; AAL11284.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     127    127
SQ   SEQUENCE   127 AA;  14861 MW;  D026508240CB69BE CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 127;
  Best Local Similarity   71.4%;  Pred. No. 65;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         71 WTANRHT 77


RESULT 36
Q9XZA5_PLAFA
ID   Q9XZA5_PLAFA PRELIMINARY;      PRT;   128 AA.
AC   Q9XZA5;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   DBL alpha protein (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=3D7;
RX   MEDLINE=20078856; PubMed=10613695; DOI=10.1016/S0166-6851(99)00159-0;
RA   Taylor H.M., Kyes S.A., Harris D., Kriek N., Newbold C.I.;
RT   "A study of var gene transcription in vitro using universal var gene
RT   primers.";
RL   Mol. Biochem. Parasitol. 105:13-23(2000).
DR   EMBL; AF133880; AAD33641.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     128    128
SQ   SEQUENCE   128 AA;  14769 MW;  FF9D18B26392F6C2 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 128;
  Best Local Similarity   71.4%;  Pred. No. 66;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         58 WTANRHT 64


RESULT 37
Q95Z31_PLAFA
ID   Q95Z31_PLAFA PRELIMINARY;      PRT;   129 AA.
AC   Q95Z31;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PfEMP1 protein (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kriek N., Kyes S.A., Christodoulou Z., Newbold C.I.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ319702; CAC41306.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  15174 MW;  0C49AF87BDF52C31 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 129;
  Best Local Similarity   71.4%;  Pred. No. 66;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         63 WTANRHT 69


RESULT 38
Q9NHL3_PLAFA
ID   Q9NHL3_PLAFA PRELIMINARY;      PRT;   129 AA.
AC   Q9NHL3;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PfEMP1 protein (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20520970; PubMed=11071291; DOI=10.1016/S0166-6851(00)00286-3;
RA   Taylor H.M., Kyes S.A., Newbold C.I.;
RT   "Var gene diversity in Plasmodium falciparum is generated by frequent
RT   recombination events.";
RL   Mol. Biochem. Parasitol. 110:391-397(2000).
DR   EMBL; AF221777; AAF36617.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  15042 MW;  9D96B0B037C24ECC CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 129;
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  Best Local Similarity   71.4%;  Pred. No. 66;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         67 WTANRHT 73


RESULT 39
O77184_PLAFA
ID   O77184_PLAFA PRELIMINARY;      PRT;   130 AA.
AC   O77184;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Erythrocyte membrane protein 1 type u (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tiwari B.;
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF084592; AAC62734.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     130    130
SQ   SEQUENCE   130 AA;  15186 MW;  A5DCCBA0B13D5214 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 130;
  Best Local Similarity   71.4%;  Pred. No. 67;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         64 WTANRHT 70


RESULT 40
Q8T4V6_PLAFA
ID   Q8T4V6_PLAFA PRELIMINARY;      PRT;   130 AA.
AC   Q8T4V6;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Erythrocyte membrane protein 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21839615; PubMed=11849711; DOI=10.1016/S0166-6851(01)00443-1;
RA   Fowler E.V., Peters J.M., Gatton M.L., Chen N., Cheng Q.;
RT   "Genetic diversity of the DBLalpha region in Plasmodium falciparum var
RT   genes among Asia-Pacific isolates.";
RL   Mol. Biochem. Parasitol. 120:117-126(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Fowler E., Peters J., Gatton M., Chen N., Cheng Q.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY054958; AAL11322.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     130    130
SQ   SEQUENCE   130 AA;  15347 MW;  768F089FB9D68D0B CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 130;
  Best Local Similarity   71.4%;  Pred. No. 67;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         58 WTANRHT 64


RESULT 41
Q9XZ84_PLAFA
ID   Q9XZ84_PLAFA PRELIMINARY;      PRT;   130 AA.
AC   Q9XZ84;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   DBL alpha protein (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=3D7;
RX   MEDLINE=20078856; PubMed=10613695; DOI=10.1016/S0166-6851(99)00159-0;
RA   Taylor H.M., Kyes S.A., Harris D., Kriek N., Newbold C.I.;
RT   "A study of var gene transcription in vitro using universal var gene
RT   primers.";
RL   Mol. Biochem. Parasitol. 105:13-23(2000).
DR   EMBL; AF133856; AAD33617.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     130    130
SQ   SEQUENCE   130 AA;  15284 MW;  089F79F4FA39C63D CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 130;
  Best Local Similarity   71.4%;  Pred. No. 67;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         60 WTANRHT 66


RESULT 42
Q868Z2_PLAFA
ID   Q868Z2_PLAFA PRELIMINARY;      PRT;   131 AA.
AC   Q868Z2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Erythrocyte membrane protein 1 variant 2 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22561043; PubMed=12672527; DOI=10.1016/S0166-6851(03)00004-5;
RA   Winter G., Chen Q., Flick K., Kremsner P., Fernandez V., Wahlgren M.;
RT   "The 3D7var5.2 (var COMMON) type var gene family is commonly expressed
RT   in non-placental Plasmodium falciparum malaria.";
RL   Mol. Biochem. Parasitol. 127:179-191(2003).
DR   EMBL; AF528111; AAO85728.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER     131    131
SQ   SEQUENCE   131 AA;  15163 MW;  DEDACFCA392223C2 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 131;
  Best Local Similarity   71.4%;  Pred. No. 67;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         63 WTANRHT 69


RESULT 43
Q8STF4_PLAFA
ID   Q8STF4_PLAFA PRELIMINARY;      PRT;   131 AA.
AC   Q8STF4;
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DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Erythrocyte membrane protein 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21839615; PubMed=11849711; DOI=10.1016/S0166-6851(01)00443-1;
RA   Fowler E.V., Peters J.M., Gatton M.L., Chen N., Cheng Q.;
RT   "Genetic diversity of the DBLalpha region in Plasmodium falciparum var
RT   genes among Asia-Pacific isolates.";
RL   Mol. Biochem. Parasitol. 120:117-126(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Fowler E., Peters J., Gatton M., Chen N., Cheng Q.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY054813; AAL11177.1; -; Genomic_DNA.
DR   EMBL; AY054923; AAL11287.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     131    131
SQ   SEQUENCE   131 AA;  15488 MW;  4859B076CBA741F2 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 131;
  Best Local Similarity   71.4%;  Pred. No. 67;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         68 WTANRHT 74


RESULT 44
Q8T4U7_PLAFA
ID   Q8T4U7_PLAFA PRELIMINARY;      PRT;   131 AA.
AC   Q8T4U7;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Erythrocyte membrane protein 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21839615; PubMed=11849711; DOI=10.1016/S0166-6851(01)00443-1;
RA   Fowler E.V., Peters J.M., Gatton M.L., Chen N., Cheng Q.;
RT   "Genetic diversity of the DBLalpha region in Plasmodium falciparum var
RT   genes among Asia-Pacific isolates.";
RL   Mol. Biochem. Parasitol. 120:117-126(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Fowler E., Peters J., Gatton M., Chen N., Cheng Q.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY054967; AAL11331.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     131    131
SQ   SEQUENCE   131 AA;  15364 MW;  89678615F986E3AA CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 131;
  Best Local Similarity   71.4%;  Pred. No. 67;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         65 WTANRHT 71


RESULT 45
Q8T4X9_PLAFA
ID   Q8T4X9_PLAFA PRELIMINARY;      PRT;   131 AA.
AC   Q8T4X9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Erythrocyte membrane protein 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21839615; PubMed=11849711; DOI=10.1016/S0166-6851(01)00443-1;
RA   Fowler E.V., Peters J.M., Gatton M.L., Chen N., Cheng Q.;
RT   "Genetic diversity of the DBLalpha region in Plasmodium falciparum var
RT   genes among Asia-Pacific isolates.";
RL   Mol. Biochem. Parasitol. 120:117-126(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Fowler E., Peters J., Gatton M., Chen N., Cheng Q.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY054933; AAL11297.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     131    131
SQ   SEQUENCE   131 AA;  15343 MW;  1E1BF7138D59B408 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 131;
  Best Local Similarity   71.4%;  Pred. No. 67;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         73 WTANRHT 79


RESULT 46
Q8T577_PLAFA
ID   Q8T577_PLAFA PRELIMINARY;      PRT;   131 AA.
AC   Q8T577;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Erythrocyte membrane protein 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21839615; PubMed=11849711; DOI=10.1016/S0166-6851(01)00443-1;
RA   Fowler E.V., Peters J.M., Gatton M.L., Chen N., Cheng Q.;
RT   "Genetic diversity of the DBLalpha region in Plasmodium falciparum var
RT   genes among Asia-Pacific isolates.";
RL   Mol. Biochem. Parasitol. 120:117-126(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Fowler E., Peters J., Gatton M., Chen N., Cheng Q.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY054802; AAL11166.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER     131    131
SQ   SEQUENCE   131 AA;  14970 MW;  7A978ED606C89209 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 131;
  Best Local Similarity   71.4%;  Pred. No. 67;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         67 WTANRHT 73


RESULT 47
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Q8T355_PLAFA
ID   Q8T355_PLAFA PRELIMINARY;      PRT;   132 AA.
AC   Q8T355;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   PfEMP1 (Fragment).
GN   Name=P132var1;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21927235; PubMed=11930336; DOI=10.1086/339684;
RA   Rowe J.A., Kyes S.A., Rogerson S.J., Babiker H.A., Raza A.;
RT   "Identification of a conserved Plasmodium falciparum var gene
RT   implicated in malaria in pregnancy.";
RL   J. Infect. Dis. 185:1207-1211(2002).
DR   EMBL; AJ420379; CAD20835.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER     132    132
SQ   SEQUENCE   132 AA;  15512 MW;  C67EF154C47D2E55 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 132;
  Best Local Similarity   71.4%;  Pred. No. 68;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         71 WTANRHT 77


RESULT 48
Q86RR3_PLAFA
ID   Q86RR3_PLAFA PRELIMINARY;      PRT;   133 AA.
AC   Q86RR3;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Erythrocyte membrane protein 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kirchgatter K., del Portillo H.A.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF416580; AAN39150.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER     133    133
SQ   SEQUENCE   133 AA;  15382 MW;  F09577B8AF5D7760 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 133;
  Best Local Similarity   71.4%;  Pred. No. 68;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         72 WTANRHT 78


RESULT 49
Q86RR4_PLAFA
ID   Q86RR4_PLAFA PRELIMINARY;      PRT;   133 AA.
AC   Q86RR4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Erythrocyte membrane protein 1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Kirchgatter K., del Portillo H.A.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF416579; AAN39149.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER     133    133
SQ   SEQUENCE   133 AA;  15440 MW;  6BF8C1618BCE875C CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 133;
  Best Local Similarity   71.4%;  Pred. No. 68;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         72 WTANRHT 78


RESULT 50
Q964S4_PLAFA
ID   Q964S4_PLAFA PRELIMINARY;      PRT;   133 AA.
AC   Q964S4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PfEMP1 (Fragment).
GN   Name=var;
OS   Plasmodium falciparum.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5833;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ItG2;
RX   MEDLINE=21918495; PubMed=11918813;
RA   Duffy M.F., Brown G.V., Basuki W., Krejany E.O., Noviyanti R.,
RA   Cowman A.F., Reeder J.C.;
RT   "Transcription of multiple var genes by individual, trophozoite-stage
RT   Plasmodium falciparum cells expressing a chondroitin sulphate A
RT   binding phenotype.";
RL   Mol. Microbiol. 43:1285-1293(2002).
DR   EMBL; AF275846; AAK69040.1; -; mRNA.
FT   NON_TER       1      1
FT   NON_TER     133    133
SQ   SEQUENCE   133 AA;  15604 MW;  1C8FDF5FC53D5289 CRC64;

  Query Match             81.4%;  Score 35;  DB 2;  Length 133;
  Best Local Similarity   71.4%;  Pred. No. 68;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||: |||
Db         68 WTANRHT 74


Search completed: March 23, 2006, 02:02:55
Job time : 88.362 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:05:22 ; Search time 15.1507 Seconds
(without alignments)
38.196 Million cell updates/sec

Title: US-10-755-382-21
Perfect score: 43
Sequence: 1 WTSTRHT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	100.0	7	1	US-08-318-157B-21	Sequence 21, Appl
2	43	100.0	7	2	US-09-253-794-21	Sequence 21, Appl
3	43	100.0	106	1	US-08-318-157B-4	Sequence 4, Appli
4	43	100.0	106	1	US-08-318-157B-19	Sequence 19, Appl
5	43	100.0	106	2	US-09-253-794-4	Sequence 4, Appli
6	43	100.0	106	2	US-09-253-794-19	Sequence 19, Appl
7	43	100.0	250	1	US-08-133-804-2	Sequence 2, Appli
8	43	100.0	250	1	US-08-461-184-8	Sequence 8, Appli
9	43	100.0	250	1	US-08-463-675-8	Sequence 8, Appli
10	43	100.0	250	1	US-08-464-589-8	Sequence 8, Appli
11	43	100.0	250	1	US-08-461-838-2	Sequence 2, Appli
12	43	100.0	250	1	US-08-461-386-2	Sequence 2, Appli
13	43	100.0	622	1	US-08-356-786-16	Sequence 16, Appl
14	39	90.7	110	2	US-10-092-246-13	Sequence 13, Appl
15	39	90.7	110	2	US-10-096-246A-13	Sequence 13, Appl
16	39	90.7	239	2	US-10-092-246-32	Sequence 32, Appl
17	39	90.7	239	2	US-10-092-246-33	Sequence 33, Appl
18	39	90.7	239	2	US-10-096-246A-32	Sequence 32, Appl
19	39	90.7	239	2	US-10-096-246A-33	Sequence 33, Appl
20	39	90.7	240	2	US-10-092-246-34	Sequence 34, Appl
21	39	90.7	240	2	US-10-092-246-35	Sequence 35, Appl
22	39	90.7	240	2	US-10-092-246-36	Sequence 36, Appl
23	39	90.7	240	2	US-10-092-246-37	Sequence 37, Appl
24	39	90.7	240	2	US-10-096-246A-34	Sequence 34, Appl
25	39	90.7	240	2	US-10-096-246A-35	Sequence 35, Appl
26	39	90.7	240	2	US-10-096-246A-36	Sequence 36, Appl
27	39	90.7	240	2	US-10-096-246A-37	Sequence 37, Appl
28	39	90.7	257	2	US-10-092-246-2	Sequence 2, Appli
29	39	90.7	257	2	US-10-096-246A-2	Sequence 2, Appli
30	38	88.4	106	2	US-09-189-129-4	Sequence 4, Appli
31	38	88.4	106	2	US-09-824-286-4	Sequence 4, Appli
32	38	88.4	107	1	US-07-634-278-50	Sequence 50, Appl
33	38	88.4	107	1	US-07-634-278-51	Sequence 51, Appl
34	38	88.4	107	1	US-08-477-728-50	Sequence 50, Appl
35	38	88.4	107	1	US-08-477-728-51	Sequence 51, Appl
36	38	88.4	107	1	US-08-474-040-50	Sequence 50, Appl
37	38	88.4	107	1	US-08-474-040-51	Sequence 51, Appl
38	38	88.4	107	1	US-08-487-200-50	Sequence 50, Appl
39	38	88.4	107	1	US-08-487-200-51	Sequence 51, Appl
40	38	88.4	107	1	US-08-491-845-4	Sequence 4, Appli
41	38	88.4	107	1	US-08-491-845-12	Sequence 12, Appl
42	38	88.4	107	2	US-08-838-682-19	Sequence 19, Appl
43	38	88.4	107	2	US-08-895-914-19	Sequence 19, Appl
44	38	88.4	107	2	US-08-484-537-50	Sequence 50, Appl
45	38	88.4	107	2	US-08-484-537-51	Sequence 51, Appl
46	38	88.4	107	2	US-09-357-710A-19	Sequence 19, Appl
47	38	88.4	107	2	US-09-357-707-19	Sequence 19, Appl
48	38	88.4	107	2	US-09-357-708-19	Sequence 19, Appl
49	38	88.4	249	1	US-08-797-689-18	Sequence 18, Appl
50	38	88.4	249	2	US-09-984-186-18	Sequence 18, Appl
51	36	83.7	228	1	US-08-484-101B-40	Sequence 40, Appl
52	36	83.7	228	2	US-08-714-524D-40	Sequence 40, Appl
53	34	79.1	7	2	US-09-406-535-9	Sequence 9, Appli
54	34	79.1	107	2	US-09-406-535-4	Sequence 4, Appli
55	34	79.1	139	2	US-09-252-991A-24538	Sequence 24538, A
56	34	79.1	260	2	US-09-540-236-3812	Sequence 3812, Ap
57	34	79.1	375	2	US-09-614-912-96	Sequence 96, Appl
58	34	79.1	501	2	US-09-134-000C-4693	Sequence 4693, Ap
59	33	76.7	108	2	US-09-232-290-18	Sequence 18, Appl
60	33	76.7	142	2	US-09-252-991A-31446	Sequence 31446, A
61	33	76.7	268	2	US-09-605-703B-658	Sequence 658, App
62	33	76.7	268	2	US-09-605-703B-660	Sequence 660, App
63	32	74.4	16	1	US-08-031-538-38	Sequence 38, Appl
64	32	74.4	157	2	US-09-270-767-35310	Sequence 35310, A
65	32	74.4	157	2	US-09-270-767-50527	Sequence 50527, A
66	32	74.4	240	2	US-10-001-189-59	Sequence 59, Appl
67	32	74.4	253	2	US-09-270-767-35268	Sequence 35268, A
68	32	74.4	253	2	US-09-270-767-50485	Sequence 50485, A
69	32	74.4	260	2	US-09-252-991A-21611	Sequence 21611, A
70	32	74.4	268	2	US-09-712-363-245	Sequence 245, App
71	32	74.4	370	1	US-08-031-538-2	Sequence 2, Appli
72	32	74.4	419	2	US-09-489-039A-8844	Sequence 8844, Ap
73	32	74.4	462	2	US-09-477-962-109	Sequence 109, App
74	32	74.4	572	2	US-10-096-571-2	Sequence 2, Appli
75	32	74.4	1232	2	US-09-902-540-14264	Sequence 14264, A
76	32	74.4	1536	2	US-09-413-814-10	Sequence 10, Appl
77	31	72.1	17	1	US-08-729-152-38	Sequence 38, Appl
78	31	72.1	107	1	US-08-399-106A-14	Sequence 14, Appl
79	31	72.1	107	1	US-08-433-105A-14	Sequence 14, Appl
80	31	72.1	107	1	US-08-434-869A-14	Sequence 14, Appl
81	31	72.1	110	2	US-09-199-637A-39	Sequence 39, Appl
82	31	72.1	205	1	US-08-729-152-8	Sequence 8, Appli
83	31	72.1	209	2	US-09-949-016-10830	Sequence 10830, A
84	31	72.1	218	2	US-09-483-588-10	Sequence 10, Appl
85	31	72.1	223	1	US-08-430-633-1	Sequence 1, Appli
86	31	72.1	223	1	US-08-936-854-1	Sequence 1, Appli
87	31	72.1	263	2	US-09-252-991A-17326	Sequence 17326, A
88	31	72.1	308	2	US-09-804-778A-2	Sequence 2, Appli
89	31	72.1	308	2	US-09-804-778A-4	Sequence 4, Appli
90	31	72.1	308	2	US-09-804-778A-6	Sequence 6, Appli
91	31	72.1	346	2	US-09-343-011B-2	Sequence 2, Appli
92	31	72.1	441	2	US-09-252-991A-18870	Sequence 18870, A
93	31	72.1	454	2	US-09-653-755A-4	Sequence 4, Appli
94	31	72.1	455	1	US-08-738-172-4	Sequence 4, Appli
95	31	72.1	462	2	US-09-653-755A-6	Sequence 6, Appli
96	31	72.1	478	2	US-09-770-916-2	Sequence 2, Appli
97	31	72.1	571	2	US-09-252-991A-30957	Sequence 30957, A
98	31	72.1	634	2	US-09-614-912-88	Sequence 88, Appl
99	31	72.1	634	2	US-09-614-912-100	Sequence 100, App
100	31	72.1	1143	1	US-08-310-912A-108	Sequence 108, App

101	31	72.1	1143	2	US-09-301-085-108	Sequence 108, App
102	31	72.1	1143	4	PCT-US95-04589-108	Sequence 108, App
103	31	72.1	1144	1	US-08-261-663A-2	Sequence 2, Appli
104	31	72.1	1144	1	US-08-261-663A-4	Sequence 4, Appli
105	31	72.1	1144	2	US-08-930-996A-9	Sequence 9, Appli
106	31	72.1	1144	2	US-09-357-206A-3	Sequence 3, Appli
107	31	72.1	1144	2	US-09-813-742A-3	Sequence 3, Appli
108	31	72.1	1144	4	PCT-US95-07754A-2	Sequence 2, Appli
109	31	72.1	1144	4	PCT-US95-07754A-4	Sequence 4, Appli
110	31	72.1	1207	1	US-07-951-715A-7	Sequence 7, Appli
111	31	72.1	1207	1	US-08-459-448A-7	Sequence 7, Appli
112	31	72.1	1207	2	US-08-459-595A-7	Sequence 7, Appli
113	31	72.1	1207	2	US-08-459-504B-7	Sequence 7, Appli
114	31	72.1	1207	2	US-08-459-444-7	Sequence 7, Appli
115	31	72.1	1207	2	US-09-053-549-8	Sequence 8, Appli
116	31	72.1	1207	2	US-09-547-422-7	Sequence 7, Appli
117	31	72.1	1207	2	US-09-988-462-7	Sequence 7, Appli
118	31	72.1	1227	2	US-09-053-549-2	Sequence 2, Appli
119	31	72.1	1228	2	US-09-661-322A-38	Sequence 38, Appl
120	30	69.8	92	2	US-09-673-395A-143	Sequence 143, App
121	30	69.8	113	2	US-09-270-767-40629	Sequence 40629, A
122	30	69.8	113	2	US-09-270-767-55845	Sequence 55845, A
123	30	69.8	123	2	US-09-248-796A-20169	Sequence 20169, A
124	30	69.8	143	2	US-09-252-991A-31561	Sequence 31561, A
125	30	69.8	148	2	US-09-252-991A-17476	Sequence 17476, A
126	30	69.8	153	2	US-09-949-016-8665	Sequence 8665, Ap
127	30	69.8	153	2	US-09-949-016-8666	Sequence 8666, Ap
128	30	69.8	153	2	US-09-949-016-8667	Sequence 8667, Ap
129	30	69.8	153	2	US-09-949-016-8668	Sequence 8668, Ap
130	30	69.8	153	2	US-09-949-016-8669	Sequence 8669, Ap
131	30	69.8	193	2	US-09-252-991A-28920	Sequence 28920, A
132	30	69.8	197	1	US-08-855-261A-1	Sequence 1, Appli
133	30	69.8	197	2	US-09-227-224-1	Sequence 1, Appli
134	30	69.8	197	2	US-09-855-288-1	Sequence 1, Appli
135	30	69.8	197	2	US-09-973-278-154	Sequence 154, App
136	30	69.8	198	2	US-09-227-357-232	Sequence 232, App
137	30	69.8	200	2	US-09-949-016-9937	Sequence 9937, Ap
138	30	69.8	209	2	US-09-724-797-60	Sequence 60, Appl
139	30	69.8	227	2	US-09-489-039A-10192	Sequence 10192, A
140	30	69.8	270	2	US-09-270-767-58225	Sequence 58225, A
141	30	69.8	282	2	US-09-252-991A-32829	Sequence 32829, A
142	30	69.8	286	2	US-09-543-681A-6982	Sequence 6982, Ap
143	30	69.8	333	2	US-09-252-991A-17113	Sequence 17113, A
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145	30	69.8	356	1	US-08-259-924-2	Sequence 2, Appli
146	30	69.8	357	2	US-09-949-016-9297	Sequence 9297, Ap
147	30	69.8	360	2	US-09-252-991A-29934	Sequence 29934, A
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149	30	69.8	362	1	US-08-487-826B-30	Sequence 30, Appl
150	30	69.8	362	2	US-09-210-288-18	Sequence 18, Appl
151	30	69.8	362	2	US-10-153-273-18	Sequence 18, Appl
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153	30	69.8	439	2	US-09-252-991A-20350	Sequence 20350, A
154	30	69.8	447	2	US-09-949-016-6956	Sequence 6956, Ap
155	30	69.8	470	2	US-09-252-991A-20500	Sequence 20500, A
156	30	69.8	497	2	US-09-949-016-6958	Sequence 6958, Ap
157	30	69.8	501	1	US-08-663-566A-9	Sequence 9, Appli
158	30	69.8	501	1	US-08-023-610-9	Sequence 9, Appli
159	30	69.8	501	1	US-08-288-065A-9	Sequence 9, Appli
160	30	69.8	501	1	US-08-362-240A-9	Sequence 9, Appli
161	30	69.8	501	2	US-08-804-372A-7	Sequence 7, Appli
162	30	69.8	501	4	PCT-US95-10245-9	Sequence 9, Appli
163	30	69.8	563	2	US-09-949-016-6955	Sequence 6955, Ap
164	30	69.8	567	2	US-09-543-681A-7515	Sequence 7515, Ap
165	30	69.8	592	2	US-09-949-016-6957	Sequence 6957, Ap
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167	30	69.8	610	2	US-09-438-185A-58	Sequence 58, Appl
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170	30	69.8	620	2	US-09-949-016-7497	Sequence 7497, Ap
171	30	69.8	620	2	US-09-949-016-7498	Sequence 7498, Ap
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183	30	69.8	1229	1	US-08-779-046-4	Sequence 4, Appli
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188	30	69.8	3969	2	US-09-538-092-1262	Sequence 1262, Ap
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190	30	69.8	4544	1	US-08-469-658-52	Sequence 52, Appl
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193	29	67.4	23	2	US-09-270-767-54175	Sequence 54175, A
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196	29	67.4	68	2	US-09-973-278-412	Sequence 412, App
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253	29	67.4	997	1	US-08-904-686A-50	Sequence 50, Appl
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263	29	67.4	1985	2	US-09-539-601-30	Sequence 30, Appl
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274	29	67.4	2620	1	US-08-384-616-32	Sequence 32, Appl
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277	29	67.4	2621	1	US-08-324-977-36	Sequence 36, Appl
278	29	67.4	2621	1	US-08-384-616-36	Sequence 36, Appl
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292	29	67.4	2955	2	US-08-443-900A-3	Sequence 3, Appli
293	29	67.4	2955	2	US-08-444-818-124	Sequence 124, App
294	29	67.4	2955	2	US-08-249-843-3	Sequence 3, Appli
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297	29	67.4	3010	1	US-08-324-977-2	Sequence 2, Appli
298	29	67.4	3010	1	US-08-324-977-14	Sequence 14, Appl
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308	29	67.4	3010	2	US-09-539-601-27	Sequence 27, Appl
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317	29	67.4	3011	1	US-08-231-368-36	Sequence 36, Appl
318	29	67.4	3011	1	US-08-440-210-36	Sequence 36, Appl
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325	29	67.4	3011	2	US-09-014-416-5	Sequence 5, Appli
326	29	67.4	3011	2	US-08-529-169A-6	Sequence 6, Appli
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335	29	67.4	3011	2	US-09-952-572-9	Sequence 9, Appli
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341	29	67.4	3011	4	PCT-US94-07280-1	Sequence 1, Appli
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346	29	67.4	3178	2	US-09-655-160-4	Sequence 4, Appli
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350	28	65.1	74	2	US-09-270-767-44875	Sequence 44875, A
351	28	65.1	82	2	US-09-270-767-35838	Sequence 35838, A
352	28	65.1	82	2	US-09-270-767-51055	Sequence 51055, A
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355	28	65.1	110	2	US-09-252-991A-32217	Sequence 32217, A
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357	28	65.1	116	2	US-09-621-976-6157	Sequence 6157, Ap
358	28	65.1	116	2	US-09-248-796A-15543	Sequence 15543, A
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363	28	65.1	159	2	US-09-252-991A-25125	Sequence 25125, A
364	28	65.1	162	2	US-09-270-767-38424	Sequence 38424, A
365	28	65.1	162	2	US-09-270-767-53641	Sequence 53641, A
366	28	65.1	163	2	US-09-252-991A-24968	Sequence 24968, A
367	28	65.1	166	2	US-09-270-767-32841	Sequence 32841, A
368	28	65.1	170	2	US-09-248-796A-17611	Sequence 17611, A
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396	28	65.1	358	2	US-09-088-337B-19	Sequence 19, Appl
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412	28	65.1	378	2	US-09-088-337B-15	Sequence 15, Appl
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416	28	65.1	378	2	US-09-170-496D-74	Sequence 74, Appl
417	28	65.1	378	2	US-09-170-496D-204	Sequence 204, App
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420	28	65.1	378	2	US-09-721-495B-7	Sequence 7, Appli
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422	28	65.1	378	4	PCT-US93-11153-15	Sequence 15, Appl
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424	28	65.1	399	2	US-08-834-033A-4	Sequence 4, Appli
425	28	65.1	399	2	US-09-363-574-4	Sequence 4, Appli
426	28	65.1	399	2	US-09-363-526-4	Sequence 4, Appli
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430	28	65.1	410	2	US-09-299-843A-7	Sequence 7, Appli
431	28	65.1	410	2	US-09-088-337B-7	Sequence 7, Appli
432	28	65.1	410	4	PCT-US93-11153-7	Sequence 7, Appli
433	28	65.1	419	2	US-10-104-047-3262	Sequence 3262, Ap
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435	28	65.1	423	2	US-09-438-185A-479	Sequence 479, App
436	28	65.1	427	2	US-09-252-991A-17391	Sequence 17391, A
437	28	65.1	447	2	US-09-252-991A-25916	Sequence 25916, A
438	28	65.1	453	2	US-09-328-352-5272	Sequence 5272, Ap
439	28	65.1	489	2	US-09-710-279-1302	Sequence 1302, Ap
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441	28	65.1	501	2	US-09-614-912-70	Sequence 70, Appl
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448	28	65.1	579	2	US-09-254-776B-59	Sequence 59, Appl
449	28	65.1	579	2	US-09-369-247-61	Sequence 61, Appl
450	28	65.1	579	2	US-10-062-548-61	Sequence 61, Appl
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456	28	65.1	613	2	US-09-254-776B-55	Sequence 55, Appl
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532	27	62.8	134	2	US-09-095-855-165	Sequence 165, App
533	27	62.8	134	2	US-09-324-542-165	Sequence 165, App
534	27	62.8	134	2	US-09-205-426-165	Sequence 165, App
535	27	62.8	141	2	US-09-489-039A-13076	Sequence 13076, A
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555	27	62.8	187	2	US-09-252-991A-17564	Sequence 17564, A
556	27	62.8	187	2	US-09-252-991A-20667	Sequence 20667, A
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564	27	62.8	211	2	US-09-107-532A-7002	Sequence 7002, Ap
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572	27	62.8	243	2	US-09-095-855-199	Sequence 199, App
573	27	62.8	243	2	US-09-205-426-199	Sequence 199, App
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575	27	62.8	245	2	US-09-644-934-2	Sequence 2, Appli
576	27	62.8	247	2	US-09-543-681A-5194	Sequence 5194, Ap
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588	27	62.8	280	2	US-09-605-703B-954	Sequence 954, App
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591	27	62.8	290	2	US-09-620-461-8	Sequence 8, Appli
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595	27	62.8	290	2	US-09-915-789A-17	Sequence 17, Appl
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613	27	62.8	340	2	US-09-234-613-26	Sequence 26, Appl
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615	27	62.8	346	2	US-09-710-279-2034	Sequence 2034, Ap
616	27	62.8	355	2	US-09-134-001C-4752	Sequence 4752, Ap
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621	27	62.8	411	2	US-09-210-288-19	Sequence 19, Appl
622	27	62.8	411	2	US-10-153-273-19	Sequence 19, Appl
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626	27	62.8	430	2	US-09-722-971-4	Sequence 4, Appli
627	27	62.8	431	2	US-09-684-855-114	Sequence 114, App
628	27	62.8	435	2	US-09-902-540-15382	Sequence 15382, A
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635	27	62.8	439	2	US-09-684-855-133	Sequence 133, App
636	27	62.8	439	2	US-09-684-855-156	Sequence 156, App
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640	27	62.8	441	2	US-09-634-493A-1	Sequence 1, Appli
641	27	62.8	441	2	US-09-684-855-115	Sequence 115, App
642	27	62.8	441	2	US-09-488-265B-14	Sequence 14, Appl
643	27	62.8	441	2	US-09-488-265B-24	Sequence 24, Appl
644	27	62.8	441	2	US-09-488-265B-98	Sequence 98, Appl
645	27	62.8	443	2	US-09-198-452A-1086	Sequence 1086, Ap
646	27	62.8	447	2	US-09-044-718-6	Sequence 6, Appli
647	27	62.8	447	2	US-10-062-848-6	Sequence 6, Appli
648	27	62.8	449	1	US-08-142-439A-5	Sequence 5, Appli
649	27	62.8	449	1	US-08-869-477-5	Sequence 5, Appli
650	27	62.8	457	2	US-08-477-928A-33	Sequence 33, Appl
651	27	62.8	463	2	US-08-477-928A-6	Sequence 6, Appli
652	27	62.8	463	2	US-08-868-435-29	Sequence 29, Appl
653	27	62.8	463	2	US-08-744-231-29	Sequence 29, Appl
654	27	62.8	463	2	US-09-273-871A-10	Sequence 10, Appl
655	27	62.8	463	2	US-10-083-452-10	Sequence 10, Appl
656	27	62.8	463	2	US-09-635-504-29	Sequence 29, Appl
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664	27	62.8	467	2	US-09-684-855-163	Sequence 163, App
665	27	62.8	467	2	US-09-684-855-167	Sequence 167, App
666	27	62.8	467	2	US-09-684-855-169	Sequence 169, App
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672	27	62.8	467	2	US-09-488-265B-35	Sequence 35, Appl
673	27	62.8	467	2	US-09-488-265B-36	Sequence 36, Appl
674	27	62.8	467	2	US-09-488-265B-91	Sequence 91, Appl
675	27	62.8	467	2	US-09-488-265B-93	Sequence 93, Appl
676	27	62.8	467	2	US-09-488-265B-95	Sequence 95, Appl
677	27	62.8	467	2	US-09-488-265B-97	Sequence 97, Appl
678	27	62.8	478	2	US-08-477-928A-32	Sequence 32, Appl
679	27	62.8	478	2	US-08-477-928A-34	Sequence 34, Appl
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689	27	62.8	496	2	US-09-252-991A-17357	Sequence 17357, A
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691	27	62.8	518	2	US-09-270-767-42683	Sequence 42683, A
692	27	62.8	519	2	US-09-248-796A-20368	Sequence 20368, A
693	27	62.8	520	2	US-09-489-039A-11384	Sequence 11384, A
694	27	62.8	522	2	US-10-104-047-2664	Sequence 2664, Ap
695	27	62.8	534	2	US-10-104-047-3403	Sequence 3403, Ap
696	27	62.8	545	2	US-09-270-767-58384	Sequence 58384, A
697	27	62.8	553	1	US-08-475-894-2	Sequence 2, Appli
698	27	62.8	553	1	US-08-484-710-2	Sequence 2, Appli
699	27	62.8	553	1	US-08-484-709-2	Sequence 2, Appli
700	27	62.8	553	2	US-08-474-697-2	Sequence 2, Appli
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704	27	62.8	596	2	US-09-107-433-4563	Sequence 4563, Ap
705	27	62.8	628	2	US-09-107-532A-5288	Sequence 5288, Ap
706	27	62.8	631	2	US-09-252-991A-26007	Sequence 26007, A
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708	27	62.8	706	2	US-09-303-518D-254	Sequence 254, App
709	27	62.8	706	2	US-09-303-518D-258	Sequence 258, App
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804	27	62.8	790	2	US-09-589-477-102	Sequence 102, App
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817	27	62.8	843	2	US-08-591-502B-45	Sequence 45, Appl
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821	27	62.8	843	2	US-08-591-502B-56	Sequence 56, Appl
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836	27	62.8	894	2	US-09-094-410-2	Sequence 2, Appli
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855	27	62.8	903	2	US-09-758-007-1	Sequence 1, Appli
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892	27	62.8	1162	2	US-08-708-123D-43	Sequence 43, Appl
893	27	62.8	1162	2	US-08-638-524B-43	Sequence 43, Appl
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897	27	62.8	1165	2	US-09-069-781B-4	Sequence 4, Appli
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934	27	62.8	2710	2	US-10-153-273-12	Sequence 12, Appl
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936	27	62.8	2864	2	US-08-488-446-394	Sequence 394, App
937	27	62.8	2864	2	US-08-467-344A-394	Sequence 394, App
938	27	62.8	2864	2	US-08-424-550B-394	Sequence 394, App
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944	26	60.5	7	1	US-09-014-880-20	Sequence 20, Appl
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948	26	60.5	7	2	US-09-563-222C-27	Sequence 27, Appl
949	26	60.5	7	2	US-09-467-903-20	Sequence 20, Appl
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952	26	60.5	7	2	US-09-339-596A-18	Sequence 18, Appl
953	26	60.5	7	2	US-10-146-305-10	Sequence 10, Appl
954	26	60.5	7	4	PCT-US93-08435-24	Sequence 24, Appl
955	26	60.5	7	4	PCT-US93-08435-37	Sequence 37, Appl
956	26	60.5	7	4	PCT-US93-08435-41	Sequence 41, Appl
957	26	60.5	17	1	US-08-729-152-37	Sequence 37, Appl
958	26	60.5	19	1	US-08-484-434C-26	Sequence 26, Appl
959	26	60.5	19	2	US-09-384-361-26	Sequence 26, Appl
960	26	60.5	53	2	US-09-621-976-7154	Sequence 7154, Ap
961	26	60.5	62	2	US-09-328-352-4341	Sequence 4341, Ap
962	26	60.5	62	2	US-09-621-976-5579	Sequence 5579, Ap
963	26	60.5	67	2	US-09-621-976-7214	Sequence 7214, Ap
964	26	60.5	67	2	US-09-621-976-7215	Sequence 7215, Ap
965	26	60.5	71	1	US-08-152-721B-28	Sequence 28, Appl
966	26	60.5	73	2	US-09-489-039A-10859	Sequence 10859, A
967	26	60.5	75	2	US-09-583-110-2743	Sequence 2743, Ap
968	26	60.5	75	2	US-09-107-433-4185	Sequence 4185, Ap
969	26	60.5	79	2	US-09-252-991A-28954	Sequence 28954, A
970	26	60.5	88	1	US-08-469-202-20	Sequence 20, Appl
971	26	60.5	88	2	US-09-424-487B-2	Sequence 2, Appli
972	26	60.5	94	2	US-09-905-243-60	Sequence 60, Appl
973	26	60.5	98	2	US-10-330-613A-56	Sequence 56, Appl
974	26	60.5	101	2	US-09-627-896B-28	Sequence 28, Appl
975	26	60.5	101	2	US-10-194-975-89	Sequence 89, Appl
976	26	60.5	101	2	US-10-330-613A-55	Sequence 55, Appl

977	26	60.5	104	2	US-10-104-047-3073	Sequence 3073, Ap
978	26	60.5	109	1	US-08-308-494A-23	Sequence 23, Appl
979	26	60.5	110	2	US-08-957-001B-5	Sequence 5, Appli
980	26	60.5	110	2	US-08-957-001B-24	Sequence 24, Appl
981	26	60.5	110	2	US-09-496-301-5	Sequence 5, Appli
982	26	60.5	110	2	US-09-496-301-24	Sequence 24, Appl
983	26	60.5	112	1	US-07-942-245-30	Sequence 30, Appl
984	26	60.5	112	1	US-07-916-098A-15	Sequence 15, Appl
985	26	60.5	112	2	US-08-435-516-4	Sequence 4, Appli
986	26	60.5	112	2	US-08-435-516-28	Sequence 28, Appl
987	26	60.5	112	2	US-09-252-991A-22629	Sequence 22629, A
988	26	60.5	113	1	US-08-690-102A-2	Sequence 2, Appli
989	26	60.5	113	1	US-08-690-102A-6	Sequence 6, Appli
990	26	60.5	113	2	US-08-483-749A-16	Sequence 16, Appl
991	26	60.5	113	2	US-09-127-902-2	Sequence 2, Appli
992	26	60.5	113	2	US-09-127-902-6	Sequence 6, Appli
993	26	60.5	113	2	US-09-155-107-2	Sequence 2, Appli
994	26	60.5	113	2	US-09-155-107-6	Sequence 6, Appli
995	26	60.5	113	2	US-09-155-107-20	Sequence 20, Appl
996	26	60.5	113	2	US-08-525-539A-80	Sequence 80, Appl
997	26	60.5	113	2	US-09-301-593-2	Sequence 2, Appli
998	26	60.5	113	2	US-09-301-593-4	Sequence 4, Appli
999	26	60.5	113	2	US-09-301-593-6	Sequence 6, Appli
1000	26	60.5	113	4	PCT-US93-11611-5	Sequence 5, Appli

ALIGNMENTS

```
RESULT 1
US-08-318-157B-21
; Sequence 21, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-21

  Query Match           100.0%;  Score 43;  DB 1;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 4.6e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db          1 WTSTRHT 7


RESULT 2
US-09-253-794-21
; Sequence 21, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 21:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 7 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-253-794-21

  Query Match           100.0%;  Score 43;  DB 2;  Length 7;
  Best Local Similarity  100.0%;  Pred. No. 4.6e+05;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db          1 WTSTRHT 7


RESULT 3
US-08-318-157B-4
; Sequence 4, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
```

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;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-4

  Query Match             100.0%;  Score 43;  DB 1;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         50 WTSTRHT 56


RESULT 4
US-08-318-157B-19
; Sequence 19, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-19

  Query Match             100.0%;  Score 43;  DB 1;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         50 WTSTRHT 56


RESULT 5
US-09-253-794-4
; Sequence 4, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 106 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-253-794-4

  Query Match             100.0%;  Score 43;  DB 2;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         50 WTSTRHT 56
```

```
RESULT 6
US-09-253-794-19
; Sequence 19, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 106 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-253-794-19

  Query Match             100.0%;  Score 43;  DB 2;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         50 WTSTRHT 56


RESULT 7
US-08-133-804-2
; Sequence 2, Application US/08133804
; Patent No. 5534254
;  GENERAL INFORMATION:
;    APPLICANT:  Huston, James S.
;    APPLICANT:  Oppermann, Hermann
;    APPLICANT:  Houston, L. L.
;    APPLICANT:  Ring, David B.
;    TITLE OF INVENTION:  Biosynthetic Binding Proteins For
;    TITLE OF INVENTION:  Imaging
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault/Patent Department
;      STREET:  Exchange Place, 53 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/133,804
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kelley, Robin D.
;      REGISTRATION NUMBER:  34,637
;      REFERENCE/DOCKET NUMBER:  2054/22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-248-7477
;      TELEFAX:  617-248-7100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-133-804-2

  Query Match             100.0%;  Score 43;  DB 1;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        185 WTSTRHT 191


RESULT 8
US-08-461-184-8
; Sequence 8, Application US/08461184
; Patent No. 5631158
;  GENERAL INFORMATION:
;    APPLICANT:  DORAI, HAIMANTI
;    APPLICANT:  OPPERMANN, HERMANN
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR HIGH PROTEIN
;    TITLE OF INVENTION:  PRODUCTION FROM NON-NATIVE DNA
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
;      STREET:  45 SOUTH STREET
;      CITY:  HOPKINTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  07148
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,184
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/143,498
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KELLEY, ROBIN D
;      REGISTRATION NUMBER:  34,637
;      REFERENCE/DOCKET NUMBER:  CRP093
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/248-7000
;      TELEFAX:  617/248-7100
;  INFORMATION FOR SEQ ID NO:  8:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-461-184-8

  Query Match             100.0%;  Score 43;  DB 1;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        185 WTSTRHT 191


RESULT 9
US-08-463-675-8
; Sequence 8, Application US/08463675
; Patent No. 5658763
;  GENERAL INFORMATION:
;    APPLICANT:  DORAI, HAIMANTI
;    APPLICANT:  OPPERMANN, HERMANN
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR HIGH PROTEIN
;    TITLE OF INVENTION:  PRODUCTION FROM NON-NATIVE DNA
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
;      STREET:  45 SOUTH STREET
;      CITY:  HOPKINTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  07148
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/463,675
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/143,498
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KELLEY, ROBIN D
;      REGISTRATION NUMBER:  34,637
;      REFERENCE/DOCKET NUMBER:  CRP093
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/248-7000
;      TELEFAX:  617/248-7100
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-463-675-8

  Query Match             100.0%;  Score 43;  DB 1;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        185 WTSTRHT 191


RESULT 10
US-08-464-589-8
; Sequence 8, Application US/08464589
; Patent No. 5733782
;  GENERAL INFORMATION:
;    APPLICANT:  DORAI, HAIMANTI
;    APPLICANT:  OPPERMANN, HERMANN
;    TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR HIGH PROTEIN
;    TITLE OF INVENTION:  PRODUCTION FROM NON-NATIVE DNA
;    NUMBER OF SEQUENCES:  10
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
;      STREET:  45 SOUTH STREET
;      CITY:  HOPKINTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  07148
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,589
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/143,498
;      FILING DATE:  25-OCT-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KELLEY, ROBIN D
;      REGISTRATION NUMBER:  34,637
;      REFERENCE/DOCKET NUMBER:  CRP093
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/248-7000
;      TELEFAX:  617/248-7100
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-464-589-8

  Query Match             100.0%;  Score 43;  DB 1;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        185 WTSTRHT 191


RESULT 11
US-08-461-838-2
; Sequence 2, Application US/08461838
; Patent No. 5753204
;  GENERAL INFORMATION:
;    APPLICANT:  Huston, James S.
;    APPLICANT:  Oppermann, Hermann
;    APPLICANT:  Houston, L. L.
;    APPLICANT:  Ring, David B.
;    TITLE OF INVENTION:  Biosynthetic Binding Proteins For
;    TITLE OF INVENTION:  Imaging
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault/Patent Department
;      STREET:  Exchange Place, 53 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
```

```
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,838
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kelley, Robin D.
;      REGISTRATION NUMBER:  34,637
;      REFERENCE/DOCKET NUMBER:  2054/22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-248-7477
;      TELEFAX:  617-248-7100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-461-838-2

  Query Match             100.0%;  Score 43;  DB 1;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        185 WTSTRHT 191


RESULT 12
US-08-461-386-2
; Sequence 2, Application US/08461386
; Patent No. 5837846
;  GENERAL INFORMATION:
;    APPLICANT:  Huston, James S.
;    APPLICANT:  Oppermann, Hermann
;    APPLICANT:  Houston, L. L.
;    APPLICANT:  Ring, David B.
;    TITLE OF INVENTION:  Biosynthetic Binding Proteins For
;    TITLE OF INVENTION:  Imaging
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Testa, Hurwitz & Thibeault/Patent Department
;      STREET:  Exchange Place, 53 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,386
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kelley, Robin D.
;      REGISTRATION NUMBER:  34,637
;      REFERENCE/DOCKET NUMBER:  2054/22
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-248-7477
;      TELEFAX:  617-248-7100
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-461-386-2

  Query Match             100.0%;  Score 43;  DB 1;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        185 WTSTRHT 191


RESULT 13
US-08-356-786-16
; Sequence 16, Application US/08356786
; Patent No. 5877305
;  GENERAL INFORMATION:
;    APPLICANT:  Huston, James S.
;    APPLICANT:  Oppermann, Hermann
;    APPLICANT:  Houston, L. L.
;    APPLICANT:  Ring, David B.
;    TITLE OF INVENTION:  Biosynthetic Binding Protein for Cancer
;    TITLE OF INVENTION:  Marker
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
;      STREET:  Exchange Place, 53 State Street
;      CITY:  Boston
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/356,786
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/831,967
;      FILING DATE:  06-FEB-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pitcher, Edmund R.
;      REGISTRATION NUMBER:  27,829
;      REFERENCE/DOCKET NUMBER:  CRP-053
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 248-7000
;      TELEFAX:  (617) 248-7100
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  622 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-356-786-16

  Query Match             100.0%;  Score 43;  DB 1;  Length 622;
  Best Local Similarity   100.0%;  Pred. No. 7.4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        185 WTSTRHT 191


RESULT 14
US-10-092-246-13
; Sequence 13, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
```

```
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/092,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-13

  Query Match             90.7%;  Score 39;  DB 2;  Length 110;
  Best Local Similarity   85.7%;  Pred. No. 6.7;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db         49 WSSTRHT 55


RESULT 15
US-10-096-246A-13
; Sequence 13, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
;  APPLICANT: Fulton, R. Elaine
;  APPLICANT:  Nagata, Leslie
;  APPLICANT:  Alvi, Azhar Z.
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
;  TITLE OF INVENTION:  Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
;  TITLE OF INVENTION:  Virus (VEE)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/096,246A
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: mouse
US-10-096-246A-13

  Query Match             90.7%;  Score 39;  DB 2;  Length 110;
  Best Local Similarity   85.7%;  Pred. No. 6.7;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db         49 WSSTRHT 55


RESULT 16
US-10-092-246-32
; Sequence 32, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/092,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-32

  Query Match             90.7%;  Score 39;  DB 2;  Length 239;
  Best Local Similarity   85.7%;  Pred. No. 14;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db        181 WSSTRHT 187


RESULT 17
US-10-092-246-33
; Sequence 33, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/092,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-33

  Query Match             90.7%;  Score 39;  DB 2;  Length 239;
  Best Local Similarity   85.7%;  Pred. No. 14;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db        181 WSSTRHT 187


RESULT 18
US-10-096-246A-32
; Sequence 32, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
;  APPLICANT: Fulton, R. Elaine
;  APPLICANT:  Nagata, Leslie
;  APPLICANT:  Alvi, Azhar Z.
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
;  TITLE OF INVENTION:  Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
;  TITLE OF INVENTION:  Virus (VEE)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/096,246A
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: mouse
US-10-096-246A-32

  Query Match             90.7%;  Score 39;  DB 2;  Length 239;
  Best Local Similarity   85.7%;  Pred. No. 14;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db        181 WSSTRHT 187


RESULT 19
US-10-096-246A-33
```

; Sequence 33, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie
; APPLICANT: Alvi, Azhar Z.
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
; TITLE OF INVENTION: Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
; TITLE OF INVENTION: Virus (VEE)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 239
; TYPE: PRT
; ORGANISM: mouse
US-10-096-246A-33

Query Match 90.7%; Score 39; DB 2; Length 239;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|:|||||
Db 181 WSSTRHT 187

RESULT 20
US-10-092-246-34
; Sequence 34, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
; TITLE OF INVENTION: scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-34

Query Match 90.7%; Score 39; DB 2; Length 240;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|:|||||
Db 182 WSSTRHT 188

RESULT 21
US-10-092-246-35
; Sequence 35, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
; TITLE OF INVENTION: scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-35

Query Match 90.7%; Score 39; DB 2; Length 240;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|:|||||
Db 182 WSSTRHT 188

RESULT 22
US-10-092-246-36
; Sequence 36, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
; TITLE OF INVENTION: scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-36

Query Match 90.7%; Score 39; DB 2; Length 240;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
|:|||||
Db 182 WSSTRHT 188

RESULT 23
US-10-092-246-37
; Sequence 37, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
; TITLE OF INVENTION: scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-37

Query Match 90.7%; Score 39; DB 2; Length 240;
Best Local Similarity 85.7%; Pred. No. 14;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WTSTRHT 7
              |:|||||
Db        182 WSSTRHT 188
```

RESULT 24
US-10-096-246A-34
; Sequence 34, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie
; APPLICANT: Alvi, Azhar Z.
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
; TITLE OF INVENTION: Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
; TITLE OF INVENTION: Virus (VEE)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 240
; TYPE: PRT
; ORGANISM: mouse
US-10-096-246A-34

Query Match 90.7%; Score 39; DB 2; Length 240;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WTSTRHT 7
              |:|||||
Db        182 WSSTRHT 188
```

RESULT 25
US-10-096-246A-35
; Sequence 35, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie
; APPLICANT: Alvi, Azhar Z.
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
; TITLE OF INVENTION: Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
; TITLE OF INVENTION: Virus (VEE)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 240
; TYPE: PRT
; ORGANISM: mouse
US-10-096-246A-35

Query Match 90.7%; Score 39; DB 2; Length 240;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 WTSTRHT 7
              |:|||||
Db        182 WSSTRHT 188
```

RESULT 26
US-10-096-246A-36
; Sequence 36, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie
; APPLICANT: Alvi, Azhar Z.
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
; TITLE OF INVENTION: Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
; TITLE OF INVENTION: Virus (VEE)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: mouse
US-10-096-246A-36

Query Match 90.7%; Score 39; DB 2; Length 240;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WTSTRHT 7
              |:|||||
Db        182 WSSTRHT 188
```

RESULT 27
US-10-096-246A-37
; Sequence 37, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
; APPLICANT: Fulton, R. Elaine
; APPLICANT: Nagata, Leslie
; APPLICANT: Alvi, Azhar Z.
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
; TITLE OF INVENTION: Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
; TITLE OF INVENTION: Virus (VEE)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/096,246A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 240
; TYPE: PRT
; ORGANISM: mouse
US-10-096-246A-37

Query Match 90.7%; Score 39; DB 2; Length 240;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WTSTRHT 7
              |:|||||
Db        182 WSSTRHT 188
```

RESULT 28
US-10-092-246-2
; Sequence 2, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor
; TITLE OF INVENTION: scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEL-0007
; CURRENT APPLICATION NUMBER: US/10/092,246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37

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;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 257
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-2

  Query Match             90.7%;  Score 39;  DB 2;  Length 257;
  Best Local Similarity   85.7%;  Pred. No. 15;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db        181 WSSTRHT 187


RESULT 29
US-10-096-246A-2
; Sequence 2, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
;  APPLICANT: Fulton, R. Elaine
;  APPLICANT:  Nagata, Leslie
;  APPLICANT:  Alvi, Azhar Z.
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
;  TITLE OF INVENTION:  Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
;  TITLE OF INVENTION:  Virus (VEE)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/096,246A
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 257
;   TYPE: PRT
;   ORGANISM: mouse
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   OTHER INFORMATION: scFv protein A116-6  1 - 239
;   OTHER INFORMATION: e-tag                240 - 257
US-10-096-246A-2

  Query Match             90.7%;  Score 39;  DB 2;  Length 257;
  Best Local Similarity   85.7%;  Pred. No. 15;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db        181 WSSTRHT 187


RESULT 30
US-09-189-129-4
; Sequence 4, Application US/09189129
; Patent No. 6323027
;  GENERAL INFORMATION:
;    APPLICANT:  Burkly, Linda C
;    APPLICANT:  Benjamin, Christopher D
;    APPLICANT:  Hession, Catherine A
;    APPLICANT:  Whitty, Adrian
;    TITLE OF INVENTION:  COMMON GAMMA CHAIN BLOCKING AGENTS
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Biogen, Inc.
;      STREET:  14 Cambridge Center
;      CITY:  Cambridge
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02142
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/189,129
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  A006 PCT CIP
;      FILING DATE:  09-MAY-1997
;      APPLICATION NUMBER:  60/017,466
;      FILING DATE:  10-MAY-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kaplan, Warren A.
;      REGISTRATION NUMBER:  34,199
;      REFERENCE/DOCKET NUMBER:  A006 PCT CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617 679-2000
;      TELEFAX:  617 679-2838
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  106 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FRAGMENT TYPE:  internal
US-09-189-129-4

  Query Match             88.4%;  Score 38;  DB 2;  Length 106;
  Best Local Similarity   85.7%;  Pred. No. 9.6;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 31
US-09-824-286-4
; Sequence 4, Application US/09824286
; Patent No. 6770745
;   GENERAL INFORMATION:
;        APPLICANT: Burkly, Linda C
;                   Benjamin, Christopher D
;                   Hession, Catherine A
;                   Whitty, Adrian
;        TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
;        NUMBER OF SEQUENCES: 17
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Biogen, Inc.
;             STREET: 14 Cambridge Center
;             CITY: Cambridge
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02142
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/824,286
;             FILING DATE: 02-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/017,466
;             FILING DATE: 10-MAY-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Kaplan, Warren A.
;             REGISTRATION NUMBER: 34,199
;             REFERENCE/DOCKET NUMBER: A006 PCT CIP
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 617 679-2000
;             TELEFAX: 617 679-2838
;   INFORMATION FOR SEQ ID NO: 4:
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;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 106 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: not relevant
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        FRAGMENT TYPE: internal
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-824-286-4

  Query Match             88.4%;  Score 38;  DB 2;  Length 106;
  Best Local Similarity   85.7%;  Pred. No. 9.6;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 32
US-07-634-278-50
; Sequence 50, Application US/07634278
; Patent No. 5530101
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,278
;      FILING DATE:  19-DEC-1990
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-634-278-50

  Query Match             88.4%;  Score 38;  DB 1;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 33
US-07-634-278-51
; Sequence 51, Application US/07634278
; Patent No. 5530101
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,278
;      FILING DATE:  19-DEC-1990
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-634-278-51

  Query Match             88.4%;  Score 38;  DB 1;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 34
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US-08-477-728-50
; Sequence 50, Application US/08477728
; Patent No. 5585089
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,728
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-477-728-50

  Query Match             88.4%;  Score 38;  DB 1;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 35
US-08-477-728-51
; Sequence 51, Application US/08477728
; Patent No. 5585089
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, 8th Floor
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94111
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,728
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-477-728-51

  Query Match             88.4%;  Score 38;  DB 1;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 36
US-08-474-040-50
; Sequence 50, Application US/08474040
; Patent No. 5693761
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
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;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,040
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-474-040-50

  Query Match             88.4%;  Score 38;  DB 1;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 37
US-08-474-040-51
; Sequence 51, Application US/08474040
; Patent No. 5693761
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,040
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-474-040-51

  Query Match             88.4%;  Score 38;  DB 1;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 38
US-08-487-200-50
; Sequence 50, Application US/08487200
; Patent No. 5693762
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,200
;      FILING DATE:  7-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
```

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;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002610
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-487-200-50

  Query Match             88.4%;  Score 38;  DB 1;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 39
US-08-487-200-51
; Sequence 51, Application US/08487200
; Patent No. 5693762
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/487,200
;      FILING DATE:  7-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/634,278
;      FILING DATE:  19-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002610
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-487-200-51

  Query Match             88.4%;  Score 38;  DB 1;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 40
US-08-491-845-4
; Sequence 4, Application US/08491845
; Patent No. 5773247
;  GENERAL INFORMATION:
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  KIMACHI, Kazuhiko
;    APPLICANT:  EDA, Yasuyuki
;    APPLICANT:  SHIOSAKI, Kouichi
;    APPLICANT:  OSATOMI, Kiyoshi
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  RECOMBINANT ANTI-HIV ANTIBODY AND
;    TITLE OF INVENTION:  PROCESS FOR PREPARING THE SAME
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Browdy and Neimark
;      STREET:  419 Seventh Street N.W. Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/491,845
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP93/00039
;      FILING DATE:  14-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Browdy, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  MAEDA=5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-491-845-4

  Query Match             88.4%;  Score 38;  DB 1;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 41
US-08-491-845-12
; Sequence 12, Application US/08491845
; Patent No. 5773247
;  GENERAL INFORMATION:
;    APPLICANT:  MAEDA, Hiroaki
;    APPLICANT:  KIMACHI, Kazuhiko
;    APPLICANT:  EDA, Yasuyuki
;    APPLICANT:  SHIOSAKI, Kouichi
;    APPLICANT:  OSATOMI, Kiyoshi
;    APPLICANT:  TOKIYOSHI, Sachio
;    TITLE OF INVENTION:  RECOMBINANT ANTI-HIV ANTIBODY AND
;    TITLE OF INVENTION:  PROCESS FOR PREPARING THE SAME
;    NUMBER OF SEQUENCES:  17
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Browdy and Neimark
;      STREET:  419 Seventh Street N.W. Ste. 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/491,845
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP93/00039
;      FILING DATE:  14-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Browdy, Roger L.
;      REGISTRATION NUMBER:  25,618
;      REFERENCE/DOCKET NUMBER:  MAEDA=5
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 628-5197
;      TELEFAX:  (202) 737-3528
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-491-845-12

  Query Match           88.4%;  Score 38;  DB 1;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 42
US-08-838-682-19
; Sequence 19, Application US/08838682
; Patent No. 6107090
;  GENERAL INFORMATION:
;    APPLICANT:  Bander M.D., Neil H.
;    TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF PROSTATE
;    TITLE OF INVENTION:  CANCER
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle LLP
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  14603-1051
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/838,682
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/016,976
;      FILING DATE:  06-MAY-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/022,125
;      FILING DATE:  18-JUL-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldman, Michael L.
;      REGISTRATION NUMBER:  30,727
;      REFERENCE/DOCKET NUMBER:  19603/1172
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716) 263-1304
;      TELEFAX:  (716) 263-1600
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-838-682-19

  Query Match           88.4%;  Score 38;  DB 2;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 43
US-08-895-914-19
; Sequence 19, Application US/08895914
; Patent No. 6136311
;  GENERAL INFORMATION:
;    APPLICANT:  Bander, Neil H.
;    TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF CANCER
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nixon, Hargrave, Devans & Doyle LLP
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  14603-1051
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/895,914
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/016,976
;      FILING DATE:  06-MAY-1996
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/022,125
;      FILING DATE:  18-JUL-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/838,682
;      FILING DATE:  09-APR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Goldman, Michael L.
;      REGISTRATION NUMBER:  30,727
;      REFERENCE/DOCKET NUMBER:  19603/1173
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (716) 263-1304
;      TELEFAX:  (716) 263-1600
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-895-914-19

  Query Match             88.4%;  Score 38;  DB 2;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 44
US-08-484-537-50
; Sequence 50, Application US/08484537
; Patent No. 6180370
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,537
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,278
;      FILING DATE:  19-DEC-1990
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  50:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-484-537-50

  Query Match             88.4%;  Score 38;  DB 2;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 45
US-08-484-537-51
; Sequence 51, Application US/08484537
; Patent No. 6180370
;  GENERAL INFORMATION:
;    APPLICANT:  QUEEN, Cary L.
;    APPLICANT:  CO, Man Sung
;    APPLICANT:  SCHNEIDER, William P.
;    APPLICANT:  LANDOLFI, Nicholas F.
;    APPLICANT:  COELINGH, Kathleen L.
;    APPLICANT:  SELICK, Harold E.
;    TITLE OF INVENTION:  IMPROVED HUMANIZED IMMUNOGLOBLINS
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend Khourie and Crew
;      STREET:  379 Lytton Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  US
;      ZIP:  94301
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,537
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/634,278
;      FILING DATE:  19-DEC-1990
;      APPLICATION NUMBER:  US 07/590,274
;      FILING DATE:  28-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/310,252
;      FILING DATE:  13-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/290,975
;      FILING DATE:  28-DEC-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith, William M
;      REGISTRATION NUMBER:  30,223
;      REFERENCE/DOCKET NUMBER:  11823-002600
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 326-2400
;      TELEFAX:  (415) 326-2422
;  INFORMATION FOR SEQ ID NO:  51:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
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;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-484-537-51

  Query Match             88.4%;  Score 38;  DB 2;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 46
US-09-357-710A-19
; Sequence 19, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
;  APPLICANT:  Bander, Neil H.
;  TITLE OF INVENTION:   TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:   Lois M. Kwasigroch: BZL 242/025
;  CURRENT APPLICATION NUMBER: US/09/357,710A
;  CURRENT FILING DATE:  1999-07-20
;  PRIOR APPLICATION NUMBER:   US 08/838,682
;  PRIOR FILING DATE:   1997-04-09
;  PRIOR APPLICATION NUMBER:   US 60/016,976
;  PRIOR FILING DATE:   1996-05-06
;  PRIOR APPLICATION NUMBER:   US 60/022,125
;  PRIOR FILING DATE:   1996-07-18
;  NUMBER OF SEQ ID NOS:   21
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-357-710A-19

  Query Match             88.4%;  Score 38;  DB 2;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 47
US-09-357-707-19
; Sequence 19, Application US/09357707
; Patent No. 6649163
; GENERAL INFORMATION:
;  APPLICANT: Bander, Neil H.
;  TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
;  FILE REFERENCE: Lois M. Kwasigroch: BZL 242/078
;  CURRENT APPLICATION NUMBER: US/09/357,707
;  CURRENT FILING DATE:  1999-07-20
;  PRIOR APPLICATION NUMBER: US 08/895,914
;  PRIOR FILING DATE: 1997-07-17
;  PRIOR APPLICATION NUMBER: US 08/838,682
;  PRIOR FILING DATE: 1997-04-09
;  PRIOR APPLICATION NUMBER: US 60/016,976
;  PRIOR FILING DATE: 1996-05-06
;  PRIOR APPLICATION NUMBER: US 60/022,125
;  PRIOR FILING DATE: 1996-07-18
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-357-707-19

  Query Match             88.4%;  Score 38;  DB 2;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 48
US-09-357-708-19
; Sequence 19, Application US/09357708
; Patent No. 6770450
; GENERAL INFORMATION:
;  APPLICANT: Bander, Neil H.
;  TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
;  FILE REFERENCE: Lois M. Kwasigroch: BZL 242/028
;  CURRENT APPLICATION NUMBER: US/09/357,708
;  CURRENT FILING DATE:  1999-07-20
;  PRIOR APPLICATION NUMBER: US 08/895,914
;  PRIOR FILING DATE: 1997-07-17
;  PRIOR APPLICATION NUMBER: US 08/838,682
;  PRIOR FILING DATE: 1997-04-09
;  PRIOR APPLICATION NUMBER: US 60/016,976
;  PRIOR FILING DATE: 1996-05-06
;  PRIOR APPLICATION NUMBER: US 60/022,125
;  PRIOR FILING DATE: 1996-07-18
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-09-357-708-19

  Query Match             88.4%;  Score 38;  DB 2;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 49
US-08-797-689-18
; Sequence 18, Application US/08797689
; Patent No. 5876969
;  GENERAL INFORMATION:
;    APPLICANT:  Fleer, Reinhard
;    APPLICANT:  Fournier, Alain
;    APPLICANT:  Guitton, Jean-Dominique
;    APPLICANT:  Jung, Gerard
;    APPLICANT:  Yeh, Patrice
;    TITLE OF INVENTION:  NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
;    TITLE OF INVENTION:  PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
;    TITLE OF INVENTION:  CONTAINING SAID POLYPEPTIDES
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Rhone-Poulenc Rorer Inc.
;      STREET:  500 Arcola Road, 3C43
;      CITY:  Collegeville
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  System 7.1
;      SOFTWARE:  Word 5.1 (PatentIn)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/797,689
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;      FILING DATE:  31-JAN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/256,927
;      FILING DATE:  28-JUL-1994
;      APPLICATION NUMBER:  FR 92/01064
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/FR93/00085
;      FILING DATE:  28-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Smith Ph.D., Julie K.
;      REGISTRATION NUMBER:  P-38,619
;      REFERENCE/DOCKET NUMBER:  ST92006-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (610) 454-3839
;      TELEFAX:  (610) 454-3808
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  249 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-797-689-18

  Query Match             88.4%;  Score 38;  DB 1;  Length 249;
  Best Local Similarity   85.7%;  Pred. No. 22;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db        192 WASTRHT 198


RESULT 50
US-09-984-186-18
; Sequence 18, Application US/09984186
; Patent No. 6686179
;   GENERAL INFORMATION:
;        APPLICANT: Fleer, Reinhard
;                   Fournier, Alain
;                   Guitton, Jean-Dominique
;                   Jung, Gerard
;                   Yeh, Patrice
;        TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
;                            PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
;                            CONTAINING SAID POLYPEPTIDES
;        NUMBER OF SEQUENCES: 36
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Rhone-Poulenc Rorer Inc.
;             STREET: 500 Arcola Road, 3C43
;             CITY: Collegeville
;             STATE: PA
;             COUNTRY: USA
;             ZIP: 19426
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: Macintosh
;             OPERATING SYSTEM: System 7.1
;             SOFTWARE: Word 5.1 (PatentIn)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/984,186
;             FILING DATE: 29-Oct-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/797,689
;             FILING DATE: 31-JAN-1997
;             APPLICATION NUMBER: US 08/256,927
;             FILING DATE: 28-JUL-1994
;             APPLICATION NUMBER: FR 92/01064
;             FILING DATE: 31-JAN-1992
;             APPLICATION NUMBER: PCT/FR93/00085
;             FILING DATE: 28-JAN-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Smith Ph.D., Julie K.
;             REGISTRATION NUMBER: P-38,619
;             REFERENCE/DOCKET NUMBER: ST92006-US
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (610) 454-3839
;             TELEFAX: (610) 454-3808
;   INFORMATION FOR SEQ ID NO: 18:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 249 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-984-186-18

  Query Match             88.4%;  Score 38;  DB 2;  Length 249;
  Best Local Similarity   85.7%;  Pred. No. 22;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
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Db        192 WASTRHT 198


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Job time : 24.1507 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:42:16 ; Search time 49.0959 Seconds
(without alignments)
59.573 Million cell updates/sec

Title: US-10-755-382-21
Perfect score: 43
Sequence: 1 WTSTRHT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	100.0	7	3	US-09-253-794-21	Sequence 21, Appl
2	43	100.0	7	4	US-10-680-734-21	Sequence 21, Appl
3	43	100.0	7	5	US-10-755-382-21	Sequence 21, Appl
4	43	100.0	106	3	US-09-253-794-4	Sequence 4, Appli
5	43	100.0	106	3	US-09-253-794-19	Sequence 19, Appl
6	43	100.0	106	4	US-10-680-734-4	Sequence 4, Appli
7	43	100.0	106	4	US-10-680-734-19	Sequence 19, Appl
8	43	100.0	106	5	US-10-755-382-4	Sequence 4, Appli
9	43	100.0	106	5	US-10-755-382-19	Sequence 19, Appl
10	43	100.0	115	4	US-10-270-073-4	Sequence 4, Appli
11	43	100.0	232	4	US-10-006-771A-6	Sequence 6, Appli
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13	43	100.0	250	3	US-09-887-853-2	Sequence 2, Appli
14	43	100.0	250	5	US-10-683-547-2	Sequence 2, Appli
15	43	100.0	256	4	US-10-270-073-6	Sequence 6, Appli
16	43	100.0	257	4	US-10-270-073-8	Sequence 8, Appli
17	43	100.0	261	4	US-10-270-071-18	Sequence 18, Appl
18	43	100.0	261	4	US-10-270-073-2	Sequence 2, Appli
19	43	100.0	261	4	US-10-328-190-6	Sequence 6, Appli
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22	43	100.0	262	4	US-10-270-071-28	Sequence 28, Appl
23	43	100.0	262	4	US-10-270-071-34	Sequence 34, Appl
24	43	100.0	358	5	US-10-829-388-12	Sequence 12, Appl
25	43	100.0	363	5	US-10-829-388-2	Sequence 2, Appli
26	43	100.0	364	5	US-10-829-388-11	Sequence 11, Appl
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28	43	100.0	391	4	US-10-328-190-14	Sequence 14, Appl
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37	39	90.7	240	4	US-10-096-246-35	Sequence 35, Appl
38	39	90.7	240	4	US-10-096-246-36	Sequence 36, Appl
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62	38	88.4	107	4	US-10-389-417-9	Sequence 9, Appli
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74	38	88.4	107	5	US-10-842-011-47	Sequence 47, Appl
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87	38	88.4	213	4	US-10-281-479A-74	Sequence 74, Appl
88	38	88.4	213	4	US-10-281-479A-75	Sequence 75, Appl
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93	38	88.4	213	4	US-10-275-180A-75	Sequence 75, Appl
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121	35	81.4	72	4	US-10-212-872-516	Sequence 516, App
122	35	81.4	103	4	US-10-425-115-221235	Sequence 221235,
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148	33	76.7	1753	4	US-10-719-385-3	Sequence 3, Appli
149	33	76.7	1753	4	US-10-719-385-4	Sequence 4, Appli
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152	33	76.7	1753	4	US-10-719-385-8	Sequence 8, Appli
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158	33	76.7	1753	4	US-10-719-385-15	Sequence 15, Appl
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202	32	74.4	370	3	US-09-954-342-57	Sequence 57, Appl
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228	31	72.1	30	3	US-09-818-683-554	Sequence 554, App
229	31	72.1	30	3	US-09-818-683-554	Sequence 554, App
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285	31	72.1	218	6	US-11-158-839-10	Sequence 10, Appl
286	31	72.1	226	4	US-10-424-599-201750	Sequence 201750,
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289	31	72.1	229	4	US-10-767-701-43021	Sequence 43021, A
290	31	72.1	229	4	US-10-425-115-345269	Sequence 345269,
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292	31	72.1	245	4	US-10-425-115-308762	Sequence 308762,
293	31	72.1	258	4	US-10-424-599-145736	Sequence 145736,
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295	31	72.1	270	3	US-09-934-455-162	Sequence 162, App
296	31	72.1	270	4	US-10-225-066A-590	Sequence 590, App
297	31	72.1	270	4	US-10-374-780A-208	Sequence 208, App
298	31	72.1	270	5	US-10-225-066A-590	Sequence 590, App
299	31	72.1	278	4	US-10-322-281-204	Sequence 204, App
300	31	72.1	310	3	US-09-800-103-30	Sequence 30, Appl
301	31	72.1	310	6	US-11-027-027-30	Sequence 30, Appl
302	31	72.1	320	4	US-10-322-281-201	Sequence 201, App
303	31	72.1	322	4	US-10-437-963-202887	Sequence 202887,
304	31	72.1	346	4	US-10-087-192-402	Sequence 402, App
305	31	72.1	346	4	US-10-205-219-181	Sequence 181, App
306	31	72.1	346	5	US-10-723-860-3814	Sequence 3814, Ap
307	31	72.1	346	5	US-10-756-149-5663	Sequence 5663, Ap
308	31	72.1	389	5	US-10-732-923-6541	Sequence 6541, Ap
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310	31	72.1	399	4	US-10-424-599-228199	Sequence 228199,
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318	31	72.1	456	3	US-09-800-103-34	Sequence 34, Appl
319	31	72.1	456	6	US-11-027-027-34	Sequence 34, Appl
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321	31	72.1	478	5	US-10-496-059-2	Sequence 2, Appli
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325	31	72.1	634	5	US-10-876-086-27	Sequence 27, Appl
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329	31	72.1	1143	4	US-10-613-765-108	Sequence 108, App
330	31	72.1	1144	3	US-09-813-742-3	Sequence 3, Appli
331	31	72.1	1207	3	US-09-988-462-7	Sequence 7, Appli
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333	31	72.1	1228	4	US-10-428-961-38	Sequence 38, Appl
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335	31	72.1	1228	4	US-10-809-953-10	Sequence 10, Appl
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341	31	72.1	6043	5	US-10-844-716-7	Sequence 7, Appli
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343	30	69.8	13	4	US-10-635-977-34	Sequence 34, Appl
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347	30	69.8	46	5	US-10-741-600-978	Sequence 978, App
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395	30	69.8	197	6	US-11-041-419-27	Sequence 27, Appl
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397	30	69.8	198	3	US-09-983-802-232	Sequence 232, App
398	30	69.8	198	3	US-09-984-490-232	Sequence 232, App
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405	30	69.8	242	4	US-10-635-977-4	Sequence 4, Appli
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485	30	69.8	4545	4	US-10-464-368-71	Sequence 71, Appl
486	30	69.8	4563	4	US-10-276-774-1723	Sequence 1723, Ap
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488	30	69.8	4599	4	US-10-464-368-70	Sequence 70, Appl
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496	29	67.4	7	4	US-10-317-747-14	Sequence 14, Appl
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518	29	67.4	68	3	US-09-984-490-639	Sequence 639, App
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993	28	65.1	313	4	US-10-029-386-33204	Sequence 33204, A
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ALIGNMENTS

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RESULT 1
US-09-253-794-21
; Sequence 21, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 21:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 7 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-253-794-21

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Db          1 WTSTRHT 7


RESULT 2
US-10-680-734-21
; Sequence 21, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 21
;   LENGTH: 7
;   TYPE: PRT
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US-10-680-734-21

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Db          1 WTSTRHT 7


RESULT 3
US-10-755-382-21
; Sequence 21, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
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;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 21:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 7 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
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US-10-755-382-21

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RESULT 4
US-09-253-794-4
; Sequence 4, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 106 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
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US-09-253-794-4

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Db         50 WTSTRHT 56


RESULT 5
US-09-253-794-19
; Sequence 19, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
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;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 106 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-253-794-19

  Query Match             100.0%;  Score 43;  DB 3;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         50 WTSTRHT 56


RESULT 6
US-10-680-734-4
; Sequence 4, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
;   LENGTH: 106
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-680-734-4

  Query Match           100.0%;  Score 43;  DB 4;  Length 106;
  Best Local Similarity  100.0%;  Pred. No. 4.1;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         50 WTSTRHT 56


RESULT 7
US-10-680-734-19
; Sequence 19, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
;   LENGTH: 106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-19

  Query Match           100.0%;  Score 43;  DB 4;  Length 106;
  Best Local Similarity  100.0%;  Pred. No. 4.1;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         50 WTSTRHT 56


RESULT 8
US-10-755-382-4
; Sequence 4, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 106 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-755-382-4

  Query Match           100.0%;  Score 43;  DB 5;  Length 106;
  Best Local Similarity  100.0%;  Pred. No. 4.1;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         50 WTSTRHT 56


RESULT 9
US-10-755-382-19
; Sequence 19, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;
```

```
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 106 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-755-382-19

  Query Match             100.0%;  Score 43;  DB 5;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 4.1;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         50 WTSTRHT 56


RESULT 10
US-10-270-073-4
; Sequence 4, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14VK deduced amino acid sequence
US-10-270-073-4

  Query Match             100.0%;  Score 43;  DB 4;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 4.4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         50 WTSTRHT 56


RESULT 11
US-10-006-771A-6
; Sequence 6, Application US/10006771A
; Publication No. US20020165360A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen
;  FILE REFERENCE: 002
;  CURRENT APPLICATION NUMBER: US/10/006,771A
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: 60/250,090
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 232
;   TYPE: PRT
;   ORGANISM: Homo sapiens and Mus sp.
US-10-006-771A-6

  Query Match             100.0%;  Score 43;  DB 4;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 8.4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         69 WTSTRHT 75


RESULT 12
US-10-377-109-4
; Sequence 4, Application US/10377109
; Publication No. US20040018557A1
; GENERAL INFORMATION:
;  APPLICANT: QU, ZHENGXING
;  APPLICANT:  HANSEN, HANS
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: BISPECIFIC ANTIBODY POINT MUTATIONS FOR ENHANCING RATE
;  TITLE OF INVENTION:  OF CLEARANCE
;  FILE REFERENCE: 018733/1159
;  CURRENT APPLICATION NUMBER: US/10/377,109
;  CURRENT FILING DATE:  2003-03-03
;  PRIOR APPLICATION NUMBER: 60/361,037
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 232
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-377-109-4

  Query Match             100.0%;  Score 43;  DB 4;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 8.4;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         69 WTSTRHT 75


RESULT 13
US-09-887-853-2
; Sequence 2, Application US/09887853
; Patent No. US20020168375A1
;   GENERAL INFORMATION:
;       APPLICANT: Huston, James S.
;                  Oppermann, Hermann
;                  Houston, L. L.
;                  Ring, David B.
;       TITLE OF INVENTION: Biosynthetic Binding Proteins For
;                           Imaging
;       NUMBER OF SEQUENCES: 11
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Testa, Hurwitz & Thibeault/Patent Department
```

```
;            STREET: Exchange Place, 53 State Street
;            CITY: Boston
;            STATE: Massachusetts
;            COUNTRY: USA
;            ZIP: 02109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/887,853
;            FILING DATE: 21-Jun-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/133,804
;            FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Kelley, Robin D.
;            REGISTRATION NUMBER: 34,637
;            REFERENCE/DOCKET NUMBER: 2054/22
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 617-248-7477
;            TELEFAX: 617-248-7100
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 250 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-887-853-2

  Query Match             100.0%;  Score 43;  DB 3;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 9;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        185 WTSTRHT 191


RESULT 14
US-10-683-547-2
; Sequence 2, Application US/10683547
; Publication No. US20050058638A1
; GENERAL INFORMATION:
;  APPLICANT: Huston, J.
;  APPLICANT:  Houston, L.L.
;  APPLICANT:  Ring, D.
;  APPLICANT:  Oppermann, H.
;  TITLE OF INVENTION: BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING
;  FILE REFERENCE: CIBT-P01-130
;  CURRENT APPLICATION NUMBER: US/10/683,547
;  CURRENT FILING DATE:  2003-10-10
;  PRIOR APPLICATION NUMBER: US/09/558,741
;  PRIOR FILING DATE: 2000-04-26
;  PRIOR APPLICATION NUMBER: 07/831,967
;  PRIOR FILING DATE: 1992-02-06
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: 741F8 sFv'
US-10-683-547-2

  Query Match             100.0%;  Score 43;  DB 5;  Length 250;
  Best Local Similarity   100.0%;  Pred. No. 9;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        185 WTSTRHT 191


RESULT 15
US-10-270-073-6
; Sequence 6, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14-0 amino acid sequence
US-10-270-073-6

  Query Match             100.0%;  Score 43;  DB 4;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 9.2;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        191 WTSTRHT 197


RESULT 16
US-10-270-073-8
; Sequence 8, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 257
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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```
;   OTHER INFORMATION: hMN-14-1G amino acid sequence
US-10-270-073-8

  Query Match             100.0%;  Score 43;  DB 4;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 9.2;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        192 WTSTRHT 198


RESULT 17
US-10-270-071-18
; Sequence 18, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of hMN14VK
US-10-270-071-18

  Query Match             100.0%;  Score 43;  DB 4;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 9.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        196 WTSTRHT 202


RESULT 18
US-10-270-073-2
; Sequence 2, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14scFv-L5 amino acid sequence
US-10-270-073-2

  Query Match             100.0%;  Score 43;  DB 4;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 9.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        196 WTSTRHT 202


RESULT 19
US-10-328-190-6
; Sequence 6, Application US/10328190
; Publication No. US20030162709A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID M.
;  TITLE OF INVENTION: METHODS OF GENERATING MULTISPECIFIC, MULTIVALENT AGENTS
;  TITLE OF INVENTION:  FROM VH AND VL DOMAINS
;  FILE REFERENCE: 042418/0115
;  CURRENT APPLICATION NUMBER: US/10/328,190
;  CURRENT FILING DATE:  2003-04-03
;  PRIOR APPLICATION NUMBER: 60/342,103
;  PRIOR FILING DATE: 2001-12-26
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: hMN14-scFv-L5
;   OTHER INFORMATION: protein sequence
US-10-328-190-6

  Query Match             100.0%;  Score 43;  DB 4;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 9.3;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        196 WTSTRHT 202


RESULT 20
US-10-270-071-20
; Sequence 20, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 262
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of polypeptide 1 of BS1
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US-10-270-071-20

Query Match 100.0%; Score 43; DB 4; Length 262;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
||||||| |
Db 197 WTSTRHT 203

RESULT 21
US-10-270-071-24
; Sequence 24, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
; APPLICANT: ROSSI, EDMUND
; APPLICANT: CHANG, CHIEN-HSING KEN
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
; FILE REFERENCE: 042418/0110
; CURRENT APPLICATION NUMBER: US/10/270,071
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/328,835
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/341,881
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; OTHER INFORMATION: sequence of polypeptide 1 of BS1.5
US-10-270-071-24

Query Match 100.0%; Score 43; DB 4; Length 262;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
||||||| |
Db 197 WTSTRHT 203

RESULT 22
US-10-270-071-28
; Sequence 28, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
; APPLICANT: ROSSI, EDMUND
; APPLICANT: CHANG, CHIEN-HSING KEN
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
; FILE REFERENCE: 042418/0110
; CURRENT APPLICATION NUMBER: US/10/270,071
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/328,835
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/341,881
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; OTHER INFORMATION: sequence of polypeptide 1 of BS2
US-10-270-071-28

Query Match 100.0%; Score 43; DB 4; Length 262;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
||||||| |
Db 197 WTSTRHT 203

RESULT 23
US-10-270-071-34
; Sequence 34, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
; APPLICANT: ROSSI, EDMUND
; APPLICANT: CHANG, CHIEN-HSING KEN
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
; FILE REFERENCE: 042418/0110
; CURRENT APPLICATION NUMBER: US/10/270,071
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/328,835
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/341,881
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; OTHER INFORMATION: sequence for polypeptide 1 of BS1.5H (h679XhMN14 bispecific
; OTHER INFORMATION: diabody)
US-10-270-071-34

Query Match 100.0%; Score 43; DB 4; Length 262;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WTSTRHT 7
||||||| |
Db 197 WTSTRHT 203

RESULT 24
US-10-829-388-12
; Sequence 12, Application US/10829388
; Publication No. US20050003403A1
; GENERAL INFORMATION:
; APPLICANT: ROSSI, EDMUND A.
; APPLICANT: CHANG, CHIEN HSING
; APPLICANT: MCBRIDE, WILLIAM J.
; TITLE OF INVENTION: POLYVALENT PROTEIN COMPLEX
; FILE REFERENCE: 41133-0006US1
; CURRENT APPLICATION NUMBER: US/10/829,388
; CURRENT FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: 60/464,532
; PRIOR FILING DATE: 2003-04-22
; PRIOR APPLICATION NUMBER: 60/525,391
; PRIOR FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric sequence from multiple species
US-10-829-388-12

Query Match 100.0%; Score 43; DB 5; Length 358;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WTSTRHT 7
              |||||||
Db         51 WTSTRHT 57


RESULT 25
US-10-829-388-2
; Sequence 2, Application US/10829388
; Publication No. US20050003403A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN HSING
;  APPLICANT:  MCBRIDE, WILLIAM J.
;  TITLE OF INVENTION: POLYVALENT PROTEIN COMPLEX
;  FILE REFERENCE: 41133-0006US1
;  CURRENT APPLICATION NUMBER: US/10/829,388
;  CURRENT FILING DATE:  2004-04-22
;  PRIOR APPLICATION NUMBER: 60/464,532
;  PRIOR FILING DATE: 2003-04-22
;  PRIOR APPLICATION NUMBER: 60/525,391
;  PRIOR FILING DATE: 2003-11-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 363
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chimeric sequence from multiple species
US-10-829-388-2

  Query Match            100.0%;  Score 43;  DB 5;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         56 WTSTRHT 62


RESULT 26
US-10-829-388-11
; Sequence 11, Application US/10829388
; Publication No. US20050003403A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN HSING
;  APPLICANT:  MCBRIDE, WILLIAM J.
;  TITLE OF INVENTION: POLYVALENT PROTEIN COMPLEX
;  FILE REFERENCE: 41133-0006US1
;  CURRENT APPLICATION NUMBER: US/10/829,388
;  CURRENT FILING DATE:  2004-04-22
;  PRIOR APPLICATION NUMBER: 60/464,532
;  PRIOR FILING DATE: 2003-04-22
;  PRIOR APPLICATION NUMBER: 60/525,391
;  PRIOR FILING DATE: 2003-11-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
;   LENGTH: 364
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chimeric sequence from multiple species
US-10-829-388-11

  Query Match            100.0%;  Score 43;  DB 5;  Length 364;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        175 WTSTRHT 181


RESULT 27
US-10-829-388-1
; Sequence 1, Application US/10829388
; Publication No. US20050003403A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN HSING
;  APPLICANT:  MCBRIDE, WILLIAM J.
;  TITLE OF INVENTION: POLYVALENT PROTEIN COMPLEX
;  FILE REFERENCE: 41133-0006US1
;  CURRENT APPLICATION NUMBER: US/10/829,388
;  CURRENT FILING DATE:  2004-04-22
;  PRIOR APPLICATION NUMBER: 60/464,532
;  PRIOR FILING DATE: 2003-04-22
;  PRIOR APPLICATION NUMBER: 60/525,391
;  PRIOR FILING DATE: 2003-11-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 370
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chimeric sequence from multiple species
US-10-829-388-1

  Query Match            100.0%;  Score 43;  DB 5;  Length 370;
  Best Local Similarity   100.0%;  Pred. No. 13;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        181 WTSTRHT 187


RESULT 28
US-10-328-190-14
; Sequence 14, Application US/10328190
; Publication No. US20030162709A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID M.
;  TITLE OF INVENTION: METHODS OF GENERATING MULTISPECIFIC, MULTIVALENT AGENTS
;  TITLE OF INVENTION:  FROM VH AND VL DOMAINS
;  FILE REFERENCE: 042418/0115
;  CURRENT APPLICATION NUMBER: US/10/328,190
;  CURRENT FILING DATE:  2003-04-03
;  PRIOR APPLICATION NUMBER: 60/342,103
;  PRIOR FILING DATE: 2001-12-26
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 391
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Protein
;   OTHER INFORMATION: sequence for VL-chain of TS1
US-10-328-190-14

  Query Match            100.0%;  Score 43;  DB 4;  Length 391;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        326 WTSTRHT 332
```

```
RESULT 29
US-10-006-773-2
; Sequence 2, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
;  FILE REFERENCE: 003
;  CURRENT APPLICATION NUMBER: US/10/006,773
;  CURRENT FILING DATE:  2001-12-10
;  PRIOR APPLICATION NUMBER: 60/250,089
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 443
;   TYPE: PRT
;   ORGANISM: Homo sapiens and Mus sp.
US-10-006-773-2

  Query Match             100.0%;  Score 43;  DB 4;  Length 443;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         69 WTSTRHT 75


RESULT 30
US-10-006-771A-2
; Sequence 2, Application US/10006771A
; Publication No. US20020165360A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen
;  FILE REFERENCE: 002
;  CURRENT APPLICATION NUMBER: US/10/006,771A
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: 60/250,090
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 443
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-006-771A-2

  Query Match             100.0%;  Score 43;  DB 4;  Length 443;
  Best Local Similarity   100.0%;  Pred. No. 15;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db         69 WTSTRHT 75


RESULT 31
US-10-900-928-3
; Sequence 3, Application US/10900928
; Publication No. US20050069552A1
; GENERAL INFORMATION:
;  APPLICANT: Bleck, Gregory T.
;  APPLICANT:  York, Donna
;  APPLICANT:  Collins, Ian
;  TITLE OF INVENTION: Fusion Antibodies
;  FILE REFERENCE: GALA-09135
;  CURRENT APPLICATION NUMBER: US/10/900,928
;  CURRENT FILING DATE:  2004-07-28
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 669
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-900-928-3

  Query Match             100.0%;  Score 43;  DB 5;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||||||
Db        506 WTSTRHT 512


RESULT 32
US-10-437-963-156937
; Sequence 156937, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  APPLICANT:  Wu, Wei
;  APPLICANT:  Boukharov, Andrey A.
;  APPLICANT:  Barbazuk, Brad
;  APPLICANT:  Li, Ping
;  TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53221)B
;  CURRENT APPLICATION NUMBER: US/10/437,963
;  CURRENT FILING DATE:  2003-05-14
;  NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 156937
;   LENGTH: 105
;   TYPE: PRT
;   ORGANISM: Oryza sativa
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT4530_56557C.1.pep
US-10-437-963-156937

  Query Match             90.7%;  Score 39;  DB 4;  Length 105;
  Best Local Similarity   85.7%;  Pred. No. 21;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db         14 WSSTRHT 20


RESULT 33
US-10-096-246-13
; Sequence 13, Application US/10096246
; Publication No. US20030100060A1
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/096,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-13
```

```
  Query Match             90.7%;  Score 39;  DB 4;  Length 110;
  Best Local Similarity   85.7%;  Pred. No. 22;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db         49 WSSTRHT 55


RESULT 34
US-10-096-246-32
; Sequence 32, Application US/10096246
; Publication No. US20030100060A1
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/096,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-32

  Query Match             90.7%;  Score 39;  DB 4;  Length 239;
  Best Local Similarity   85.7%;  Pred. No. 45;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db        181 WSSTRHT 187


RESULT 35
US-10-096-246-33
; Sequence 33, Application US/10096246
; Publication No. US20030100060A1
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/096,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
;   LENGTH: 239
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-33

  Query Match             90.7%;  Score 39;  DB 4;  Length 239;
  Best Local Similarity   85.7%;  Pred. No. 45;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db        181 WSSTRHT 187


RESULT 36
US-10-096-246-34
; Sequence 34, Application US/10096246
; Publication No. US20030100060A1
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/096,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-34

  Query Match             90.7%;  Score 39;  DB 4;  Length 240;
  Best Local Similarity   85.7%;  Pred. No. 45;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db        182 WSSTRHT 188


RESULT 37
US-10-096-246-35
; Sequence 35, Application US/10096246
; Publication No. US20030100060A1
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/096,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-35

  Query Match             90.7%;  Score 39;  DB 4;  Length 240;
  Best Local Similarity   85.7%;  Pred. No. 45;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db        182 WSSTRHT 188


RESULT 38
US-10-096-246-36
; Sequence 36, Application US/10096246
; Publication No. US20030100060A1
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
;  FILE REFERENCE: NEL-0007
```

```
;  CURRENT APPLICATION NUMBER: US/10/096,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-36

  Query Match             90.7%;  Score 39;  DB 4;  Length 240;
  Best Local Similarity   85.7%;  Pred. No. 45;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db        182 WSSTRHT 188


RESULT 39
US-10-096-246-37
; Sequence 37, Application US/10096246
; Publication No. US20030100060A1
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/096,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 240
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-37

  Query Match             90.7%;  Score 39;  DB 4;  Length 240;
  Best Local Similarity   85.7%;  Pred. No. 45;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db        182 WSSTRHT 188


RESULT 40
US-10-096-246-2
; Sequence 2, Application US/10096246
; Publication No. US20030100060A1
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mo
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/096,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 257
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-096-246-2

  Query Match             90.7%;  Score 39;  DB 4;  Length 257;
  Best Local Similarity   85.7%;  Pred. No. 48;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db        181 WSSTRHT 187


RESULT 41
US-10-784-305-2
; Sequence 2, Application US/10784305
; Publication No. US20050118569A1
; GENERAL INFORMATION:
;  APPLICANT: Fulton, R. Elaine
;  APPLICANT:  Nagata, Leslie P.
;  APPLICANT:  Alvi, Azhar  Z.
;  APPLICANT:  Hu, Wei-Gang
;  TITLE OF INVENTION: Genetic Engineering of Streptavidin-Binding Peptide Tagged
;  TITLE OF INVENTION:  Single-Chain Variable Fragment Antibody to Venezuelan Equine
;  TITLE OF INVENTION:  Encephalitis Virus
;  FILE REFERENCE: NEL-0018
;  CURRENT APPLICATION NUMBER: US/10/784,305
;  CURRENT FILING DATE:  2004-02-24
;  PRIOR APPLICATION NUMBER: 60/448,902
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 7
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 296
;   TYPE: PRT
;   ORGANISM: Mouse
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   OTHER INFORMATION: scFv: 1-269:
;   OTHER INFORMATION: SBP,6His and spacers: 270-296
US-10-784-305-2

  Query Match             90.7%;  Score 39;  DB 5;  Length 296;
  Best Local Similarity   85.7%;  Pred. No. 55;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |:|||||
Db        207 WSSTRHT 213


RESULT 42
US-10-378-832A-2
; Sequence 2, Application US/10378832A
; Publication No. US20040005333A1
; GENERAL INFORMATION:
;  APPLICANT: Her Majesty the Queen in right of Canada, as represented by the Minister
;  APPLICANT:  of National Defence
;  APPLICANT:  Nagata, Leslie  P
;  APPLICANT:  Fulton, R. Elaine
;  APPLICANT:  Hu, Weigang
;  APPLICANT:  Alvi, Azhar Z
;  TITLE OF INVENTION: No. US20040005333A1el Fusion Protein of Human IgG1 Heavy Chain Cor
;  TITLE OF INVENTION:  Antibody Against Venezuaelan Equine Encephalitis Virus
;  FILE REFERENCE: NEL-0013
;  CURRENT APPLICATION NUMBER: US/10/378,832A
;  CURRENT FILING DATE:  2003-03-05
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 622
;   TYPE: PRT
;   ORGANISM: mouse hybridome cells and human lymphocytes
US-10-378-832A-2

  Query Match             90.7%;  Score 39;  DB 4;  Length 622;
  Best Local Similarity   85.7%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 WTSTRHT 7
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Db        241 WSSTRHT 247


RESULT 43
US-10-281-479A-29
; Sequence 29, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  Oshumi, Jun
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THER
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 21085.0029U6
;  CURRENT APPLICATION NUMBER: US/10/281,479A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 60/391,478
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe
US-10-281-479A-29

  Query Match             88.4%;  Score 38;  DB 4;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 1.7e+06;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db          1 WASTRHT 7


RESULT 44
US-10-160-506-5
; Sequence 5, Application US/10160506
; Publication No. US20030161832A1
; GENERAL INFORMATION:
;  APPLICANT: Bander, Neil H.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
;  TITLE OF INVENTION:  SKIN DISORDERS USING BINDING AGENTS SPECIFIC FOR
;  TITLE OF INVENTION:  PROSTATE SPECIFIC MEMBRANE ANTIGEN
;  FILE REFERENCE: 10448-162001
;  CURRENT APPLICATION NUMBER: US/10/160,506
;  CURRENT FILING DATE:  2002-05-30
;  PRIOR APPLICATION NUMBER: 60/324,100
;  PRIOR FILING DATE: 2001-09-20
;  PRIOR APPLICATION NUMBER: 60/362,612
;  PRIOR FILING DATE: 2002-03-08
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-160-506-5

  Query Match             88.4%;  Score 38;  DB 4;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 1.7e+06;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db          1 WASTRHT 7


RESULT 45
US-10-275-180A-29
; Sequence 29, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSI
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-275-180A-29

  Query Match             88.4%;  Score 38;  DB 4;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 1.7e+06;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db          1 WASTRHT 7


RESULT 46
US-10-286-132A-29
; Sequence 29, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
;  APPLICANT: Zhou, Tong
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
;  TITLE OF INVENTION:  APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U7
;  CURRENT APPLICATION NUMBER: US/10/286,132A
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: US 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
;   LENGTH: 7
;   TYPE: PRT
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;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-29

  Query Match             88.4%;  Score 38;  DB 4;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 1.7e+06;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db          1 WASTRHT 7


RESULT 47
US-10-449-379-5
; Sequence 5, Application US/10449379
; Publication No. US20040120958A1
; GENERAL INFORMATION:
;  APPLICANT: Bander, Neil H.
;  TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
;  TITLE OF INVENTION:  MEMBRANE ANTIGEN AND USES THEREOF
;  FILE REFERENCE: 10448-163002
;  CURRENT APPLICATION NUMBER: US/10/449,379
;  CURRENT FILING DATE:  2003-05-30
;  PRIOR APPLICATION NUMBER: 10/160,505
;  PRIOR FILING DATE: 2002-05-30
;  PRIOR APPLICATION NUMBER: 60/323,585
;  PRIOR FILING DATE: 2001-09-20
;  PRIOR APPLICATION NUMBER: 60/362,810
;  PRIOR FILING DATE: 2002-03-08
;  PRIOR APPLICATION NUMBER: 60/295,214
;  PRIOR FILING DATE: 2001-06-01
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-449-379-5

  Query Match             88.4%;  Score 38;  DB 4;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 1.7e+06;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db          1 WASTRHT 7


RESULT 48
US-10-297-371A-12
; Sequence 12, Application US/10297371A
; Publication No. US20040131607A1
; GENERAL INFORMATION:
;  APPLICANT: Carroll, Michael C.
;  APPLICANT:  Moore, Jr., Francis D.
;  APPLICANT:  Hechtman, Herbert B.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING
;  TITLE OF INVENTION:  IMMUNOGLOBULIN-MEDIATED REPERFUSION INJURY
;  FILE REFERENCE: 10861-024US1
;  CURRENT APPLICATION NUMBER: US/10/297,371A
;  CURRENT FILING DATE:  2004-01-02
;  PRIOR APPLICATION NUMBER: PCT/US01/18510
;  PRIOR FILING DATE: 2001-06-08
;  PRIOR APPLICATION NUMBER: US 60/210,272
;  PRIOR FILING DATE: 2000-06-08
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-297-371A-12

  Query Match             88.4%;  Score 38;  DB 4;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 1.7e+06;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db          1 WASTRHT 7


RESULT 49
US-10-688-015-5
; Sequence 5, Application US/10688015
; Publication No. US20040136998A1
; GENERAL INFORMATION:
;  APPLICANT: Bander, Neil H.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING OR PREVENTING
;  TITLE OF INVENTION:  INSULIN-RELATED DISORDERS USING BINDING AGENTS SPECIFIC FOR
;  TITLE OF INVENTION:  PROSTATE SPECIFIC MEMBRANE ANTIGEN
;  FILE REFERENCE: 10448-196001
;  CURRENT APPLICATION NUMBER: US/10/688,015
;  CURRENT FILING DATE:  2003-10-17
;  PRIOR APPLICATION NUMBER: 60/422,396
;  PRIOR FILING DATE: 2002-10-30
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-688-015-5

  Query Match             88.4%;  Score 38;  DB 4;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 1.7e+06;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db          1 WASTRHT 7


RESULT 50
US-10-160-505-5
; Sequence 5, Application US/10160505
; Publication No. US20040213791A1
; GENERAL INFORMATION:
;  APPLICANT: Bander, Neil H.
;  APPLICANT:  Carr, Francis J.
;  APPLICANT:  Hamilton, Anita A.
;  TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
;  TITLE OF INVENTION:  MEMBRANE ANTIGEN AND USES THEREOF
;  FILE REFERENCE: 10448-163001
;  CURRENT APPLICATION NUMBER: US/10/160,505
;  CURRENT FILING DATE:  2002-05-30
;  PRIOR APPLICATION NUMBER: 60/323,585
;  PRIOR FILING DATE: 2001-09-20
;  PRIOR APPLICATION NUMBER: 60/362,810
;  PRIOR FILING DATE: 2002-03-08
;  PRIOR APPLICATION NUMBER: 60/295,214
;  PRIOR FILING DATE: 2001-06-01
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-10-160-505-5

  Query Match             88.4%;  Score 38;  DB 4;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 1.7e+06;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 WTSTRHT 7
              | |||||
Db          1 WASTRHT 7
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Search completed: March 23, 2006, 02:51:59
Job time : 62.2387 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:44:01 ; Search time 5.94521 Seconds
(without alignments)
33.701 Million cell updates/sec

Title: US-10-755-382-21
Perfect score: 43
Sequence: 1 WTSTRHT 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	38	88.4	7	6	US-10-982-357-19	Sequence 19, Appl
2	38	88.4	7	6	US-10-982-357-36	Sequence 36, Appl
3	38	88.4	8	7	US-11-097-812-132	Sequence 132, App
4	38	88.4	105	7	US-11-097-812-53	Sequence 53, Appl
5	38	88.4	107	6	US-10-982-357-6	Sequence 6, Appli
6	38	88.4	107	6	US-10-982-357-42	Sequence 42, Appl
7	38	88.4	107	6	US-10-982-357-44	Sequence 44, Appl
8	38	88.4	107	6	US-10-982-357-48	Sequence 48, Appl
9	38	88.4	107	6	US-10-982-357-50	Sequence 50, Appl
10	38	88.4	108	7	US-11-097-812-45	Sequence 45, Appl
11	38	88.4	108	7	US-11-097-812-50	Sequence 50, Appl
12	38	88.4	109	7	US-11-097-812-113	Sequence 113, App
13	38	88.4	109	7	US-11-037-199-7	Sequence 7, Appli
14	38	88.4	127	6	US-10-982-357-28	Sequence 28, Appl
15	37	86.0	738	7	US-11-140-625-11	Sequence 11, Appl
16	36	83.7	352	7	US-11-087-099-3380	Sequence 3380, Ap
17	36	83.7	461	7	US-11-077-619-56	Sequence 56, Appl
18	32	74.4	527	7	US-11-098-686-10607	Sequence 10607, A
19	31	72.1	78	7	US-11-096-568A-14196	Sequence 14196, A
20	31	72.1	218	7	US-11-218-821-8	Sequence 8, Appli
21	31	72.1	346	7	US-11-169-041-208	Sequence 208, App
22	31	72.1	353	7	US-11-024-959-473	Sequence 473, App
23	31	72.1	473	6	US-10-203-486-10	Sequence 10, Appl
24	31	72.1	1207	6	US-10-755-092-7	Sequence 7, Appli
25	30	69.8	153	7	US-11-096-568A-21041	Sequence 21041, A
26	30	69.8	185	7	US-11-096-568A-25833	Sequence 25833, A
27	30	69.8	210	6	US-10-467-657-2812	Sequence 2812, Ap
28	30	69.8	314	7	US-11-096-568A-18747	Sequence 18747, A
29	30	69.8	420	7	US-11-096-568A-18746	Sequence 18746, A
30	30	69.8	427	7	US-11-096-568A-18745	Sequence 18745, A
31	30	69.8	435	7	US-11-087-099-10693	Sequence 10693, A
32	30	69.8	437	7	US-11-087-099-5390	Sequence 5390, Ap
33	30	69.8	645	6	US-10-510-386-32	Sequence 32, Appl
34	30	69.8	4544	6	US-10-501-035-214	Sequence 214, App
35	30	69.8	4544	7	US-11-076-427A-32	Sequence 32, Appl
36	29	67.4	38	6	US-10-467-657-7398	Sequence 7398, Ap
37	29	67.4	48	6	US-10-467-657-1750	Sequence 1750, Ap
38	29	67.4	108	7	US-11-097-812-52	Sequence 52, Appl
39	29	67.4	115	7	US-11-097-812-38	Sequence 38, Appl
40	29	67.4	166	7	US-11-087-099-4793	Sequence 4793, Ap
41	29	67.4	184	7	US-11-096-568A-11521	Sequence 11521, A
42	29	67.4	193	7	US-11-096-568A-11520	Sequence 11520, A
43	29	67.4	210	7	US-11-096-568A-20894	Sequence 20894, A
44	29	67.4	216	7	US-11-087-099-11293	Sequence 11293, A
45	29	67.4	251	7	US-11-087-099-5492	Sequence 5492, Ap
46	29	67.4	277	7	US-11-096-568A-20893	Sequence 20893, A
47	29	67.4	317	7	US-11-096-568A-11519	Sequence 11519, A
48	29	67.4	350	7	US-11-087-099-1450	Sequence 1450, Ap
49	29	67.4	451	6	US-10-508-263-68	Sequence 68, Appl
50	29	67.4	451	6	US-10-508-263-70	Sequence 70, Appl
51	29	67.4	855	7	US-11-024-959-506	Sequence 506, App
52	29	67.4	1717	7	US-11-182-016-20	Sequence 20, Appl
53	29	67.4	1985	7	US-11-119-330-2	Sequence 2, Appli
54	29	67.4	1985	7	US-11-173-792-3	Sequence 3, Appli
55	29	67.4	1985	7	US-11-173-792-15	Sequence 15, Appl
56	29	67.4	1985	7	US-11-173-792-17	Sequence 17, Appl
57	29	67.4	2335	6	US-10-821-234-1610	Sequence 1610, Ap
58	29	67.4	3011	6	US-10-985-205-3	Sequence 3, Appli
59	28	65.1	224	7	US-11-072-512-3751	Sequence 3751, Ap
60	28	65.1	224	7	US-11-096-568A-31411	Sequence 31411, A
61	28	65.1	268	6	US-10-467-657-6098	Sequence 6098, Ap
62	28	65.1	307	7	US-11-098-686-10143	Sequence 10143, A
63	28	65.1	335	7	US-11-096-568A-8475	Sequence 8475, Ap
64	28	65.1	339	7	US-11-096-568A-8474	Sequence 8474, Ap
65	28	65.1	347	7	US-11-087-099-6748	Sequence 6748, Ap
66	28	65.1	360	7	US-11-194-246-307	Sequence 307, App
67	28	65.1	393	7	US-11-096-568A-8473	Sequence 8473, Ap
68	28	65.1	399	7	US-11-087-099-1609	Sequence 1609, Ap
69	28	65.1	400	7	US-11-087-099-1421	Sequence 1421, Ap
70	28	65.1	400	7	US-11-087-099-7481	Sequence 7481, Ap
71	28	65.1	400	7	US-11-087-099-10687	Sequence 10687, A
72	28	65.1	401	7	US-11-146-428-43	Sequence 43, Appl
73	28	65.1	419	7	US-11-072-512-3262	Sequence 3262, Ap
74	28	65.1	444	7	US-11-024-959-337	Sequence 337, App
75	28	65.1	445	6	US-10-467-657-4578	Sequence 4578, Ap
76	28	65.1	489	6	US-10-793-626-1302	Sequence 1302, Ap
77	28	65.1	575	6	US-10-131-826A-128	Sequence 128, App
78	28	65.1	575	6	US-10-973-115B-128	Sequence 128, App
79	28	65.1	739	7	US-11-057-047-2	Sequence 2, Appli
80	28	65.1	761	7	US-11-057-047-6	Sequence 6, Appli
81	28	65.1	764	7	US-11-057-047-1	Sequence 1, Appli
82	28	65.1	798	6	US-10-821-234-1034	Sequence 1034, Ap
83	28	65.1	976	7	US-11-155-288-20	Sequence 20, Appl
84	28	65.1	1023	6	US-10-131-826A-200	Sequence 200, App
85	28	65.1	1023	6	US-10-973-115B-200	Sequence 200, App
86	27.5	64.0	221	7	US-11-051-720-1776	Sequence 1776, Ap
87	27.5	64.0	221	7	US-11-043-806-574	Sequence 574, App
88	27.5	64.0	490	7	US-11-051-720-325	Sequence 325, App
89	27.5	64.0	490	7	US-11-043-806-369	Sequence 369, App
90	27	62.8	21	7	US-11-004-399-1490	Sequence 1490, Ap
91	27	62.8	44	6	US-10-957-887B-110	Sequence 110, App
92	27	62.8	90	7	US-11-096-568A-9033	Sequence 9033, Ap
93	27	62.8	104	7	US-11-096-568A-16210	Sequence 16210, A
94	27	62.8	156	6	US-10-467-657-3148	Sequence 3148, Ap
95	27	62.8	169	6	US-10-453-372-838	Sequence 838, App
96	27	62.8	174	7	US-11-004-399-944	Sequence 944, App
97	27	62.8	178	6	US-10-453-372-846	Sequence 846, App
98	27	62.8	192	7	US-11-096-568A-9032	Sequence 9032, Ap

99	27	62.8	197	7	US-11-096-568A-9031	Sequence 9031, Ap
100	27	62.8	216	6	US-10-821-234-925	Sequence 925, App
101	27	62.8	219	7	US-11-098-686-10314	Sequence 10314, A
102	27	62.8	222	6	US-10-453-372-844	Sequence 844, App
103	27	62.8	227	7	US-11-072-512-2179	Sequence 2179, Ap
104	27	62.8	245	6	US-10-115-609-2	Sequence 2, Appli
105	27	62.8	251	7	US-11-055-822-404	Sequence 404, App
106	27	62.8	278	7	US-11-087-099-4872	Sequence 4872, Ap
107	27	62.8	283	6	US-10-453-372-850	Sequence 850, App
108	27	62.8	290	6	US-10-453-372-836	Sequence 836, App
109	27	62.8	290	6	US-10-453-372-842	Sequence 842, App
110	27	62.8	290	6	US-10-453-372-848	Sequence 848, App
111	27	62.8	290	6	US-10-115-609-4	Sequence 4, Appli
112	27	62.8	290	7	US-11-113-424-77	Sequence 77, Appl
113	27	62.8	295	6	US-10-453-372-840	Sequence 840, App
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116	27	62.8	341	7	US-11-072-512-3424	Sequence 3424, Ap
117	27	62.8	342	7	US-11-087-099-7659	Sequence 7659, Ap
118	27	62.8	346	6	US-10-793-626-2034	Sequence 2034, Ap
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120	27	62.8	354	7	US-11-087-099-659	Sequence 659, App
121	27	62.8	377	7	US-11-055-822-448	Sequence 448, App
122	27	62.8	378	7	US-11-096-568A-13078	Sequence 13078, A
123	27	62.8	379	7	US-11-055-822-446	Sequence 446, App
124	27	62.8	422	7	US-11-230-251-26	Sequence 26, Appl
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126	27	62.8	463	7	US-11-087-099-933	Sequence 933, App
127	27	62.8	470	7	US-11-096-568A-24810	Sequence 24810, A
128	27	62.8	475	7	US-11-096-568A-13077	Sequence 13077, A
129	27	62.8	479	6	US-10-821-234-871	Sequence 871, App
130	27	62.8	522	7	US-11-072-512-2664	Sequence 2664, Ap
131	27	62.8	528	7	US-11-096-568A-24809	Sequence 24809, A
132	27	62.8	534	7	US-11-072-512-3403	Sequence 3403, Ap
133	27	62.8	549	7	US-11-096-568A-4707	Sequence 4707, Ap
134	27	62.8	557	7	US-11-096-568A-4706	Sequence 4706, Ap
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138	27	62.8	585	7	US-11-096-568A-4705	Sequence 4705, Ap
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144	27	62.8	740	7	US-11-140-625-12	Sequence 12, Appl
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152	27	62.8	746	7	US-11-087-099-11798	Sequence 11798, A
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155	27	62.8	749	7	US-11-087-099-4239	Sequence 4239, Ap
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242	27	62.8	752	7	US-11-087-099-9357	Sequence 9357, Ap
243	27	62.8	752	7	US-11-087-099-9943	Sequence 9943, Ap
244	27	62.8	753	7	US-11-087-099-7485	Sequence 7485, Ap

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248	27	62.8	832	7	US-11-108-172-1081	Sequence 1081, Ap
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251	27	62.8	842	7	US-11-221-470-51	Sequence 51, Appl
252	27	62.8	843	7	US-11-221-470-45	Sequence 45, Appl
253	27	62.8	843	7	US-11-221-470-47	Sequence 47, Appl
254	27	62.8	843	7	US-11-221-470-48	Sequence 48, Appl
255	27	62.8	843	7	US-11-221-470-55	Sequence 55, Appl
256	27	62.8	843	7	US-11-221-470-56	Sequence 56, Appl
257	27	62.8	843	7	US-11-221-470-59	Sequence 59, Appl
258	27	62.8	845	7	US-11-094-519A-42	Sequence 42, Appl
259	27	62.8	845	7	US-11-221-470-11	Sequence 11, Appl
260	27	62.8	845	7	US-11-221-470-46	Sequence 46, Appl
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262	27	62.8	883	6	US-10-858-730-207	Sequence 207, App
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265	27	62.8	898	7	US-11-166-730-3	Sequence 3, Appli
266	27	62.8	923	7	US-11-192-219-4	Sequence 4, Appli
267	27	62.8	933	7	US-11-072-512-2928	Sequence 2928, Ap
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269	27	62.8	1017	7	US-11-087-099-6494	Sequence 6494, Ap
270	27	62.8	1162	7	US-11-202-330-43	Sequence 43, Appl
271	27	62.8	1165	7	US-11-192-219-2	Sequence 2, Appli
272	27	62.8	1165	7	US-11-202-330-4	Sequence 4, Appli
273	27	62.8	1332	7	US-11-091-643-18	Sequence 18, Appl
274	27	62.8	1344	7	US-11-072-512-2452	Sequence 2452, Ap
275	27	62.8	1730	7	US-11-182-016-19	Sequence 19, Appl
276	27	62.8	3482	7	US-11-087-099-2068	Sequence 2068, Ap
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279	26.5	61.6	312	7	US-11-096-568A-32766	Sequence 32766, A
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283	26	60.5	14	6	US-10-939-890-20	Sequence 20, Appl
284	26	60.5	18	6	US-10-939-890-375	Sequence 375, App
285	26	60.5	22	6	US-10-939-890-263	Sequence 263, App
286	26	60.5	52	7	US-11-033-105A-10	Sequence 10, Appl
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290	26	60.5	101	7	US-11-084-554-120	Sequence 120, App
291	26	60.5	101	7	US-11-004-590-94	Sequence 94, Appl
292	26	60.5	101	7	US-11-136-250-120	Sequence 120, App
293	26	60.5	104	7	US-11-072-512-3073	Sequence 3073, Ap
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295	26	60.5	109	6	US-10-771-257-105	Sequence 105, App
296	26	60.5	109	6	US-10-771-257-107	Sequence 107, App
297	26	60.5	109	6	US-10-771-257-112	Sequence 112, App
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302	26	60.5	112	7	US-11-136-559-22	Sequence 22, Appl
303	26	60.5	114	6	US-10-771-257-68	Sequence 68, Appl
304	26	60.5	114	6	US-10-771-257-72	Sequence 72, Appl
305	26	60.5	114	6	US-10-771-257-74	Sequence 74, Appl
306	26	60.5	114	6	US-10-834-397-17	Sequence 17, Appl
307	26	60.5	114	7	US-11-127-677-27	Sequence 27, Appl
308	26	60.5	114	7	US-11-127-677-66	Sequence 66, Appl
309	26	60.5	114	7	US-11-127-677-70	Sequence 70, Appl
310	26	60.5	114	7	US-11-127-677-72	Sequence 72, Appl
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313	26	60.5	115	6	US-10-834-397-49	Sequence 49, Appl
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316	26	60.5	116	7	US-11-096-046-1	Sequence 1, Appli
317	26	60.5	116	7	US-11-096-046-3	Sequence 3, Appli
318	26	60.5	118	7	US-11-072-512-3051	Sequence 3051, Ap
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321	26	60.5	125	7	US-11-127-677-6	Sequence 6, Appli
322	26	60.5	135	7	US-11-158-505-35	Sequence 35, Appl
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324	26	60.5	153	7	US-11-096-568A-24489	Sequence 24489, A
325	26	60.5	171	7	US-11-096-568A-14292	Sequence 14292, A
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328	26	60.5	211	7	US-11-052-554A-301	Sequence 301, App
329	26	60.5	244	7	US-11-096-568A-20817	Sequence 20817, A
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331	26	60.5	253	7	US-11-054-515-860	Sequence 860, App
332	26	60.5	259	6	US-10-512-184-31	Sequence 31, Appl
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334	26	60.5	259	6	US-10-631-558-4	Sequence 4, Appli
335	26	60.5	259	7	US-11-098-686-11154	Sequence 11154, A
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345	26	60.5	329	6	US-10-512-184-68	Sequence 68, Appl
346	26	60.5	329	6	US-10-512-184-70	Sequence 70, Appl
347	26	60.5	341	5	US-09-978-360A-686	Sequence 686, App
348	26	60.5	341	6	US-10-131-826A-256	Sequence 256, App
349	26	60.5	341	6	US-10-973-115B-256	Sequence 256, App
350	26	60.5	341	7	US-11-099-691-6	Sequence 6, Appli
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354	26	60.5	383	7	US-11-096-568A-22981	Sequence 22981, A
355	26	60.5	391	7	US-11-096-568A-22980	Sequence 22980, A
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361	26	60.5	430	7	US-11-126-313-36	Sequence 36, Appl
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363	26	60.5	434	7	US-11-123-013-4	Sequence 4, Appli
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366	26	60.5	471	7	US-11-096-568A-13313	Sequence 13313, A
367	26	60.5	494	7	US-11-087-099-4883	Sequence 4883, Ap
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369	26	60.5	495	7	US-11-087-099-373	Sequence 373, App
370	26	60.5	506	6	US-10-485-517-344	Sequence 344, App
371	26	60.5	517	7	US-11-096-568A-13312	Sequence 13312, A
372	26	60.5	527	7	US-11-096-568A-13311	Sequence 13311, A
373	26	60.5	528	7	US-11-096-568A-14618	Sequence 14618, A
374	26	60.5	566	7	US-11-087-099-9603	Sequence 9603, Ap
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377	26	60.5	579	6	US-10-524-750-6	Sequence 6, Appli
378	26	60.5	579	6	US-10-524-750-8	Sequence 8, Appli
379	26	60.5	590	7	US-11-096-568A-14617	Sequence 14617, A
380	26	60.5	597	6	US-10-884-730-381	Sequence 381, App
381	26	60.5	602	7	US-11-096-568A-14616	Sequence 14616, A
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383	26	60.5	615	7	US-11-198-819-18	Sequence 18, Appl
384	26	60.5	642	6	US-10-995-561-631	Sequence 631, App
385	26	60.5	651	7	US-11-198-819-22	Sequence 22, Appl
386	26	60.5	657	6	US-10-995-561-622	Sequence 622, App
387	26	60.5	657	7	US-11-193-561-27	Sequence 27, Appl
388	26	60.5	657	7	US-11-193-771-27	Sequence 27, Appl
389	26	60.5	657	7	US-11-193-789-27	Sequence 27, Appl
390	26	60.5	657	7	US-11-193-806-27	Sequence 27, Appl

391	26	60.5	657	7	US-11-193-857-27	Sequence 27, Appl
392	26	60.5	666	6	US-10-981-356A-25	Sequence 25, Appl
393	26	60.5	666	6	US-10-981-356A-27	Sequence 27, Appl
394	26	60.5	666	6	US-10-981-356A-28	Sequence 28, Appl
395	26	60.5	666	6	US-10-981-356A-29	Sequence 29, Appl
396	26	60.5	666	7	US-11-096-046-27	Sequence 27, Appl
397	26	60.5	667	7	US-11-096-046-25	Sequence 25, Appl
398	26	60.5	667	7	US-11-096-046-28	Sequence 28, Appl
399	26	60.5	667	7	US-11-096-046-29	Sequence 29, Appl
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401	26	60.5	695	7	US-11-096-046-26	Sequence 26, Appl
402	26	60.5	719	6	US-10-467-657-762	Sequence 762, App
403	26	60.5	754	7	US-11-140-625-10	Sequence 10, Appl
404	26	60.5	796	6	US-10-995-561-954	Sequence 954, App
405	26	60.5	798	6	US-10-770-726-64	Sequence 64, Appl
406	26	60.5	803	7	US-11-200-296B-63	Sequence 63, Appl
407	26	60.5	808	7	US-11-096-568A-26949	Sequence 26949, A
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410	26	60.5	897	7	US-11-096-568A-26948	Sequence 26948, A
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412	26	60.5	928	7	US-11-201-801-8	Sequence 8, Appli
413	26	60.5	984	6	US-10-995-561-629	Sequence 629, App
414	26	60.5	1010	7	US-11-052-554A-89	Sequence 89, Appl
415	26	60.5	1047	7	US-11-124-367A-388	Sequence 388, App
416	26	60.5	1048	6	US-10-912-580-6	Sequence 6, Appli
417	26	60.5	1048	6	US-10-912-581-1	Sequence 1, Appli
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419	26	60.5	1062	7	US-11-124-367A-387	Sequence 387, App
420	26	60.5	1074	6	US-10-501-035-311	Sequence 311, App
421	26	60.5	1207	7	US-11-124-368A-263	Sequence 263, App
422	26	60.5	1451	7	US-11-046-346-1	Sequence 1, Appli
423	26	60.5	1490	7	US-11-257-883-2	Sequence 2, Appli
424	26	60.5	1871	6	US-10-877-346-42	Sequence 42, Appl
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426	26	60.5	2176	7	US-11-193-771-25	Sequence 25, Appl
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429	26	60.5	2176	7	US-11-193-857-25	Sequence 25, Appl
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432	26	60.5	2217	7	US-11-193-789-38	Sequence 38, Appl
433	26	60.5	2217	7	US-11-193-806-38	Sequence 38, Appl
434	26	60.5	2217	7	US-11-193-857-38	Sequence 38, Appl
435	26	60.5	2296	6	US-10-995-561-633	Sequence 633, App
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442	26	60.5	2330	7	US-11-193-771-21	Sequence 21, Appl
443	26	60.5	2330	7	US-11-193-789-21	Sequence 21, Appl
444	26	60.5	2330	7	US-11-193-806-21	Sequence 21, Appl
445	26	60.5	2330	7	US-11-193-857-21	Sequence 21, Appl
446	26	60.5	2355	6	US-10-995-561-623	Sequence 623, App
447	26	60.5	2355	6	US-10-995-561-627	Sequence 627, App
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449	26	60.5	2355	7	US-11-193-771-19	Sequence 19, Appl
450	26	60.5	2355	7	US-11-193-789-19	Sequence 19, Appl
451	26	60.5	2355	7	US-11-193-806-19	Sequence 19, Appl
452	26	60.5	2355	7	US-11-193-857-19	Sequence 19, Appl
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456	26	60.5	2421	7	US-11-193-771-17	Sequence 17, Appl
457	26	60.5	2421	7	US-11-193-789-17	Sequence 17, Appl
458	26	60.5	2421	7	US-11-193-806-17	Sequence 17, Appl
459	26	60.5	2421	7	US-11-193-857-17	Sequence 17, Appl
460	26	60.5	2477	7	US-11-193-561-15	Sequence 15, Appl
461	26	60.5	2477	7	US-11-193-771-15	Sequence 15, Appl
462	26	60.5	2477	7	US-11-193-789-15	Sequence 15, Appl
463	26	60.5	2477	7	US-11-193-806-15	Sequence 15, Appl
464	26	60.5	2477	7	US-11-193-857-15	Sequence 15, Appl
465	26	60.5	3716	7	US-11-052-554A-141	Sequence 141, App
466	25	58.1	51	6	US-10-467-657-7274	Sequence 7274, Ap
467	25	58.1	51	6	US-10-467-657-8152	Sequence 8152, Ap
468	25	58.1	52	7	US-11-004-399-3481	Sequence 3481, Ap
469	25	58.1	61	7	US-11-096-568A-25322	Sequence 25322, A
470	25	58.1	78	7	US-11-004-399-882	Sequence 882, App
471	25	58.1	87	6	US-10-485-788A-729	Sequence 729, App
472	25	58.1	87	7	US-11-053-076-99	Sequence 99, Appl
473	25	58.1	87	7	US-11-166-609-16	Sequence 16, Appl
474	25	58.1	101	7	US-11-096-568A-25321	Sequence 25321, A
475	25	58.1	112	7	US-11-031-206-88	Sequence 88, Appl
476	25	58.1	161	7	US-11-087-099-7866	Sequence 7866, Ap
477	25	58.1	172	7	US-11-072-512-3926	Sequence 3926, Ap
478	25	58.1	173	7	US-11-096-568A-10438	Sequence 10438, A
479	25	58.1	178	6	US-10-491-468-36	Sequence 36, Appl
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483	25	58.1	194	7	US-11-072-512-2233	Sequence 2233, Ap
484	25	58.1	197	7	US-11-096-568A-20126	Sequence 20126, A
485	25	58.1	198	7	US-11-096-568A-17131	Sequence 17131, A
486	25	58.1	219	7	US-11-040-595-11	Sequence 11, Appl
487	25	58.1	241	7	US-11-096-568A-20547	Sequence 20547, A
488	25	58.1	241	7	US-11-234-250-3	Sequence 3, Appli
489	25	58.1	244	6	US-10-524-647-102	Sequence 102, App
490	25	58.1	244	6	US-10-524-972-86	Sequence 86, Appl
491	25	58.1	256	7	US-11-096-568A-878	Sequence 878, App
492	25	58.1	257	7	US-11-096-568A-877	Sequence 877, App
493	25	58.1	272	7	US-11-096-568A-24761	Sequence 24761, A
494	25	58.1	295	7	US-11-096-568A-876	Sequence 876, App
495	25	58.1	300	7	US-11-179-977-4	Sequence 4, Appli
496	25	58.1	303	7	US-11-096-568A-14763	Sequence 14763, A
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499	25	58.1	308	7	US-11-244-219-5	Sequence 5, Appli
500	25	58.1	315	7	US-11-087-099-5128	Sequence 5128, Ap
501	25	58.1	322	7	US-11-082-389-188	Sequence 188, App
502	25	58.1	325	7	US-11-098-686-10395	Sequence 10395, A
503	25	58.1	329	7	US-11-087-099-3224	Sequence 3224, Ap
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508	25	58.1	353	7	US-11-096-568A-18704	Sequence 18704, A
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510	25	58.1	355	7	US-11-087-099-10302	Sequence 10302, A
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514	25	58.1	389	7	US-11-219-282-22	Sequence 22, Appl
515	25	58.1	390	7	US-11-019-711-62	Sequence 62, Appl
516	25	58.1	391	6	US-10-623-155-110	Sequence 110, App
517	25	58.1	391	7	US-11-019-711-61	Sequence 61, Appl
518	25	58.1	391	7	US-11-019-711-63	Sequence 63, Appl
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520	25	58.1	397	7	US-11-096-568A-21921	Sequence 21921, A
521	25	58.1	399	7	US-11-096-568A-24759	Sequence 24759, A
522	25	58.1	400	6	US-10-623-155-112	Sequence 112, App
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524	25	58.1	400	7	US-11-019-711-12	Sequence 12, Appl
525	25	58.1	400	7	US-11-019-711-14	Sequence 14, Appl
526	25	58.1	400	7	US-11-202-566-27	Sequence 27, Appl
527	25	58.1	411	7	US-11-096-568A-14761	Sequence 14761, A
528	25	58.1	412	7	US-11-087-099-899	Sequence 899, App
529	25	58.1	416	7	US-11-087-099-8746	Sequence 8746, Ap
530	25	58.1	417	7	US-11-087-099-11336	Sequence 11336, A
531	25	58.1	420	7	US-11-087-099-8718	Sequence 8718, Ap
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533	25	58.1	438	6	US-10-525-710-2	Sequence 2, Appli
534	25	58.1	440	6	US-10-606-302-9	Sequence 9, Appli
535	25	58.1	442	6	US-10-873-528-6	Sequence 6, Appli
536	25	58.1	443	6	US-10-873-528-152	Sequence 152, App

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539	25	58.1	461	7	US-11-087-099-1753	Sequence 1753, Ap
540	25	58.1	461	7	US-11-087-099-3481	Sequence 3481, Ap
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542	25	58.1	466	7	US-11-087-099-11743	Sequence 11743, A
543	25	58.1	469	7	US-11-072-512-2219	Sequence 2219, Ap
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545	25	58.1	481	7	US-11-087-099-3447	Sequence 3447, Ap
546	25	58.1	484	7	US-11-096-568A-2232	Sequence 2232, Ap
547	25	58.1	486	7	US-11-087-099-10037	Sequence 10037, A
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551	25	58.1	502	6	US-10-510-941-12	Sequence 12, Appl
552	25	58.1	503	7	US-11-087-099-1826	Sequence 1826, Ap
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554	25	58.1	511	6	US-10-520-820-15	Sequence 15, Appl
555	25	58.1	512	7	US-11-087-099-12218	Sequence 12218, A
556	25	58.1	517	6	US-10-055-877-304	Sequence 304, App
557	25	58.1	519	7	US-11-096-568A-22132	Sequence 22132, A
558	25	58.1	534	7	US-11-055-822-268	Sequence 268, App
559	25	58.1	553	7	US-11-055-822-266	Sequence 266, App
560	25	58.1	567	6	US-10-501-035-257	Sequence 257, App
561	25	58.1	577	7	US-11-124-368A-213	Sequence 213, App
562	25	58.1	616	7	US-11-120-308-42	Sequence 42, Appl
563	25	58.1	617	7	US-11-087-099-9501	Sequence 9501, Ap
564	25	58.1	647	7	US-11-096-568A-27741	Sequence 27741, A
565	25	58.1	648	7	US-11-072-512-2032	Sequence 2032, Ap
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568	25	58.1	658	7	US-11-072-175-163	Sequence 163, App
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571	25	58.1	730	7	US-11-113-424-50	Sequence 50, Appl
572	25	58.1	737	7	US-11-052-554A-305	Sequence 305, App
573	25	58.1	772	7	US-11-147-238-2	Sequence 2, Appli
574	25	58.1	772	7	US-11-147-238-5	Sequence 5, Appli
575	25	58.1	788	7	US-11-096-568A-30431	Sequence 30431, A
576	25	58.1	804	7	US-11-096-568A-27739	Sequence 27739, A
577	25	58.1	806	7	US-11-096-568A-30430	Sequence 30430, A
578	25	58.1	808	7	US-11-072-512-2654	Sequence 2654, Ap
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581	25	58.1	816	7	US-11-087-099-10395	Sequence 10395, A
582	25	58.1	818	7	US-11-096-568A-30445	Sequence 30445, A
583	25	58.1	832	7	US-11-087-099-11497	Sequence 11497, A
584	25	58.1	851	7	US-11-072-512-2451	Sequence 2451, Ap
585	25	58.1	862	7	US-11-087-099-4029	Sequence 4029, Ap
586	25	58.1	865	7	US-11-087-099-1496	Sequence 1496, Ap
587	25	58.1	867	6	US-10-725-475-19	Sequence 19, Appl
588	25	58.1	895	7	US-11-150-406-2	Sequence 2, Appli
589	25	58.1	901	7	US-11-087-099-1818	Sequence 1818, Ap
590	25	58.1	912	7	US-11-096-568A-31185	Sequence 31185, A
591	25	58.1	915	6	US-10-821-234-1514	Sequence 1514, Ap
592	25	58.1	915	6	US-10-995-561-1003	Sequence 1003, Ap
593	25	58.1	917	6	US-10-995-561-1000	Sequence 1000, Ap
594	25	58.1	920	6	US-10-821-234-1129	Sequence 1129, Ap
595	25	58.1	936	7	US-11-096-568A-31184	Sequence 31184, A
596	25	58.1	940	6	US-10-995-561-1004	Sequence 1004, Ap
597	25	58.1	955	7	US-11-096-568A-29121	Sequence 29121, A
598	25	58.1	969	6	US-10-995-561-1001	Sequence 1001, Ap
599	25	58.1	971	6	US-10-995-561-998	Sequence 998, App
600	25	58.1	979	7	US-11-096-568A-29120	Sequence 29120, A
601	25	58.1	984	7	US-11-055-822-508	Sequence 508, App
602	25	58.1	984	7	US-11-055-822-594	Sequence 594, App
603	25	58.1	994	6	US-10-995-561-997	Sequence 997, App
604	25	58.1	1026	7	US-11-096-568A-31183	Sequence 31183, A
605	25	58.1	1069	7	US-11-096-568A-29119	Sequence 29119, A
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607	25	58.1	1253	7	US-11-096-568A-28513	Sequence 28513, A
608	25	58.1	1340	7	US-11-070-575-6	Sequence 6, Appli
609	25	58.1	1344	7	US-11-091-643-20	Sequence 20, Appl
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611	25	58.1	1476	7	US-11-019-711-114	Sequence 114, App
612	25	58.1	1704	7	US-11-075-046-40	Sequence 40, Appl
613	25	58.1	1783	7	US-11-126-313-38	Sequence 38, Appl
614	25	58.1	1857	7	US-11-057-058-60	Sequence 60, Appl
615	25	58.1	1857	7	US-11-057-058-61	Sequence 61, Appl
616	25	58.1	2417	6	US-10-453-372-228	Sequence 228, App
617	25	58.1	2516	6	US-10-647-956A-2	Sequence 2, Appli
618	25	58.1	2769	7	US-11-113-424-14	Sequence 14, Appl
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622	25	58.1	3570	6	US-10-453-372-196	Sequence 196, App
623	25	58.1	3570	6	US-10-453-372-198	Sequence 198, App
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625	25	58.1	3570	6	US-10-453-372-202	Sequence 202, App
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627	25	58.1	3570	6	US-10-453-372-206	Sequence 206, App
628	25	58.1	3803	6	US-10-995-561-773	Sequence 773, App
629	25	58.1	3960	6	US-10-995-561-771	Sequence 771, App
630	25	58.1	5335	6	US-10-995-561-777	Sequence 777, App
631	25	58.1	5406	6	US-10-995-561-774	Sequence 774, App
632	25	58.1	5415	6	US-10-995-561-779	Sequence 779, App
633	25	58.1	5464	6	US-10-995-561-775	Sequence 775, App
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635	24.5	57.0	260	7	US-11-096-568A-24480	Sequence 24480, A
636	24.5	57.0	334	7	US-11-096-568A-31671	Sequence 31671, A
637	24.5	57.0	335	6	US-10-873-528-4	Sequence 4, Appli
638	24.5	57.0	354	7	US-11-096-568A-24479	Sequence 24479, A
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641	24	55.8	33	7	US-11-004-399-1730	Sequence 1730, Ap
642	24	55.8	35	7	US-11-083-624-55	Sequence 55, Appl
643	24	55.8	44	6	US-10-957-887B-111	Sequence 111, App
644	24	55.8	45	7	US-11-004-399-1835	Sequence 1835, Ap
645	24	55.8	49	7	US-11-123-896-90	Sequence 90, Appl
646	24	55.8	64	7	US-11-096-568A-25338	Sequence 25338, A
647	24	55.8	72	7	US-11-096-568A-780	Sequence 780, App
648	24	55.8	80	7	US-11-123-896-89	Sequence 89, Appl
649	24	55.8	82	7	US-11-123-896-284	Sequence 284, App
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651	24	55.8	93	7	US-11-201-519-35	Sequence 35, Appl
652	24	55.8	97	7	US-11-096-568A-8531	Sequence 8531, Ap
653	24	55.8	100	6	US-10-999-866-3	Sequence 3, Appli
654	24	55.8	100	6	US-10-935-005B-33	Sequence 33, Appl
655	24	55.8	100	7	US-11-061-821-3	Sequence 3, Appli
656	24	55.8	102	7	US-11-096-568A-24941	Sequence 24941, A
657	24	55.8	103	6	US-10-485-788A-647	Sequence 647, App
658	24	55.8	103	7	US-11-053-076-119	Sequence 119, App
659	24	55.8	121	7	US-11-072-512-2980	Sequence 2980, Ap
660	24	55.8	121	7	US-11-096-568A-23566	Sequence 23566, A
661	24	55.8	123	7	US-11-072-512-2295	Sequence 2295, Ap
662	24	55.8	130	7	US-11-096-568A-203	Sequence 203, App
663	24	55.8	130	7	US-11-096-568A-32836	Sequence 32836, A
664	24	55.8	134	7	US-11-096-568A-4045	Sequence 4045, Ap
665	24	55.8	135	6	US-10-131-826A-276	Sequence 276, App
666	24	55.8	135	6	US-10-973-115B-276	Sequence 276, App
667	24	55.8	135	7	US-11-087-099-10742	Sequence 10742, A
668	24	55.8	136	7	US-11-096-568A-202	Sequence 202, App
669	24	55.8	136	7	US-11-096-568A-32835	Sequence 32835, A
670	24	55.8	139	6	US-10-467-657-2748	Sequence 2748, Ap
671	24	55.8	139	7	US-11-096-568A-29981	Sequence 29981, A
672	24	55.8	146	7	US-11-176-830-675	Sequence 675, App
673	24	55.8	149	7	US-11-096-568A-13819	Sequence 13819, A
674	24	55.8	154	7	US-11-087-099-1172	Sequence 1172, Ap
675	24	55.8	158	6	US-10-530-253-26	Sequence 26, Appl
676	24	55.8	162	7	US-11-096-568A-22117	Sequence 22117, A
677	24	55.8	163	7	US-11-024-959-435	Sequence 435, App
678	24	55.8	163	7	US-11-096-568A-32834	Sequence 32834, A
679	24	55.8	164	7	US-11-055-822-1114	Sequence 1114, Ap
680	24	55.8	165	7	US-11-128-059-26	Sequence 26, Appl
681	24	55.8	165	7	US-11-096-568A-201	Sequence 201, App
682	24	55.8	165	7	US-11-096-568A-204	Sequence 204, App

683	24	55.8	165	7	US-11-096-568A-20455	Sequence 20455, A
684	24	55.8	165	7	US-11-096-568A-26495	Sequence 26495, A
685	24	55.8	167	6	US-10-793-626-1502	Sequence 1502, Ap
686	24	55.8	168	7	US-11-044-111-27	Sequence 27, Appl
687	24	55.8	171	7	US-11-087-099-9583	Sequence 9583, Ap
688	24	55.8	173	7	US-11-098-686-11192	Sequence 11192, A
689	24	55.8	173	7	US-11-087-099-5249	Sequence 5249, Ap
690	24	55.8	174	7	US-11-087-099-8578	Sequence 8578, Ap
691	24	55.8	174	7	US-11-096-568A-26494	Sequence 26494, A
692	24	55.8	175	7	US-11-096-568A-23153	Sequence 23153, A
693	24	55.8	175	7	US-11-096-568A-29980	Sequence 29980, A
694	24	55.8	175	7	US-11-096-568A-33229	Sequence 33229, A
695	24	55.8	177	7	US-11-096-568A-29979	Sequence 29979, A
696	24	55.8	178	7	US-11-096-568A-11302	Sequence 11302, A
697	24	55.8	183	7	US-11-096-568A-23152	Sequence 23152, A
698	24	55.8	184	7	US-11-096-568A-23151	Sequence 23151, A
699	24	55.8	185	7	US-11-087-099-10740	Sequence 10740, A
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701	24	55.8	197	7	US-11-096-568A-24940	Sequence 24940, A
702	24	55.8	198	7	US-11-087-099-5759	Sequence 5759, Ap
703	24	55.8	200	7	US-11-055-822-296	Sequence 296, App
704	24	55.8	201	7	US-11-072-512-2087	Sequence 2087, Ap
705	24	55.8	208	6	US-10-757-832-4	Sequence 4, Appli
706	24	55.8	210	7	US-11-096-568A-8162	Sequence 8162, Ap
707	24	55.8	218	7	US-11-082-389-318	Sequence 318, App
708	24	55.8	218	7	US-11-087-099-8257	Sequence 8257, Ap
709	24	55.8	219	7	US-11-098-686-10094	Sequence 10094, A
710	24	55.8	223	7	US-11-096-568A-19101	Sequence 19101, A
711	24	55.8	228	7	US-11-087-099-7494	Sequence 7494, Ap
712	24	55.8	230	7	US-11-096-568A-21243	Sequence 21243, A
713	24	55.8	231	7	US-11-096-568A-26474	Sequence 26474, A
714	24	55.8	233	7	US-11-096-568A-33228	Sequence 33228, A
715	24	55.8	236	7	US-11-096-568A-17403	Sequence 17403, A
716	24	55.8	242	7	US-11-087-099-3609	Sequence 3609, Ap
717	24	55.8	247	6	US-10-510-386-242	Sequence 242, App
718	24	55.8	247	6	US-10-995-561-790	Sequence 790, App
719	24	55.8	248	7	US-11-087-099-5977	Sequence 5977, Ap
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721	24	55.8	250	7	US-11-096-568A-23438	Sequence 23438, A
722	24	55.8	252	7	US-11-096-568A-21242	Sequence 21242, A
723	24	55.8	253	7	US-11-096-568A-7429	Sequence 7429, Ap
724	24	55.8	255	7	US-11-054-281-304	Sequence 304, App
725	24	55.8	255	7	US-11-096-568A-33227	Sequence 33227, A
726	24	55.8	256	7	US-11-128-059-68	Sequence 68, Appl
727	24	55.8	256	7	US-11-087-099-614	Sequence 614, App
728	24	55.8	261	7	US-11-083-624-2	Sequence 2, Appli
729	24	55.8	272	7	US-11-096-568A-17402	Sequence 17402, A
730	24	55.8	282	7	US-11-077-619-54	Sequence 54, Appl
731	24	55.8	283	6	US-10-055-877-167	Sequence 167, App
732	24	55.8	285	7	US-11-096-568A-17401	Sequence 17401, A
733	24	55.8	287	7	US-11-087-099-9514	Sequence 9514, Ap
734	24	55.8	288	7	US-11-087-099-8633	Sequence 8633, Ap
735	24	55.8	290	6	US-10-115-609-23	Sequence 23, Appl
736	24	55.8	290	7	US-11-113-424-78	Sequence 78, Appl
737	24	55.8	291	6	US-10-793-626-1458	Sequence 1458, Ap
738	24	55.8	293	7	US-11-096-568A-25602	Sequence 25602, A
739	24	55.8	295	6	US-10-467-657-6466	Sequence 6466, Ap
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741	24	55.8	296	7	US-11-096-568A-23305	Sequence 23305, A
742	24	55.8	298	7	US-11-096-568A-19100	Sequence 19100, A
743	24	55.8	299	7	US-11-096-568A-15962	Sequence 15962, A
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746	24	55.8	306	7	US-11-096-568A-33762	Sequence 33762, A
747	24	55.8	308	7	US-11-096-568A-25601	Sequence 25601, A
748	24	55.8	309	7	US-11-096-568A-33702	Sequence 33702, A
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753	24	55.8	311	7	US-11-096-568A-21202	Sequence 21202, A
754	24	55.8	311	7	US-11-096-568A-21241	Sequence 21241, A
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757	24	55.8	316	7	US-11-087-099-7594	Sequence 7594, Ap
758	24	55.8	318	7	US-11-096-568A-716	Sequence 716, App
759	24	55.8	319	7	US-11-096-568A-7033	Sequence 7033, Ap
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761	24	55.8	323	7	US-11-087-099-408	Sequence 408, App
762	24	55.8	324	7	US-11-096-568A-33701	Sequence 33701, A
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764	24	55.8	328	7	US-11-096-568A-20454	Sequence 20454, A
765	24	55.8	328	7	US-11-096-568A-21201	Sequence 21201, A
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767	24	55.8	330	7	US-11-096-568A-25600	Sequence 25600, A
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769	24	55.8	332	7	US-11-087-099-682	Sequence 682, App
770	24	55.8	332	7	US-11-096-568A-19004	Sequence 19004, A
771	24	55.8	338	7	US-11-087-099-8709	Sequence 8709, Ap
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773	24	55.8	340	7	US-11-087-099-10548	Sequence 10548, A
774	24	55.8	342	7	US-11-096-568A-21200	Sequence 21200, A
775	24	55.8	342	7	US-11-096-568A-22642	Sequence 22642, A
776	24	55.8	345	6	US-10-467-657-252	Sequence 252, App
777	24	55.8	345	6	US-10-467-657-3086	Sequence 3086, Ap
778	24	55.8	347	7	US-11-224-624-136	Sequence 136, App
779	24	55.8	347	7	US-11-096-568A-715	Sequence 715, App
780	24	55.8	349	6	US-10-055-877-169	Sequence 169, App
781	24	55.8	349	6	US-10-055-877-170	Sequence 170, App
782	24	55.8	349	6	US-10-055-877-171	Sequence 171, App
783	24	55.8	349	7	US-11-096-568A-13569	Sequence 13569, A
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787	24	55.8	359	7	US-11-087-099-4377	Sequence 4377, Ap
788	24	55.8	361	7	US-11-087-099-8389	Sequence 8389, Ap
789	24	55.8	364	7	US-11-096-568A-15960	Sequence 15960, A
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791	24	55.8	369	7	US-11-096-568A-3260	Sequence 3260, Ap
792	24	55.8	371	7	US-11-096-568A-16077	Sequence 16077, A
793	24	55.8	374	7	US-11-087-099-1718	Sequence 1718, Ap
794	24	55.8	377	7	US-11-087-099-2447	Sequence 2447, Ap
795	24	55.8	377	7	US-11-087-099-6533	Sequence 6533, Ap
796	24	55.8	378	7	US-11-087-099-465	Sequence 465, App
797	24	55.8	378	7	US-11-087-099-10139	Sequence 10139, A
798	24	55.8	378	7	US-11-087-099-12336	Sequence 12336, A
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802	24	55.8	383	7	US-11-096-568A-3261	Sequence 3261, Ap
803	24	55.8	384	7	US-11-096-568A-22641	Sequence 22641, A
804	24	55.8	385	7	US-11-087-099-7112	Sequence 7112, Ap
805	24	55.8	389	6	US-10-980-388-116	Sequence 116, App
806	24	55.8	389	7	US-11-096-568A-15113	Sequence 15113, A
807	24	55.8	391	7	US-11-096-568A-15545	Sequence 15545, A
808	24	55.8	392	7	US-11-087-099-4369	Sequence 4369, Ap
809	24	55.8	393	7	US-11-096-568A-6909	Sequence 6909, Ap
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811	24	55.8	402	7	US-11-096-568A-15544	Sequence 15544, A
812	24	55.8	404	7	US-11-052-554A-322	Sequence 322, App
813	24	55.8	404	7	US-11-096-568A-13568	Sequence 13568, A
814	24	55.8	404	7	US-11-096-568A-29207	Sequence 29207, A
815	24	55.8	406	6	US-10-330-773-602	Sequence 602, App
816	24	55.8	406	7	US-11-087-099-9153	Sequence 9153, Ap
817	24	55.8	408	7	US-11-096-568A-15112	Sequence 15112, A
818	24	55.8	410	7	US-11-096-568A-15543	Sequence 15543, A
819	24	55.8	414	7	US-11-087-099-3464	Sequence 3464, Ap
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821	24	55.8	417	6	US-10-613-744-2	Sequence 2, Appli
822	24	55.8	417	6	US-10-995-561-791	Sequence 791, App
823	24	55.8	417	7	US-11-110-851-61	Sequence 61, Appl
824	24	55.8	419	7	US-11-087-099-7538	Sequence 7538, Ap
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826	24	55.8	431	7	US-11-096-568A-33761	Sequence 33761, A
827	24	55.8	432	7	US-11-055-822-292	Sequence 292, App
828	24	55.8	437	7	US-11-087-099-840	Sequence 840, App

829	24	55.8	446	7	US-11-082-389-316	Sequence 316, App
830	24	55.8	446	7	US-11-096-568A-13567	Sequence 13567, A
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833	24	55.8	451	7	US-11-087-099-2650	Sequence 2650, Ap
834	24	55.8	451	7	US-11-096-568A-1960	Sequence 1960, Ap
835	24	55.8	453	7	US-11-087-099-7775	Sequence 7775, Ap
836	24	55.8	459	6	US-10-793-626-1246	Sequence 1246, Ap
837	24	55.8	459	6	US-10-793-626-2554	Sequence 2554, Ap
838	24	55.8	466	7	US-11-096-568A-23972	Sequence 23972, A
839	24	55.8	467	7	US-11-096-568A-3258	Sequence 3258, Ap
840	24	55.8	467	7	US-11-096-568A-22640	Sequence 22640, A
841	24	55.8	476	7	US-11-096-568A-20043	Sequence 20043, A
842	24	55.8	478	6	US-10-131-826A-138	Sequence 138, App
843	24	55.8	478	6	US-10-973-115B-138	Sequence 138, App
844	24	55.8	478	7	US-11-174-150-27	Sequence 27, Appl
845	24	55.8	480	7	US-11-087-099-12327	Sequence 12327, A
846	24	55.8	481	7	US-11-146-428-98	Sequence 98, Appl
847	24	55.8	482	7	US-11-087-099-7371	Sequence 7371, Ap
848	24	55.8	482	7	US-11-087-099-11565	Sequence 11565, A
849	24	55.8	482	7	US-11-096-568A-15111	Sequence 15111, A
850	24	55.8	484	7	US-11-126-313-24	Sequence 24, Appl
851	24	55.8	484	7	US-11-096-568A-7428	Sequence 7428, Ap
852	24	55.8	487	7	US-11-096-568A-22730	Sequence 22730, A
853	24	55.8	490	6	US-10-131-826A-310	Sequence 310, App
854	24	55.8	490	6	US-10-973-115B-310	Sequence 310, App
855	24	55.8	492	7	US-11-096-568A-22729	Sequence 22729, A
856	24	55.8	493	7	US-11-096-568A-6908	Sequence 6908, Ap
857	24	55.8	498	7	US-11-098-686-10205	Sequence 10205, A
858	24	55.8	504	7	US-11-096-568A-29206	Sequence 29206, A
859	24	55.8	509	7	US-11-155-288-8	Sequence 8, Appli
860	24	55.8	511	7	US-11-087-099-2235	Sequence 2235, Ap
861	24	55.8	513	7	US-11-087-099-7975	Sequence 7975, Ap
862	24	55.8	513	7	US-11-096-568A-28076	Sequence 28076, A
863	24	55.8	520	7	US-11-112-882-26	Sequence 26, Appl
864	24	55.8	521	7	US-11-143-980-32	Sequence 32, Appl
865	24	55.8	523	6	US-10-453-372-1006	Sequence 1006, Ap
866	24	55.8	523	6	US-10-453-372-1008	Sequence 1008, Ap
867	24	55.8	530	7	US-11-096-568A-22728	Sequence 22728, A
868	24	55.8	531	7	US-11-096-568A-28075	Sequence 28075, A
869	24	55.8	533	7	US-11-096-568A-20042	Sequence 20042, A
870	24	55.8	534	7	US-11-096-568A-23971	Sequence 23971, A
871	24	55.8	536	7	US-11-096-568A-23970	Sequence 23970, A
872	24	55.8	542	7	US-11-205-109-35	Sequence 35, Appl
873	24	55.8	542	7	US-11-087-099-10766	Sequence 10766, A
874	24	55.8	555	7	US-11-096-568A-28074	Sequence 28074, A
875	24	55.8	556	7	US-11-154-227-98	Sequence 98, Appl
876	24	55.8	562	7	US-11-207-721-2	Sequence 2, Appli
877	24	55.8	562	7	US-11-072-512-3214	Sequence 3214, Ap
878	24	55.8	570	7	US-11-113-424-71	Sequence 71, Appl
879	24	55.8	578	7	US-11-087-099-2668	Sequence 2668, Ap
880	24	55.8	597	6	US-10-055-877-303	Sequence 303, App
881	24	55.8	604	6	US-10-467-657-2280	Sequence 2280, Ap
882	24	55.8	613	6	US-10-131-826A-190	Sequence 190, App
883	24	55.8	613	6	US-10-973-115B-190	Sequence 190, App
884	24	55.8	613	7	US-11-166-994-4	Sequence 4, Appli
885	24	55.8	616	7	US-11-096-568A-2186	Sequence 2186, Ap
886	24	55.8	619	6	US-10-537-002-102	Sequence 102, App
887	24	55.8	625	7	US-11-072-512-3210	Sequence 3210, Ap
888	24	55.8	630	7	US-11-096-568A-2185	Sequence 2185, Ap
889	24	55.8	646	6	US-10-517-696-98	Sequence 98, Appl
890	24	55.8	646	7	US-11-126-022-35	Sequence 35, Appl
891	24	55.8	665	6	US-10-793-626-1232	Sequence 1232, Ap
892	24	55.8	678	6	US-10-055-877-202	Sequence 202, App
893	24	55.8	684	6	US-10-714-781A-55	Sequence 55, Appl
894	24	55.8	684	6	US-10-714-781A-57	Sequence 57, Appl
895	24	55.8	684	6	US-10-714-781A-61	Sequence 61, Appl
896	24	55.8	686	6	US-10-714-781A-59	Sequence 59, Appl
897	24	55.8	698	7	US-11-087-099-7907	Sequence 7907, Ap
898	24	55.8	709	6	US-10-131-826A-202	Sequence 202, App
899	24	55.8	709	6	US-10-519-238-3	Sequence 3, Appli
900	24	55.8	709	6	US-10-973-115B-202	Sequence 202, App
901	24	55.8	729	7	US-11-099-691-3	Sequence 3, Appli
902	24	55.8	743	7	US-11-096-568A-27531	Sequence 27531, A
903	24	55.8	747	6	US-10-501-035-224	Sequence 224, App
904	24	55.8	750	7	US-11-096-568A-30499	Sequence 30499, A
905	24	55.8	756	7	US-11-096-568A-27530	Sequence 27530, A
906	24	55.8	769	7	US-11-087-099-4295	Sequence 4295, Ap
907	24	55.8	814	7	US-11-096-568A-27529	Sequence 27529, A
908	24	55.8	824	7	US-11-072-512-2515	Sequence 2515, Ap
909	24	55.8	855	7	US-11-104-110-1	Sequence 1, Appli
910	24	55.8	855	7	US-11-019-711-132	Sequence 132, App
911	24	55.8	855	7	US-11-104-111-22	Sequence 22, Appl
912	24	55.8	885	7	US-11-096-568A-30498	Sequence 30498, A
913	24	55.8	894	7	US-11-124-367A-429	Sequence 429, App
914	24	55.8	896	7	US-11-080-991-98	Sequence 98, Appl
915	24	55.8	908	6	US-10-517-939-360	Sequence 360, App
916	24	55.8	911	7	US-11-096-568A-30497	Sequence 30497, A
917	24	55.8	916	6	US-10-501-035-299	Sequence 299, App
918	24	55.8	928	6	US-10-880-144-4	Sequence 4, Appli
919	24	55.8	934	7	US-11-108-864-19	Sequence 19, Appl
920	24	55.8	934	7	US-11-052-554A-10	Sequence 10, Appl
921	24	55.8	1011	6	US-10-330-773-924	Sequence 924, App
922	24	55.8	1014	6	US-10-491-468-7	Sequence 7, Appli
923	24	55.8	1024	6	US-10-330-773-927	Sequence 927, App
924	24	55.8	1070	6	US-10-537-002-14	Sequence 14, Appl
925	24	55.8	1073	6	US-10-537-002-11	Sequence 11, Appl
926	24	55.8	1074	7	US-11-096-568A-28522	Sequence 28522, A
927	24	55.8	1077	7	US-11-072-512-2291	Sequence 2291, Ap
928	24	55.8	1092	7	US-11-096-568A-28521	Sequence 28521, A
929	24	55.8	1117	7	US-11-087-099-6893	Sequence 6893, Ap
930	24	55.8	1118	7	US-11-087-099-9174	Sequence 9174, Ap
931	24	55.8	1124	7	US-11-087-099-1938	Sequence 1938, Ap
932	24	55.8	1124	7	US-11-087-099-2565	Sequence 2565, Ap
933	24	55.8	1124	7	US-11-087-099-4855	Sequence 4855, Ap
934	24	55.8	1125	7	US-11-024-959-360	Sequence 360, App
935	24	55.8	1136	7	US-11-096-568A-28520	Sequence 28520, A
936	24	55.8	1161	6	US-10-511-538-99	Sequence 99, Appl
937	24	55.8	1190	7	US-11-043-889-20	Sequence 20, Appl
938	24	55.8	1252	6	US-10-493-909-89	Sequence 89, Appl
939	24	55.8	1256	6	US-10-493-909-90	Sequence 90, Appl
940	24	55.8	1274	7	US-11-096-568A-29137	Sequence 29137, A
941	24	55.8	1283	7	US-11-096-568A-29136	Sequence 29136, A
942	24	55.8	1286	7	US-11-096-568A-29135	Sequence 29135, A
943	24	55.8	1359	7	US-11-152-569-20	Sequence 20, Appl
944	24	55.8	1402	6	US-10-971-982-2	Sequence 2, Appli
945	24	55.8	1494	7	US-11-128-059-78	Sequence 78, Appl
946	24	55.8	1591	6	US-10-495-083-5	Sequence 5, Appli
947	24	55.8	1607	7	US-11-098-686-10178	Sequence 10178, A
948	24	55.8	1735	6	US-10-495-083-3	Sequence 3, Appli
949	24	55.8	1752	6	US-10-495-083-9	Sequence 9, Appli
950	24	55.8	1854	7	US-11-180-074-4	Sequence 4, Appli
951	24	55.8	2204	6	US-10-495-083-8	Sequence 8, Appli
952	24	55.8	2333	6	US-10-453-372-170	Sequence 170, App
953	24	55.8	2333	7	US-11-096-281-13	Sequence 13, Appl
954	24	55.8	2385	6	US-10-510-941-8	Sequence 8, Appli
955	24	55.8	2662	6	US-10-453-372-114	Sequence 114, App
956	24	55.8	2724	6	US-10-453-372-148	Sequence 148, App
957	24	55.8	2725	7	US-11-113-424-52	Sequence 52, Appl
958	24	55.8	2733	6	US-10-453-372-136	Sequence 136, App
959	24	55.8	2733	6	US-10-453-372-142	Sequence 142, App
960	24	55.8	2733	6	US-10-453-372-146	Sequence 146, App
961	24	55.8	2733	6	US-10-453-372-150	Sequence 150, App
962	24	55.8	2733	6	US-10-453-372-154	Sequence 154, App
963	24	55.8	2759	6	US-10-453-372-168	Sequence 168, App
964	24	55.8	2764	6	US-10-995-561-691	Sequence 691, App
965	24	55.8	2765	6	US-10-453-372-116	Sequence 116, App
966	24	55.8	2813	6	US-10-995-561-688	Sequence 688, App
967	24	55.8	2919	6	US-10-821-234-1133	Sequence 1133, Ap
968	24	55.8	3433	6	US-10-714-781A-67	Sequence 67, Appl
969	24	55.8	3689	7	US-11-075-185-4	Sequence 4, Appli
970	24	55.8	7968	7	US-11-143-980-49	Sequence 49, Appl
971	23.5	54.7	68	7	US-11-090-878-50	Sequence 50, Appl
972	23.5	54.7	72	7	US-11-090-878-48	Sequence 48, Appl
973	23.5	54.7	72	7	US-11-090-878-52	Sequence 52, Appl
974	23.5	54.7	72	7	US-11-090-878-61	Sequence 61, Appl

975	23.5	54.7	211	7	US-11-090-878-46	Sequence 46, Appl
976	23.5	54.7	244	7	US-11-090-878-66	Sequence 66, Appl
977	23.5	54.7	244	7	US-11-090-878-68	Sequence 68, Appl
978	23.5	54.7	244	7	US-11-090-878-69	Sequence 69, Appl
979	23.5	54.7	245	6	US-10-948-429A-10	Sequence 10, Appl
980	23.5	54.7	267	7	US-11-231-104-3	Sequence 3, Appli
981	23.5	54.7	268	7	US-11-096-568A-17499	Sequence 17499, A
982	23.5	54.7	283	7	US-11-087-099-9598	Sequence 9598, Ap
983	23.5	54.7	305	7	US-11-096-568A-17498	Sequence 17498, A
984	23.5	54.7	312	7	US-11-096-568A-17497	Sequence 17497, A
985	23.5	54.7	360	6	US-10-858-730-110	Sequence 110, App
986	23	53.5	6	6	US-10-857-435A-489	Sequence 489, App
987	23	53.5	10	7	US-11-011-666-3	Sequence 3, Appli
988	23	53.5	11	7	US-11-004-399-1211	Sequence 1211, Ap
989	23	53.5	11	7	US-11-004-399-1251	Sequence 1251, Ap
990	23	53.5	15	6	US-10-718-264-115	Sequence 115, App
991	23	53.5	15	6	US-10-718-264-116	Sequence 116, App
992	23	53.5	15	6	US-10-718-264-117	Sequence 117, App
993	23	53.5	15	6	US-10-718-264-141	Sequence 141, App
994	23	53.5	15	6	US-10-718-264-142	Sequence 142, App
995	23	53.5	15	6	US-10-718-264-143	Sequence 143, App
996	23	53.5	15	6	US-10-718-264-115	Sequence 115, App
997	23	53.5	15	6	US-10-718-264-116	Sequence 116, App
998	23	53.5	15	6	US-10-718-264-117	Sequence 117, App
999	23	53.5	15	6	US-10-718-264-141	Sequence 141, App
1000	23	53.5	15	6	US-10-718-264-142	Sequence 142, App

ALIGNMENTS

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RESULT 1
US-10-982-357-19
; Sequence 19, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-19

  Query Match             88.4%;  Score 38;  DB 6;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 1.3e+05;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db          1 WASTRHT 7


RESULT 2
US-10-982-357-36
; Sequence 36, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-36

  Query Match             88.4%;  Score 38;  DB 6;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 1.3e+05;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db          1 WASTRHT 7


RESULT 3
US-11-097-812-132
; Sequence 132, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 132
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-132

  Query Match             88.4%;  Score 38;  DB 7;  Length 8;
  Best Local Similarity   85.7%;  Pred. No. 1.3e+05;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db          1 WASTRHT 7


RESULT 4
US-11-097-812-53
; Sequence 53, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
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;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
;   LENGTH: 105
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-53

  Query Match             88.4%;  Score 38;  DB 7;  Length 105;
  Best Local Similarity   85.7%;  Pred. No. 1.4;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 5
US-10-982-357-6
; Sequence 6, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-6

  Query Match             88.4%;  Score 38;  DB 6;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 1.4;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 6
US-10-982-357-42
; Sequence 42, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-42

  Query Match             88.4%;  Score 38;  DB 6;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 1.4;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 7
US-10-982-357-44
; Sequence 44, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-982-357-44

  Query Match             88.4%;  Score 38;  DB 6;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 1.4;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 8
US-10-982-357-48
; Sequence 48, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-48

  Query Match             88.4%;  Score 38;  DB 6;  Length 107;
  Best Local Similarity   85.7%;  Pred. No. 1.4;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 9
US-10-982-357-50
; Sequence 50, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-982-357-50

  Query Match             88.4%;  Score 38;  DB 6;  Length 107;
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  Best Local Similarity   85.7%;  Pred. No. 1.4;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 10
US-11-097-812-45
; Sequence 45, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-45

  Query Match             88.4%;  Score 38;  DB 7;  Length 108;
  Best Local Similarity   85.7%;  Pred. No. 1.4;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         49 WASTRHT 55


RESULT 11
US-11-097-812-50
; Sequence 50, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-50

  Query Match             88.4%;  Score 38;  DB 7;  Length 108;
  Best Local Similarity   85.7%;  Pred. No. 1.4;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         49 WASTRHT 55


RESULT 12
US-11-097-812-113
; Sequence 113, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 113
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: mouse
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (6)..(6)
;   OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-097-812-113

  Query Match             88.4%;  Score 38;  DB 7;  Length 109;
  Best Local Similarity   85.7%;  Pred. No. 1.4;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 13
US-11-037-199-7
; Sequence 7, Application US/11037199
; Publication No. US20060030015A1
; GENERAL INFORMATION:
;  APPLICANT: Japan Science and Technology Corporation
;  TITLE OF INVENTION: Novel methods of producing antibody-enzyme, the antibody-enzymes,
;  TITLE OF INVENTION:  and the use thereof
;  FILE REFERENCE: A251-01/PCT
;  CURRENT APPLICATION NUMBER: US/11/037,199
;  CURRENT FILING DATE:  2005-01-19
;  PRIOR APPLICATION NUMBER: JP 2002-211756
;  PRIOR FILING DATE: 2002-7-19
;  PRIOR APPLICATION NUMBER: JP 2002-211768
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;  PRIOR FILING DATE: 2002-7-19
;  PRIOR APPLICATION NUMBER: JP 2003-051943
;  PRIOR FILING DATE: 2003-2-27
;  PRIOR APPLICATION NUMBER: JP 2003-198270
;  PRIOR FILING DATE: 2003-7-17
;  PRIOR APPLICATION NUMBER: JP 2003-198281
;  PRIOR FILING DATE: 2003-7-17
;  PRIOR APPLICATION NUMBER: JP 2003-198292
;  PRIOR FILING DATE: 2003-7-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 109
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-037-199-7

  Query Match             88.4%;  Score 38;  DB 7;  Length 109;
  Best Local Similarity   85.7%;  Pred. No. 1.4;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         50 WASTRHT 56


RESULT 14
US-10-982-357-28
; Sequence 28, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-28

  Query Match             88.4%;  Score 38;  DB 6;  Length 127;
  Best Local Similarity   85.7%;  Pred. No. 1.6;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |||||
Db         70 WASTRHT 76


RESULT 15
US-11-140-625-11
; Sequence 11, Application US/11140625
; Publication No. US20060026706A1
; GENERAL INFORMATION:
;  APPLICANT: Van Wezel, Gilles P.
;  APPLICANT:  Vijgenboom, Erik
;  TITLE OF INVENTION: A method for marker-less integration of a sequence of interest
;  TITLE OF INVENTION:  into the genome of a cell
;  FILE REFERENCE: P62377SUS00
;  CURRENT APPLICATION NUMBER: US/11/140,625
;  CURRENT FILING DATE:  2005-05-27
;  PRIOR APPLICATION NUMBER: EP 02080000.9
;  PRIOR FILING DATE: 2002-11-28
;  PRIOR APPLICATION NUMBER: PCT/NL2003/000835
;  PRIOR FILING DATE: 2003-11-27
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
;   LENGTH: 738
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: ETR1 homologue derived from Nicotiana tabacum
US-11-140-625-11

  Query Match             86.0%;  Score 37;  DB 7;  Length 738;
  Best Local Similarity   85.7%;  Pred. No. 12;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||| ||
Db         73 WTSTAHT 79


RESULT 16
US-11-087-099-3380
; Sequence 3380, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3380
;   LENGTH: 352
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
US-11-087-099-3380

  Query Match             83.7%;  Score 36;  DB 7;  Length 352;
  Best Local Similarity   85.7%;  Pred. No. 9.7;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||| ||
Db         75 WTSTLHT 81


RESULT 17
US-11-077-619-56
; Sequence 56, Application US/11077619
; Publication No. US20060040279A1
; GENERAL INFORMATION:
;  APPLICANT: Feesche, Joerg
;  APPLICANT:  Maurer, Karl-Heinz
;  APPLICANT:  Breves, Roland
;  APPLICANT:  Schweder, Thomas
;  APPLICANT:  Hecker, Michael
;  APPLICANT:  Juergen, Britta
;  APPLICANT:  Voigt, Birgit
;  TITLE OF INVENTION: DNA CHIPS USED FOR BIOPROCESS CONTROL
;  FILE REFERENCE: HENK-0122 / H5692
;  CURRENT APPLICATION NUMBER: US/11/077,619
;  CURRENT FILING DATE:  2005-03-11
;  PRIOR APPLICATION NUMBER: PCT/EP2003/009979
;  PRIOR FILING DATE: 2003-09-09
;  PRIOR APPLICATION NUMBER: DE 10242433.0
;  PRIOR FILING DATE: 2002-09-11
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56
;   LENGTH: 461
;   TYPE: PRT
;   ORGANISM: Bacillus subtilis
US-11-077-619-56

  Query Match             83.7%;  Score 36;  DB 7;  Length 461;
  Best Local Similarity   85.7%;  Pred. No. 12;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          1 WTSTRHT 7
              |||| ||
Db        418 WTSTDHT 424


RESULT 18
US-11-098-686-10607
; Sequence 10607, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
;  APPLICANT: Kapur, Vivek and Gebhart, Connie J.
;  TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
;  TITLE OF INVENTION:  FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
;  FILE REFERENCE: 09531-128001
;  CURRENT APPLICATION NUMBER: US/11/098,686
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: PCT/US03/31318
;  PRIOR FILING DATE: 2003-10-01
;  PRIOR APPLICATION NUMBER: US 60/416,395
;  PRIOR FILING DATE: 2002-10-04
;  NUMBER OF SEQ ID NOS: 11433
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10607
;   LENGTH: 527
;   TYPE: PRT
;   ORGANISM: Lawsonia intracellularis
US-11-098-686-10607

  Query Match             74.4%;  Score 32;  DB 7;  Length 527;
  Best Local Similarity   83.3%;  Pred. No. 79;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRH 6
              ||| ||
Db        449 WTSIRH 454


RESULT 19
US-11-096-568A-14196
; Sequence 14196, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 14196
;   LENGTH: 78
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(78)
;   OTHER INFORMATION: Ceres Seq. ID no. 2733454
US-11-096-568A-14196

  Query Match             72.1%;  Score 31;  DB 7;  Length 78;
  Best Local Similarity   71.4%;  Pred. No. 22;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||:| |
Db         35 WTSSRRT 41


RESULT 20
US-11-218-821-8
; Sequence 8, Application US/11218821
; Publication No. US20060025576A1
; GENERAL INFORMATION:
;  APPLICANT: Miller, Kathy L.
;  APPLICANT:  Presta, Leonard G.
;  TITLE OF INVENTION: MULTIVALENT ANTIBODIES AND USES THEREFOR
;  FILE REFERENCE: P1780R1C1
;  CURRENT APPLICATION NUMBER: US/11/218,821
;  CURRENT FILING DATE:  2005-09-02
;  PRIOR APPLICATION NUMBER: US 09/813,341
;  PRIOR FILING DATE: 2001-03-20
;  PRIOR APPLICATION NUMBER: US 60/195,819
;  PRIOR FILING DATE: 2000-04-11
;  NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 8
;   LENGTH: 218
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-218-821-8

  Query Match             72.1%;  Score 31;  DB 7;  Length 218;
  Best Local Similarity   71.4%;  Pred. No. 56;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||  ||
Db        152 WTSNGHT 158


RESULT 21
US-11-169-041-208
; Sequence 208, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
;  TITLE OF INVENTION:  COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
;  TITLE OF INVENTION:  KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
;  TITLE OF INVENTION:  CELLS
;  FILE REFERENCE: 10001 NP
;  CURRENT APPLICATION NUMBER: US/11/169,041
;  CURRENT FILING DATE:  2005-06-28
;  PRIOR APPLICATION NUMBER: 60/584,405
;  PRIOR FILING DATE: 2004-06-30
;  NUMBER OF SEQ ID NOS: 527
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 208
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-169-041-208

  Query Match             72.1%;  Score 31;  DB 7;  Length 346;
  Best Local Similarity   66.7%;  Pred. No. 84;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRH 6
              ||::||
Db        321 WTNSRH 326


RESULT 22
US-11-024-959-473
; Sequence 473, Application US/11024959
; Publication No. US20060010516A1
; GENERAL INFORMATION:
;  APPLICANT: FORSTER, RICHARD L.
;  APPLICANT:  CONNETT, MARIE B.
;  APPLICANT:  EMERSON, SARAH JANE
;  APPLICANT:  GRIGOR, MURRAY ROBERT
;  APPLICANT:  HIGGINS, COLLEEN M.
;  APPLICANT:  LUND, STEVEN TROY
;  APPLICANT:  MAGUSIN, ANDREAS
;  APPLICANT:  KODRZYCKI, BOB
;  TITLE OF INVENTION: CELL CYCLE GENES AND RELATED METHODS
;  FILE REFERENCE: 044463-0360
```

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;  CURRENT APPLICATION NUMBER: US/11/024,959
;  CURRENT FILING DATE:  2004-12-30
;  PRIOR APPLICATION NUMBER: 60/533,036
;  PRIOR FILING DATE: 2003-12-30
;  NUMBER OF SEQ ID NOS: 782
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 473
;   LENGTH: 353
;   TYPE: PRT
;   ORGANISM: Pinus radiata
US-11-024-959-473

  Query Match             72.1%;  Score 31;  DB 7;  Length 353;
  Best Local Similarity   71.4%;  Pred. No. 86;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              || | ||
Db         46 WTVTAHT 52


RESULT 23
US-10-203-486-10
; Sequence 10, Application US/10203486
; Publication No. US20060035315A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  YUE, Henry
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  POLICKY, Jennifer L.
;  APPLICANT:  NGUYEN, Danniel B.
;  APPLICANT:  AU-YOUNG, Janice
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  KHAN, Farrah A.
;  APPLICANT:  WALIA, Narinder K.
;  APPLICANT:  GANDHI, Ameena R.
;  APPLICANT:  TRIBOULEY, Cathernie M.
;  APPLICANT:  PATTERSON, Chandra
;  APPLICANT:  THORNTON, Michael
;  APPLICANT:  GREENE, Barrie D.
;  APPLICANT:  HERNANDEZ, Roberto
;  APPLICANT:  BOROWSKY, Mark L.
;  APPLICANT:  SANJANWALA, Madhu S.
;  TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
;  FILE REFERENCE: PI-0042 PCT
;  CURRENT APPLICATION NUMBER: US/10/203,486
;  CURRENT FILING DATE:  2002-08-08
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PERL Program
; SEQ ID NO 10
;   LENGTH: 473
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 4297813CD1
US-10-203-486-10

  Query Match             72.1%;  Score 31;  DB 6;  Length 473;
  Best Local Similarity   71.4%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||  |||
Db         10 WTVRRHT 16


RESULT 24
US-10-755-092-7
; Sequence 7, Application US/10755092
; Publication No. US20060021095A1
;   GENERAL INFORMATION:
;       APPLICANT: Koziel, Michael G.
;                  Desai, Nalini M.
;                  Lewis, Kelly S.
;                  Kramer, Vance C.
;                  Warren, Gregory W.
;                  Evola, Stephen V.
;                  Crossland, Lyle D.
;                  Wright, Martha S.
;                  Merlin, Ellis J.
;                  Launis, Karen L.
;       TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
;                           INSECTICIDAL ACTIVITY IN MAIZE
;       NUMBER OF SEQUENCES: 94
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Syngenta Biotechnology, Inc.
;            STREET: 3054 Cornwallis Road
;            CITY: Research Triangle Park
;            STATE: NC
;            COUNTRY: USA
;            ZIP: 27709
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/755,092
;            FILING DATE: 08-Jan-2004
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/988,462
;            FILING DATE: 20-Nov-2001
;            APPLICATION NUMBER: US 09/547,422
;            FILING DATE: 11-APR-2000
;            APPLICATION NUMBER: US 08/459,504
;            FILING DATE: 02-JUN-1995
;            APPLICATION NUMBER: US 07/951,715
;            FILING DATE: 25-SEP-1992
;            APPLICATION NUMBER: US 07/772,027
;            FILING DATE: 04-OCT-1991
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Meigs, J. Timothy
;            REGISTRATION NUMBER: 38,241
;            REFERENCE/DOCKET NUMBER: S-18805I
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (919)541-8587
;            TELEFAX: (919)541-8689
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1207 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-755-092-7

  Query Match             72.1%;  Score 31;  DB 6;  Length 1207;
  Best Local Similarity   66.7%;  Pred. No. 2.6e+02;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTRH 6
              |::|||
Db        319 WSNTRH 324


RESULT 25
US-11-096-568A-21041
; Sequence 21041, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
```

```
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 21041
;   LENGTH: 153
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(153)
;   OTHER INFORMATION: Ceres Seq. ID no. 12400451
US-11-096-568A-21041

  Query Match             69.8%;  Score 30;  DB 7;  Length 153;
  Best Local Similarity   71.4%;  Pred. No. 63;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              |||:| |
Db         65 WTSSRST 71


RESULT 26
US-11-096-568A-25833
; Sequence 25833, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25833
;   LENGTH: 185
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(185)
;   OTHER INFORMATION: Ceres Seq. ID no. 15222925
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (86)..(86)
;   OTHER INFORMATION: Xaa is any aa, unknown or other
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (99)..(99)
;   OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-25833

  Query Match             69.8%;  Score 30;  DB 7;  Length 185;
  Best Local Similarity   100.0%;  Pred. No. 74;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WTSTR 5
              |||||
Db        169 WTSTR 173


RESULT 27
US-10-467-657-2812
; Sequence 2812, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2812
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2812

  Query Match             69.8%;  Score 30;  DB 6;  Length 210;
  Best Local Similarity   71.4%;  Pred. No. 83;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||  |||
Db         85 WTVFRHT 91


RESULT 28
US-11-096-568A-18747
; Sequence 18747, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18747
;   LENGTH: 314
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(314)
;   OTHER INFORMATION: Ceres Seq. ID no. 12366913
US-11-096-568A-18747

  Query Match             69.8%;  Score 30;  DB 7;  Length 314;
  Best Local Similarity   57.1%;  Pred. No. 1.2e+02;
  Matches    4;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | |::||
Db         68 WPSSKHT 74


RESULT 29
US-11-096-568A-18746
; Sequence 18746, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18746
;   LENGTH: 420
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(420)
;   OTHER INFORMATION: Ceres Seq. ID no. 12366912
```

US-11-096-568A-18746

Query Match 69.8%; Score 30; DB 7; Length 420;
Best Local Similarity 57.1%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 WTSTRHT 7
              | |::||
Db        174 WPSSKHT 180
```

RESULT 30
US-11-096-568A-18745
; Sequence 18745, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18745
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(427)
; OTHER INFORMATION: Ceres Seq. ID no. 12366911
US-11-096-568A-18745

Query Match 69.8%; Score 30; DB 7; Length 427;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 WTSTRHT 7
              | |::||
Db        181 WPSSKHT 187
```

RESULT 31
US-11-087-099-10693
; Sequence 10693, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 10693
; LENGTH: 435
; TYPE: PRT
; ORGANISM: Zea mays
US-11-087-099-10693

Query Match 69.8%; Score 30; DB 7; Length 435;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 WTSTRH 6
              | :|||
Db        126 WATTRH 131
```

RESULT 32
US-11-087-099-5390
; Sequence 5390, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5390
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Oryza sativa
US-11-087-099-5390

Query Match 69.8%; Score 30; DB 7; Length 437;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 WTSTRH 6
              | :|||
Db        124 WATTRH 129
```

RESULT 33
US-10-510-386-32
; Sequence 32, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
; APPLICANT: Andersen, Jens Tonne
; APPLICANT: Clausen, Ib Groth
; APPLICANT: Jorgensen, Steen Troels
; APPLICANT: Olsen, Peter Bjarke
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: Improved Bacillus Host Cell
; FILE REFERENCE: 10294.204-US
; CURRENT APPLICATION NUMBER: US/10/510,386
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 248
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 645
; TYPE: PRT
; ORGANISM: Bacillus licheniformis
US-10-510-386-32

Query Match 69.8%; Score 30; DB 6; Length 645;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 WTSTRH 6
              || |:|
Db        547 WTMTKH 552
```

RESULT 34
US-10-501-035-214
; Sequence 214, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASES
; TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 214
; LENGTH: 4544
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-214

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  Query Match             69.8%;  Score 30;  DB 6;  Length 4544;
  Best Local Similarity   53.8%;  Pred. No. 1.3e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    6;  Gaps    1;

Qy          1 WTS------TRHT 7
              |||       ||||
Db       2299 WTSYTTSTITRHT 2311


RESULT 35
US-11-076-427A-32
; Sequence 32, Application US/11076427A
; Publication No. US20060025338A1
; GENERAL INFORMATION:
;  APPLICANT: Alitalo, et al.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OF LYMPHATIC AND VENOU
;  TITLE OF INVENTION:  VESSEL ARTERIALIZATION
;  FILE REFERENCE: 28967/40008A
;  CURRENT APPLICATION NUMBER: US/11/076,427A
;  CURRENT FILING DATE:  2005-03-08
;  PRIOR APPLICATION NUMBER: US 60/551,581
;  PRIOR FILING DATE: 2004-03-08
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
;   LENGTH: 4544
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-076-427A-32

  Query Match             69.8%;  Score 30;  DB 7;  Length 4544;
  Best Local Similarity   53.8%;  Pred. No. 1.3e+03;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    6;  Gaps    1;

Qy          1 WTS------TRHT 7
              |||       ||||
Db       2299 WTSYTTSTITRHT 2311


RESULT 36
US-10-467-657-7398
; Sequence 7398, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 7398
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7398

  Query Match             67.4%;  Score 29;  DB 6;  Length 38;
  Best Local Similarity   57.1%;  Pred. No. 28;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | | ||:
Db          7 WASVRHS 13


RESULT 37
US-10-467-657-1750
; Sequence 1750, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1750
;   LENGTH: 48
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1750

  Query Match             67.4%;  Score 29;  DB 6;  Length 48;
  Best Local Similarity   57.1%;  Pred. No. 35;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              | | ||:
Db          7 WASVRHS 13


RESULT 38
US-11-097-812-52
; Sequence 52, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
;   LENGTH: 108
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-52

  Query Match             67.4%;  Score 29;  DB 7;  Length 108;
  Best Local Similarity   71.4%;  Pred. No. 71;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              : |||||
Db         49 YASTRHT 55
```

```
RESULT 39
US-11-097-812-38
; Sequence 38, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-38

  Query Match             67.4%;  Score 29;  DB 7;  Length 115;
  Best Local Similarity   71.4%;  Pred. No. 75;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              : |||||
Db         49 YASTRHT 55


RESULT 40
US-11-087-099-4793
; Sequence 4793, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 4793
;   LENGTH: 166
;   TYPE: PRT
;   ORGANISM: Pyrococcus furiosus DSM 3638
US-11-087-099-4793

  Query Match             67.4%;  Score 29;  DB 7;  Length 166;
  Best Local Similarity   66.7%;  Pred. No. 1e+02;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRH 6
              | |:||
Db        145 WVSSRH 150


RESULT 41
US-11-096-568A-11521
; Sequence 11521, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11521
;   LENGTH: 184
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(184)
;   OTHER INFORMATION: Ceres Seq. ID no. 15219207
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (73)..(73)
;   OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-11521

  Query Match             67.4%;  Score 29;  DB 7;  Length 184;
  Best Local Similarity   71.4%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||| | |
Db          2 WTSCRQT 8


RESULT 42
US-11-096-568A-11520
; Sequence 11520, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11520
;   LENGTH: 193
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(193)
;   OTHER INFORMATION: Ceres Seq. ID no. 15219206
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (82)..(82)
;   OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-11520

  Query Match             67.4%;  Score 29;  DB 7;  Length 193;
  Best Local Similarity   71.4%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||| | |
Db         11 WTSCRQT 17


RESULT 43
US-11-096-568A-20894
; Sequence 20894, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
```

```
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20894
;   LENGTH: 210
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(210)
;   OTHER INFORMATION: Ceres Seq. ID no. 12390165
US-11-096-568A-20894

  Query Match             67.4%;  Score 29;  DB 7;  Length 210;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRH 6
              |  |||
Db         41 WNKTRH 46


RESULT 44
US-11-087-099-11293
; Sequence 11293, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 11293
;   LENGTH: 216
;   TYPE: PRT
;   ORGANISM: Salmonella typhimurium LT2
US-11-087-099-11293

  Query Match             67.4%;  Score 29;  DB 7;  Length 216;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRH 6
              ||: ||
Db         69 WTTDRH 74


RESULT 45
US-11-087-099-5492
; Sequence 5492, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5492
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Oryza sativa
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(251)
;   OTHER INFORMATION: unsure at all Xaa locations
US-11-087-099-5492

  Query Match             67.4%;  Score 29;  DB 7;  Length 251;
  Best Local Similarity   57.1%;  Pred. No. 1.5e+02;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              || | |:
Db          8 WTRTHHS 14


RESULT 46
US-11-096-568A-20893
; Sequence 20893, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 20893
;   LENGTH: 277
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(277)
;   OTHER INFORMATION: Ceres Seq. ID no. 12390164
US-11-096-568A-20893

  Query Match             67.4%;  Score 29;  DB 7;  Length 277;
  Best Local Similarity   66.7%;  Pred. No. 1.6e+02;
  Matches    4;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRH 6
              |  |||
Db        108 WNKTRH 113


RESULT 47
US-11-096-568A-11519
; Sequence 11519, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11519
;   LENGTH: 317
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(317)
;   OTHER INFORMATION: Ceres Seq. ID no. 15219205
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (206)..(206)
;   OTHER INFORMATION: Xaa is any aa, unknown or other
US-11-096-568A-11519

  Query Match             67.4%;  Score 29;  DB 7;  Length 317;
  Best Local Similarity   71.4%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||| | |
Db        135 WTSCRQT 141


RESULT 48
US-11-087-099-1450
; Sequence 1450, Application US/11087099
```

```
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1450
;   LENGTH: 350
;   TYPE: PRT
;   ORGANISM: Streptomyces nogalater
US-11-087-099-1450

  Query Match            67.4%;  Score 29;  DB 7;  Length 350;
  Best Local Similarity   66.7%;  Pred. No. 2e+02;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WTSTRH 6
              |:| ||
Db        276 WSSVRH 281


RESULT 49
US-10-508-263-68
; Sequence 68, Application US/10508263
; Publication No. US20050260754A1
; GENERAL INFORMATION:
;  APPLICANT: BASF Plant Science GmbH
;  TITLE OF INVENTION: Constructs and methods for regulating gene expression
;  FILE REFERENCE: 53262-20085.00
;  CURRENT APPLICATION NUMBER: US/10/508,263
;  CURRENT FILING DATE:  2004-09-20
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-508-263-68

  Query Match            67.4%;  Score 29;  DB 6;  Length 451;
  Best Local Similarity   57.1%;  Pred. No. 2.5e+02;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||:  ||
Db        334 WTANAHT 340


RESULT 50
US-10-508-263-70
; Sequence 70, Application US/10508263
; Publication No. US20050260754A1
; GENERAL INFORMATION:
;  APPLICANT: BASF Plant Science GmbH
;  TITLE OF INVENTION: Constructs and methods for regulating gene expression
;  FILE REFERENCE: 53262-20085.00
;  CURRENT APPLICATION NUMBER: US/10/508,263
;  CURRENT FILING DATE:  2004-09-20
;  NUMBER OF SEQ ID NOS: 126
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
;   LENGTH: 451
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
US-10-508-263-70

  Query Match            67.4%;  Score 29;  DB 6;  Length 451;
  Best Local Similarity   57.1%;  Pred. No. 2.5e+02;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 WTSTRHT 7
              ||:  ||
Db        334 WTANAHT 340


Search completed: March 23, 2006, 02:52:58
Job time : 11.9452 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:40:10 ; Search time 69.589 Seconds
(without alignments)
50.511 Million cell updates/sec

Title: US-10-755-382-22
Perfect score: 41
Sequence: 1 QQYSLYRS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	100.0	8	2	AAR97315	Aar97315 Humanised
2	41	100.0	8	8	ADM95104	Adm95104 Murine MN
3	41	100.0	8	8	ADM98313	Adm98313 Humanised
4	41	100.0	106	2	AAR97337	Aar97337 Humanised
5	41	100.0	106	2	AAR97335	Aar97335 Murine NE
6	41	100.0	106	8	ADM95097	Adm95097 Murine MN
7	41	100.0	106	8	ADM95100	Adm95100 Humanised
8	41	100.0	106	8	ADM98320	Adm98320 Murine MN
9	41	100.0	106	8	ADM98322	Adm98322 Humanised
10	41	100.0	115	6	ABR42756	Abr42756 Anti-CEA
11	41	100.0	232	6	ABG76490	Abg76490 Light cha
12	41	100.0	232	7	ADE64204	Ade64204 MN14LC pr
13	41	100.0	232	7	ADF60817	Adf60817 hMN-14 li
14	41	100.0	256	6	ABR42757	Abr42757 Anti-CEA
15	41	100.0	257	6	ABR42758	Abr42758 Anti-CEA
16	41	100.0	261	6	ABR42289	Abr42289 Diabody 6
17	41	100.0	261	6	ABR42754	Abr42754 Anti-CEA
18	41	100.0	261	6	ABR83645	Abr83645 hMN14-scF
19	41	100.0	262	6	ABR42295	Abr42295 Bispecifi
20	41	100.0	262	6	ABR42293	Abr42293 Bispecifi
21	41	100.0	262	6	ABR42298	Abr42298 Bispecifi
22	41	100.0	262	6	ABR42290	Abr42290 Diabody h
23	41	100.0	262	6	ABR42291	Abr42291 Bispecifi
24	41	100.0	358	8	ADU26571	Adu26571 Chimeric
25	41	100.0	363	8	ADU26561	Adu26561 Chimeric
26	41	100.0	364	8	ADU26570	Adu26570 Chimeric
27	41	100.0	370	8	ADU26560	Adu26560 Chimeric
28	41	100.0	391	6	ABR83649	Abr83649 TS1 VL ch
29	41	100.0	443	6	ABG76488	Abg76488 Humanised
30	41	100.0	443	6	ABG74240	Abg74240 Chimaeric
31	41	100.0	669	9	ADY97271	Ady97271 Exemplary
32	33	80.5	79	3	AAB43069	Aab43069 Human ORF
33	33	80.5	368	3	AAB43084	Aab43084 Human ORF
34	33	80.5	393	7	ADJ70573	Adj70573 Human hea
35	33	80.5	640	4	AAM93645	Aam93645 Human pol
36	33	80.5	640	8	ADL31470	Adl31470 Human pro
37	33	80.5	731	8	ADR10222	Adr10222 Human pro
38	33	80.5	1025	4	AAB93899	Aab93899 Human pro
39	33	80.5	1025	5	ABB75711	Abb75711 Human pol
40	33	80.5	1025	9	ADY18562	Ady18562 PRO polyp
41	33	80.5	1040	9	ABM91906	Abm91906 M. xanthu
42	32	78.0	8	5	AAU72808	Aau72808 TRA-8 lig
43	32	78.0	8	6	AAO29876	Aao29876 Mouse ant
44	32	78.0	8	7	ADJ79794	Adj79794 TRA-8 lig
45	32	78.0	107	6	ABP58451	Abp58451 Humanised
46	32	78.0	107	6	ABP58449	Abp58449 Humanised
47	32	78.0	107	6	ABP58450	Abp58450 Humanised
48	32	78.0	212	5	AAU72815	Aau72815 DNA encod
49	32	78.0	212	6	AAO29883	Aao29883 LM1 fusio
50	32	78.0	212	7	ADJ79836	Adj79836 LM1-type
51	32	78.0	213	5	AAU72810	Aau72810 TRA-8 lig
52	32	78.0	213	5	AAU72819	Aau72819 DNA encod
53	32	78.0	213	5	AAU72818	Aau72818 DNA encod
54	32	78.0	213	5	AAU72817	Aau72817 DNA encod
55	32	78.0	213	5	AAU72816	Aau72816 DNA encod
56	32	78.0	213	6	AAO29886	Aao29886 LM5 fusio
57	32	78.0	213	6	AAO29878	Aao29878 LM2 fusio
58	32	78.0	213	6	AAO29884	Aao29884 LM3 fusio
59	32	78.0	213	6	AAO29887	Aao29887 LM6 fusio
60	32	78.0	213	6	AAO29885	Aao29885 LM4 fusio
61	32	78.0	213	7	ADJ79838	Adj79838 LM4-type
62	32	78.0	213	7	ADJ79837	Adj79837 LM3-type
63	32	78.0	213	7	ADJ79810	Adj79810 Humanized
64	32	78.0	213	7	ADJ79839	Adj79839 LM5-type
65	32	78.0	213	7	ADJ79840	Adj79840 LM6-type
66	32	78.0	234	5	AAU72802	Aau72802 TRA-8 lig
67	32	78.0	234	6	AAO29870	Aao29870 Mouse ant
68	32	78.0	234	7	ADJ79788	Adj79788 TRA-8 ant
69	32	78.0	364	4	ABB69876	Abb69876 Drosophil
70	32	78.0	414	7	ADF07152	Adf07152 Bacterial
71	32	78.0	722	4	ABB60747	Abb60747 Drosophil
72	31	75.6	72	6	ABU11354	Abu11354 Protein e
73	31	75.6	104	8	ADS44269	Ads44269 Bacterial
74	31	75.6	110	6	ADA34605	Ada34605 Acinetoba
75	31	75.6	192	4	ABB70679	Abb70679 Drosophil
76	31	75.6	268	6	ABU40461	Abu40461 Protein e
77	31	75.6	277	7	ADF07952	Adf07952 Bacterial
78	31	75.6	446	9	ADZ74344	Adz74344 Drosophil
79	31	75.6	446	9	AEB55415	Aeb55415 Drosophil
80	31	75.6	447	4	ABB63609	Abb63609 Drosophil
81	31	75.6	1033	6	ABR52728	Abr52728 Protein s
82	31	75.6	1033	7	ADK61964	Adk61964 Disease t
83	31	75.6	1083	2	AAY25169	Aay25169 Human RSC
84	31	75.6	1083	6	ABP98334	Abp98334 Amino aci
85	31	75.6	1083	8	ADU60236	Adu60236 Housekeep
86	31	75.6	1083	9	ADX05791	Adx05791 Cyclin-de
87	31	75.6	1160	4	ABG28234	Abg28234 Novel hum
88	31	75.6	1444	8	ADN61347	Adn61347 Paenibaci
89	31	75.6	1444	8	ADR21520	Adr21520 Paenibaci
90	31	75.6	1541	2	AAW33361	Aaw33361 Rat canal
91	30	73.2	194	5	ABB06807	Abb06807 Human nGP
92	30	73.2	214	5	ABB76125	Abb76125 Recombina
93	30	73.2	316	9	ABM92264	Abm92264 M. xanthu
94	30	73.2	324	8	ADS29217	Ads29217 Bacterial
95	30	73.2	363	9	AEA19988	Aea19988 Novel hum
96	30	73.2	456	4	ABG27995	Abg27995 Novel hum
97	30	73.2	522	9	AEA63536	Aea63536 C. lauren

98	30	73.2	522	9	AEB04153
99	30	73.2	805	7	ADF07615
100	30	73.2	1290	2	AAW98269
101	30	73.2	1290	8	ADU05610
102	30	73.2	1296	2	AAR41198
103	29	70.7	12	7	ADC44765
104	29	70.7	72	6	ABP79175
105	29	70.7	90	5	ABJ05387
106	29	70.7	102	2	AAY36896
107	29	70.7	105	4	ABG27151
108	29	70.7	107	4	ABG27152
109	29	70.7	156	4	ABB10699
110	29	70.7	156	4	AAM92997
111	29	70.7	184	7	ADF77049
112	29	70.7	207	6	ABU27972
113	29	70.7	217	6	AAE35235
114	29	70.7	218	6	AAE35238
115	29	70.7	221	6	AAE35237
116	29	70.7	222	6	AAE35239
117	29	70.7	222	6	AAE35236
118	29	70.7	226	3	AAG34439
119	29	70.7	226	6	AAE35234
120	29	70.7	236	5	AAO19236
121	29	70.7	236	6	AAE35232
122	29	70.7	236	6	AAE35233
123	29	70.7	237	6	ABR53357
124	29	70.7	237	7	ADK63396
125	29	70.7	238	6	AAE35241
126	29	70.7	243	3	AAG34438
127	29	70.7	252	9	AEB40784
128	29	70.7	265	6	ABM69559
129	29	70.7	267	9	AEB37470
130	29	70.7	273	9	AEB03438
131	29	70.7	273	9	AEA79341
132	29	70.7	285	4	ABG07524
133	29	70.7	288	7	ADH85694
134	29	70.7	289	2	AAW20569
135	29	70.7	289	2	AAW82548
136	29	70.7	289	3	AAB04173
137	29	70.7	289	8	ADP24404
138	29	70.7	289	9	ADV91570
139	29	70.7	306	6	ABM69568
140	29	70.7	310	3	AAY96296
141	29	70.7	310	8	ADL13078
142	29	70.7	345	5	ABP69768
143	29	70.7	367	8	ADX74777
144	29	70.7	375	4	ABG27153
145	29	70.7	379	8	ABM84661
146	29	70.7	385	4	AAE10199
147	29	70.7	394	2	AAW20710
148	29	70.7	395	7	ADH87335
149	29	70.7	416	9	AEB42281
150	29	70.7	419	9	AEB40003
151	29	70.7	421	9	AEB36278
152	29	70.7	423	9	AEB36611
153	29	70.7	427	2	AAW69231
154	29	70.7	427	7	ADG46570
155	29	70.7	427	8	ADR28644
156	29	70.7	431	2	AAW62781
157	29	70.7	431	2	AAW62778
158	29	70.7	439	2	AAW82546
159	29	70.7	439	2	AAW53464
160	29	70.7	439	2	AAW62777
161	29	70.7	439	3	AAB04171
162	29	70.7	439	8	ADO24389
163	29	70.7	439	8	ADP23998
164	29	70.7	439	9	ADV91566
165	29	70.7	439	9	ADW38513
166	29	70.7	439	9	AEA23627
167	29	70.7	445	4	AAM78722
168	29	70.7	445	6	ABJ25933
169	29	70.7	445	6	ABP57342
170	29	70.7	445	9	ADY20645

Aeb04153	Cryptococ
Adf07615	Bacterial
Aaw98269	H. pylori
Adu05610	H. pylori
Aar41198	CT. 3/200
Adc44765	Endotheli
Abp79175	N. gonorr
Abj05387	Caenorhab
Aay36896	Protein i
Abg27151	Novel hum
Abg27152	Novel hum
Abb10699	Human pan
Aam92997	Human dig
Adf77049	Novel hum
Abu27972	Protein e
Aae35235	Cryptococ
Aae35238	Cryptococ
Aae35237	Cryptococ
Aae35239	Cryptococ
Aae35236	Cryptococ
Aag34439	Arabidops
Aae35234	Cryptococ
Aao19236	Human LIR
Aae35232	Cryptococ
Aae35233	Cryptococ
Abr53357	Protein s
Adk63396	Disease t
Aae35241	Cryptococ
Aag34438	Arabidops
Aeb40784	L. pneumo
Abm69559	Photorhab
Aeb37470	L. pneumo
Aeb03438	Haemophil
Aea79341	Novel H.
Abg07524	Novel hum
Adh85694	Enterococ
Aaw20569	H. pylori
Aaw82548	Human LIR
Aab04173	Leukocyte
Adp24404	PRO polyp
Adv91570	Leukocyte
Abm69568	Photorhab
Aay96296	Human IGF
Adl13078	Human ste
Abp69768	Human pol
Adx74777	Plant ful
Abg27153	Novel hum
Abm84661	Human dia
Aae10199	Human bon
Aaw20710	H. pylori
Adh87335	Enterococ
Aeb42281	L. pneumo
Aeb40003	L. pneumo
Aeb36278	L. pneumo
Aeb36611	L. pneumo
Aaw69231	FcR-I pro
Adg46570	Human Fc
Adr28644	Human Fc
Aaw62781	Protein e
Aaw62778	Protein e
Aaw82546	Human LIR
Aaw53464	Human gp4
Aaw62777	Protein e
Aab04171	Leukocyte
Ado24389	Human PRO
Adp23998	PRO polyp
Adv91566	Leukocyte
Adw38513	Immunomod
Aea23627	Human PRO
Aam78722	Human pro
Abj25933	Aspergill
Abp57342	Human sec
Ady20645	PRO polyp

171	29	70.7	473	4	ABG27154
172	29	70.7	477	6	ABU40091
173	29	70.7	478	4	ABG27155
174	29	70.7	480	4	AAU33686
175	29	70.7	480	6	ABU15661
176	29	70.7	487	8	ADJ48555
177	29	70.7	489	2	AAW82549
178	29	70.7	489	3	AAB04174
179	29	70.7	489	8	ADJ48629
180	29	70.7	489	8	ADP24066
181	29	70.7	489	9	ADV91572
182	29	70.7	509	7	ABO74436
183	29	70.7	510	8	ADM67221
184	29	70.7	532	7	ADM26827
185	29	70.7	541	8	ADY14129
186	29	70.7	545	5	ABP66300
187	29	70.7	556	8	ABM82529
188	29	70.7	564	8	ADQ66631
189	29	70.7	593	7	ABM85957
190	29	70.7	596	8	ADX95115
191	29	70.7	597	6	ABU09632
192	29	70.7	597	8	ADP24382
193	29	70.7	598	2	AAW82547
194	29	70.7	598	3	AAB04172
195	29	70.7	598	7	ABR44280
196	29	70.7	598	8	ADP24046
197	29	70.7	598	9	ADV91568
198	29	70.7	605	6	ADA54509
199	29	70.7	615	2	AAW62780
200	29	70.7	615	2	AAW62779
201	29	70.7	619	8	ABM82530
202	29	70.7	635	3	AAY53888
203	29	70.7	649	7	ADC01266
204	29	70.7	650	2	AAW82544
205	29	70.7	650	3	AAB04169
206	29	70.7	650	8	ADL83062
207	29	70.7	650	8	ADR14195
208	29	70.7	650	9	ADV91560
209	29	70.7	651	2	AAW62782
210	29	70.7	651	7	ADF90906
211	29	70.7	652	2	AAW82545
212	29	70.7	652	3	AAB04170
213	29	70.7	652	9	ADV91562
214	29	70.7	654	8	ADN02616
215	29	70.7	654	8	ADQ65760
216	29	70.7	680	6	ADB23150
217	29	70.7	680	7	ADD30304
218	29	70.7	680	8	ADI44209
219	29	70.7	699	4	ABB68965
220	29	70.7	723	7	ADK67247
221	29	70.7	914	6	ABP98919
222	29	70.7	982	4	ABB64431
223	29	70.7	1381	6	ABP76824
224	29	70.7	1381	6	ABP78598
225	29	70.7	1589	8	ADP18469
226	29	70.7	1759	5	ABP69142
227	29	70.7	1767	6	ABU00719
228	29	70.7	1767	6	ABP81319
229	29	70.7	1767	8	ADK47460
230	29	70.7	1767	8	ADT50082
231	29	70.7	1767	9	ADY03847
232	29	70.7	1767	9	AEB91662
233	29	70.7	1769	8	ADR95041
234	29	70.7	1769	9	AEA58911
235	29	70.7	1902	4	ABB65387
236	28	68.3	9	2	AAY47857
237	28	68.3	48	4	ABB60117
238	28	68.3	51	3	AAG01743
239	28	68.3	90	5	ABP29189
240	28	68.3	92	2	AAY85796
241	28	68.3	92	6	ABU01849
242	28	68.3	92	8	ADK46989
243	28	68.3	94	5	ABB53895

Abg27154	Novel hum
Abu40091	Protein e
Abg27155	Novel hum
Aau33686	Pseudomon
Abu15661	Protein e
Adj48555	Oil-assoc
Aaw82549	Human LIR
Aab04174	Leukocyte
Adj48629	Oil-assoc
Adp24066	PRO polyp
Adv91572	Leukocyte
Abo74436	Pseudomon
Adm67221	Human adi
Adm26827	Hyperther
Ady14129	Plant ful
Abp66300	Bifidobac
Abm82529	Human dia
Adq66631	Novel hum
Abm85957	Rice abio
Adx95115	Plant ful
Abu09632	Human mon
Adp24382	PRO polyp
Aaw82547	Human LIR
Aab04172	Leukocyte
Abr44280	Human leu
Adp24046	PRO polyp
Adv91568	Leukocyte
Ada54509	Human pro
Aaw62780	Protein e
Aaw62779	Protein e
Abm82530	Human dia
Aay53888	A suppres
Adc01266	Enterohae
Aaw82544	Human LIR
Aab04169	Leukocyte
Adl83062	Human PRO
Adr14195	Human NF-
Adv91560	Leukocyte
Aaw62782	Protein e
Adf90906	Human hep
Aaw82545	Human LIR
Aab04170	Leukocyte
Adv91562	Leukocyte
Adn02616	Liver dis
Adq65760	Novel hum
Adb23150	Environme
Add30304	Plant yie
Adi44209	Plant tra
Abb68965	Drosophil
Adk67247	Human can
Abp98919	Human mol
Abb64431	Drosophil
Abp76824	N. gonorr
Abp78598	N. gonorr
Adp18469	S pneumon
Abp69142	Human pol
Abu00719	S. pneumo
Abp81319	Streptoco
Adk47460	Streptoco
Adt50082	S_pneumon
Ady03847	Streptoco
Aeb91662	Microbial
Adr95041	Novel S.
Aea58911	Streptoco
Abb65387	Drosophil
Aay47857	Immunogen
Abb60117	Drosophil
Aag01743	Human sec
Abp29189	Streptoco
Aay85796	S. pneumo
Abu01849	S. pneumo
Adk46989	Streptoco
Abb53895	Lactococc

244	28	68.3	96	8	ADY13163	Ady13163	Plant ful
245	28	68.3	97	8	ADX92455	Adx92455	Plant ful
246	28	68.3	99	9	AEA32788	Aea32788	HTH_AraC
247	28	68.3	101	4	AAE01825	Aae01825	Human gen
248	28	68.3	101	4	AAE04124	Aae04124	Human gen
249	28	68.3	101	5	ABG64172	Abg64172	Human alb
250	28	68.3	101	5	ABG64364	Abg64364	Human alb
251	28	68.3	101	8	ADL77437	Adl77437	Albumin f
252	28	68.3	101	8	ADL77631	Adl77631	Albumin f
253	28	68.3	105	4	AAO03172	Aao03172	Human pol
254	28	68.3	109	2	AAR40956	Aar40956	Human ger
255	28	68.3	110	8	ADN72179	Adn72179	Thale cre
256	28	68.3	111	4	ABB66515	Abb66515	Drosophil
257	28	68.3	141	6	ABU02436	Abu02436	S. pneumo
258	28	68.3	141	8	ADK47141	Adk47141	Streptoco
259	28	68.3	147	8	ADR95748	Adr95748	Novel S.
260	28	68.3	147	9	AEA59618	Aea59618	Streptoco
261	28	68.3	149	6	ABU40551	Abu40551	Protein e
262	28	68.3	150	8	ADP07875	Adp07875	Human sec
263	28	68.3	159	4	ABB60102	Abb60102	Drosophil
264	28	68.3	159	4	ABB59680	Abb59680	Drosophil
265	28	68.3	159	4	ABB66590	Abb66590	Drosophil
266	28	68.3	167	7	ADF05503	Adf05503	Bacterial
267	28	68.3	170	2	AAY08890	Aay08890	A. thalia
268	28	68.3	172	8	ADY12741	Ady12741	Plant ful
269	28	68.3	178	4	AAB99860	Aab99860	Physcomit
270	28	68.3	186	1	AAP90417	Aap90417	Plasmodiu
271	28	68.3	200	6	ABO00651	Abo00651	Novel hum
272	28	68.3	215	4	AAG81717	Aag81717	S. epider
273	28	68.3	227	8	ADY11724	Ady11724	Plant ful
274	28	68.3	229	2	AAW55404	Aaw55404	H. pylori
275	28	68.3	229	2	AAW55628	Aaw55628	H. pylori
276	28	68.3	230	8	ADS29980	Ads29980	Bacterial
277	28	68.3	236	6	AAE35240	Aae35240	Cryptococ
278	28	68.3	238	8	ADS41784	Ads41784	Bacterial
279	28	68.3	242	8	ADX71222	Adx71222	Plant ful
280	28	68.3	244	8	ADT57497	Adt57497	Plant pol
281	28	68.3	245	8	ADT56865	Adt56865	Plant pol
282	28	68.3	255	8	ADY22900	Ady22900	Plant ful
283	28	68.3	265	8	ADQ66394	Adq66394	Novel hum
284	28	68.3	270	2	AAW55727	Aaw55727	H. pylori
285	28	68.3	270	2	AAW98205	Aaw98205	H. pylori
286	28	68.3	270	2	AAY17200	Aay17200	H. pylori
287	28	68.3	271	3	AAG50452	Aag50452	Arabidops
288	28	68.3	273	4	ADM20107	Adm20107	Protein e
289	28	68.3	288	3	AAG50451	Aag50451	Arabidops
290	28	68.3	294	7	ADF07357	Adf07357	Bacterial
291	28	68.3	297	3	AAG50450	Aag50450	Arabidops
292	28	68.3	306	4	ABB65928	Abb65928	Drosophil
293	28	68.3	310	6	ABM68572	Abm68572	Photorhab
294	28	68.3	314	8	ADN08342	Adn08342	3T3 cell
295	28	68.3	317	6	ABM70767	Abm70767	Staphyloc
296	28	68.3	349	7	ADC94287	Adc94287	E. faeciu
297	28	68.3	351	8	ADN21155	Adn21155	Bacterial
298	28	68.3	354	5	ABP73242	Abp73242	Candida a
299	28	68.3	354	8	ADS45223	Ads45223	Bacterial
300	28	68.3	358	7	ABO60672	Abo60672	Klebsiell
301	28	68.3	366	8	ADS30689	Ads30689	Bacterial
302	28	68.3	372	7	ADD68137	Add68137	Plant GnT
303	28	68.3	376	4	AAG78660	Aag78660	Beta-tran
304	28	68.3	376	8	ADX82420	Adx82420	Human bet
305	28	68.3	377	9	ABM94734	Abm94734	M. xanthu
306	28	68.3	382	8	ADX92507	Adx92507	Plant ful
307	28	68.3	384	5	AAE28167	Aae28167	Human RET
308	28	68.3	385	6	ABM73371	Abm73371	Staphyloc
309	28	68.3	385	7	ABM90139	Abm90139	Rice abio
310	28	68.3	385	7	ABM87422	Abm87422	Rice abio
311	28	68.3	396	4	AAU27683	Aau27683	Mouse ful
312	28	68.3	396	8	ABM82271	Abm82271	Tumour-as
313	28	68.3	404	8	ADQ19228	Adq19228	Human sof
314	28	68.3	406	5	ABJ11094	Abj11094	Yeast sel
315	28	68.3	410	6	ADA55232	Ada55232	Human pro
316	28	68.3	410	8	ABM84738	Abm84738	Human dia
317	28	68.3	422	4	ABB61986	Abb61986	Drosophil
318	28	68.3	427	3	AAG22179	Aag22179	Arabidops
319	28	68.3	429	4	AAB36588	Aab36588	Human FLE
320	28	68.3	444	3	AAG22178	Aag22178	Arabidops
321	28	68.3	446	2	AAY08889	Aay08889	Tobacco G
322	28	68.3	454	3	AAG22177	Aag22177	Arabidops
323	28	68.3	469	8	ADS14887	Ads14887	Pseudomon
324	28	68.3	472	8	ADQ37049	Adq37049	Cell prol
325	28	68.3	476	4	AAM39720	Aam39720	Human pol
326	28	68.3	476	5	AAE28163	Aae28163	Human RET
327	28	68.3	476	6	ABP58348	Abp58348	Human cel
328	28	68.3	476	7	ADB65505	Adb65505	Human pro
329	28	68.3	478	4	ADM19864	Adm19864	Protein e
330	28	68.3	489	4	AAM41506	Aam41506	Human pol
331	28	68.3	493	6	ABM67023	Abm67023	Photorhab
332	28	68.3	502	5	AAE28168	Aae28168	Human RET
333	28	68.3	509	7	ABO81497	Abo81497	Pseudomon
334	28	68.3	512	5	AAE28164	Aae28164	Human RET
335	28	68.3	530	7	ABM87757	Abm87757	Rice abio
336	28	68.3	543	7	ADC03366	Adc03366	Rice flow
337	28	68.3	543	7	ABM87494	Abm87494	Rice abio
338	28	68.3	575	5	ABP27731	Abp27731	Streptoco
339	28	68.3	576	7	ADF04705	Adf04705	Bacterial
340	28	68.3	594	5	ABP35609	Abp35609	Fungal ZB
341	28	68.3	624	5	ABP73446	Abp73446	Candida a
342	28	68.3	687	4	AAM38788	Aam38788	Human pol
343	28	68.3	687	4	AAG67138	Aag67138	Amino aci
344	28	68.3	695	9	ADZ02800	Adz02800	Wheat sta
345	28	68.3	697	8	ADN61375	Adn61375	Paenibaci
346	28	68.3	698	4	AAM40574	Aam40574	Human pol
347	28	68.3	700	6	ABU24605	Abu24605	Protein e
348	28	68.3	713	4	ABB70890	Abb70890	Drosophil
349	28	68.3	757	7	ABO77172	Abo77172	Pseudomon
350	28	68.3	763	6	ADB12177	Adb12177	Alloiococ
351	28	68.3	764	7	ADJ69070	Adj69070	Human hea
352	28	68.3	764	7	ABM85709	Abm85709	Human pro
353	28	68.3	764	8	ABO84904	Abo84904	Human can
354	28	68.3	765	6	ADB12175	Adb12175	Alloiococ
355	28	68.3	789	2	AAR47519	Aar47519	EHV-4 rib
356	28	68.3	799	2	AAW19212	Aaw19212	Corn star
357	28	68.3	799	2	AAW56489	Aaw56489	Zea mays
358	28	68.3	799	7	ABW02050	Abw02050	Maize sta
359	28	68.3	825	2	AAR60811	Aar60811	Rice star
360	28	68.3	829	9	ADZ02803	Adz02803	BArley st
361	28	68.3	849	4	ABU53175	Abu53175	Human tra
362	28	68.3	855	5	AAU76219	Aau76219	Wheat sta
363	28	68.3	855	9	ADZ02802	Adz02802	Wheat sta
364	28	68.3	871	2	AAW70895	Aaw70895	Maize bra
365	28	68.3	878	8	ADS42750	Ads42750	Bacterial
366	28	68.3	878	8	ADN17821	Adn17821	Bacterial
367	28	68.3	879	6	ABM68626	Abm68626	Photorhab
368	28	68.3	892	7	ADF08029	Adf08029	Bacterial
369	28	68.3	953	7	ADC37587	Adc37587	Human nuc
370	28	68.3	979	7	ABM85708	Abm85708	Mouse pro
371	28	68.3	1063	5	ABP35715	Abp35715	Fungal ZB
372	28	68.3	1066	5	ABB48876	Abb48876	Listeria
373	28	68.3	1066	6	ABU32802	Abu32802	Protein e
374	28	68.3	1068	5	ABP35714	Abp35714	Fungal ZB
375	28	68.3	1068	7	ADK63116	Adk63116	Disease t
376	28	68.3	1166	3	AAB18268	Aab18268	Plasmodiu
377	28	68.3	2208	8	ADN72815	Adn72815	Thale cre
378	28	68.3	2570	4	ABG06375	Abg06375	Novel hum
379	27	65.9	8	8	ADK09496	Adk09496	Human pap
380	27	65.9	8	8	ADK09495	Adk09495	Human pap
381	27	65.9	9	2	AAY47692	Aay47692	Immunogen
382	27	65.9	9	5	AAU76520	Aau76520	Anti-Inte
383	27	65.9	9	5	AAE19662	Aae19662	Human tum
384	27	65.9	9	5	AAE15818	Aae15818	Human mAb
385	27	65.9	9	8	ADK09540	Adk09540	Human pap
386	27	65.9	9	8	ADK09541	Adk09541	Human pap
387	27	65.9	9	8	ADK09542	Adk09542	Human pap
388	27	65.9	9	8	ADN68413	Adn68413	Human 273
389	27	65.9	9	8	ADN69501	Adn69501	Human 273

390	27	65.9	9	8	ADN66612
391	27	65.9	9	8	ADN66895
392	27	65.9	9	8	ADN66869
393	27	65.9	9	8	ADN66127
394	27	65.9	9	8	ADN68450
395	27	65.9	9	8	ADQ07651
396	27	65.9	9	9	ADX26938
397	27	65.9	10	2	AAY47707
398	27	65.9	10	7	ADW30604
399	27	65.9	10	7	ADW32629
400	27	65.9	10	7	ADW30913
401	27	65.9	10	8	ADK09610
402	27	65.9	10	8	ADN66254
403	27	65.9	10	8	ADN66970
404	27	65.9	10	8	ADN69913
405	27	65.9	10	8	ADN66695
406	27	65.9	10	8	ADN69856
407	27	65.9	10	8	ADN66682
408	27	65.9	10	8	ADN67000
409	27	65.9	10	8	ADN66964
410	27	65.9	15	8	ADN71699
411	27	65.9	15	8	ADN71310
412	27	65.9	15	8	ADN71312
413	27	65.9	15	8	ADN71491
414	27	65.9	15	8	ADN71005
415	27	65.9	15	8	ADN71139
416	27	65.9	15	8	ADN70607
417	27	65.9	15	8	ADN71311
418	27	65.9	15	8	ADN71680
419	27	65.9	15	8	ADN70633
420	27	65.9	15	8	ADN71718
421	27	65.9	15	8	ADN70725
422	27	65.9	15	8	ADN71490
423	27	65.9	15	8	ADN71681
424	27	65.9	15	8	ADU68094
425	27	65.9	15	9	ADV11484
426	27	65.9	20	2	AAR15544
427	27	65.9	43	8	ADN04720
428	27	65.9	46	4	AAM95048
429	27	65.9	46	4	ABB95754
430	27	65.9	48	5	ABJ10314
431	27	65.9	48	6	ADA98217
432	27	65.9	48	6	ADA44063
433	27	65.9	48	7	ADC20382
434	27	65.9	48	7	ADF10711
435	27	65.9	49	4	AAB64895
436	27	65.9	53	4	AAM19202
437	27	65.9	53	4	AAM14372
438	27	65.9	53	4	ABB33320
439	27	65.9	53	4	ABB38409
440	27	65.9	53	4	AAM31847
441	27	65.9	53	4	AAM26785
442	27	65.9	53	4	ABB28145
443	27	65.9	53	4	ABB18780
444	27	65.9	53	4	ABB23587
445	27	65.9	53	4	AAM71549
446	27	65.9	53	4	AAM66499
447	27	65.9	53	4	AAM54109
448	27	65.9	53	4	AAM59019
449	27	65.9	53	4	ABG53231
450	27	65.9	53	4	ABG48169
451	27	65.9	53	4	AAM02101
452	27	65.9	53	5	ABG41360
453	27	65.9	53	5	ABG36151
454	27	65.9	54	4	AAG76153
455	27	65.9	55	3	AAG28141
456	27	65.9	62	4	AAM16237
457	27	65.9	62	4	ABB35218
458	27	65.9	62	4	AAM28727
459	27	65.9	62	4	ABB30047
460	27	65.9	62	4	ABB20659
461	27	65.9	62	4	AAM68422
462	27	65.9	62	4	AAM56050

Adn66612	Human 273
Adn66895	Human 273
Adn66869	Human 273
Adn66127	Human 273
Adn68450	Human 273
Adq07651	Light cha
Adx26938	Murine mo
Aay47707	Immunogen
Adw30604	HLA bindi
Adw32629	HLA bindi
Adw30913	HLA bindi
Adk09610	Human pap
Adn66254	Human 273
Adn66970	Human 273
Adn69913	Human 273
Adn66695	Human 273
Adn69856	Human 273
Adn66682	Human 273
Adn67000	Human 273
Adn66964	Human 273
Adn71699	Human 273
Adn71310	Human 273
Adn71312	Human 273
Adn71491	Human 273
Adn71005	Human 273
Adn71139	Human 273
Adn70607	Human 273
Adn71311	Human 273
Adn71680	Human 273
Adn70633	Human 273
Adn71718	Human 273
Adn70725	Human 273
Adn71490	Human 273
Adn71681	Human 273
Adu68094	Human pap
Adv11484	HPV type
Aar15544	Immunopep
Adn04720	Antipsori
Aam95048	Human rep
Abb95754	Human tes
Abj10314	Human lun
Ada98217	Human sec
Ada44063	Human sec
Adc20382	Human sec
Adf10711	Human sec
Aab64895	Human sec
Aam19202	Peptide #
Aam14372	Peptide #
Abb33320	Peptide #
Abb38409	Peptide #
Aam31847	Peptide #
Aam26785	Peptide #
Abb28145	Human pep
Abb18780	Protein #
Abb23587	Protein #
Aam71549	Human bon
Aam66499	Human bon
Aam54109	Human bra
Aam59019	Human bra
Abg53231	Human liv
Abg48169	Human liv
Aam02101	Peptide #
Abg41360	Human pep
Abg36151	Human pep
Aag76153	Human col
Aag28141	Arabidops
Aam16237	Peptide #
Abb35218	Peptide #
Aam28727	Peptide #
Abb30047	Peptide #
Abb20659	Protein #
Aam68422	Human bon
Aam56050	Human bra

463	27	65.9	62	4	ABG50094
464	27	65.9	62	4	AAM03967
465	27	65.9	62	5	ABG37995
466	27	65.9	64	4	AAM21990
467	27	65.9	64	4	ABB44368
468	27	65.9	64	4	AAM38336
469	27	65.9	64	4	ABB27225
470	27	65.9	64	4	AAM78109
471	27	65.9	64	4	AAM65434
472	27	65.9	64	4	ABG59741
473	27	65.9	64	5	ABG47120
474	27	65.9	66	4	AAU63413
475	27	65.9	66	6	ABM59932
476	27	65.9	73	7	ADC00790
477	27	65.9	73	8	ADR16173
478	27	65.9	76	7	ABO66991
479	27	65.9	79	7	ADC01150
480	27	65.9	80	2	AAR70741
481	27	65.9	80	2	AAW18386
482	27	65.9	80	8	ADR16169
483	27	65.9	83	8	ADR16171
484	27	65.9	83	8	ADX92035
485	27	65.9	90	9	AEB39792
486	27	65.9	93	5	ABP02067
487	27	65.9	96	3	AAG01103
488	27	65.9	97	3	AAG59052
489	27	65.9	99	9	AEB36377
490	27	65.9	100	4	ABG26990
491	27	65.9	101	5	ABP04111
492	27	65.9	104	2	AAR81795
493	27	65.9	107	2	AAW01591
494	27	65.9	107	5	AAE19664
495	27	65.9	107	5	AAE19665
496	27	65.9	107	5	AAE15812
497	27	65.9	107	9	ADX27047
498	27	65.9	107	9	ADX27048
499	27	65.9	108	5	AAU76522
500	27	65.9	108	5	AAE19684
501	27	65.9	108	5	ABP51464
502	27	65.9	108	8	ADQ07679
503	27	65.9	108	9	ADX27051
504	27	65.9	116	3	AAG58394
505	27	65.9	119	3	AAG59050
506	27	65.9	121	7	ABO64177
507	27	65.9	123	2	AAR86317
508	27	65.9	123	2	AAW23784
509	27	65.9	123	2	AAW31574
510	27	65.9	123	2	AAW42317
511	27	65.9	123	2	AAW33739
512	27	65.9	123	2	AAW69305
513	27	65.9	123	2	AAW40120
514	27	65.9	123	2	AAY29437
515	27	65.9	123	3	AAY77742
516	27	65.9	123	3	AAB30299
517	27	65.9	123	6	ABU13776
518	27	65.9	123	6	ABU59489
519	27	65.9	123	7	AAE39072
520	27	65.9	129	8	ADQ65796
521	27	65.9	133	9	AEA20996
522	27	65.9	134	6	ABU07056
523	27	65.9	137	4	ABG02934
524	27	65.9	148	4	AAB93762
525	27	65.9	148	7	ADB64748
526	27	65.9	148	8	ADO44081
527	27	65.9	148	9	AEA98536
528	27	65.9	150	5	ABB53776
529	27	65.9	154	3	AAG39746
530	27	65.9	154	3	AAG24830
531	27	65.9	157	5	ABB54740
532	27	65.9	170	4	AAG74676
533	27	65.9	182	7	ADC87179
534	27	65.9	182	7	ADC86921
535	27	65.9	182	7	ADC87083

Abg50094	Human liv
Aam03967	Peptide #
Abg37995	Human pep
Aam21990	Peptide #
Abb44368	Peptide #
Aam38336	Peptide #
Abb27225	Protein #
Aam78109	Human bon
Aam65434	Human bra
Abg59741	Human liv
Abg47120	Human pep
Aau63413	Propionib
Abm59932	Propionib
Adc00790	Enterohae
Adr16173	Escherich
Abo66991	Klebsiell
Adc01150	Enterohae
Aar70741	PrgI gene
Aaw18386	S. typhim
Adr16169	Salmonell
Adr16171	Shigella
Adx92035	Plant ful
Aeb39792	L. pneumo
Abp02067	Human ORF
Aag01103	Human sec
Aag59052	Arabidops
Aeb36377	L. pneumo
Abg26990	Novel hum
Abp04111	Human ORF
Aar81795	Y/A-Dex i
Aaw01591	Lead bind
Aae19664	Human TNF
Aae19665	Human TNF
Aae15812	Human mAb
Adx27047	Human gro
Adx27048	Human gro
Aau76522	Anti-Inte
Aae19684	Mouse-hum
Abp51464	Human MDD
Adq07679	Amino aci
Adx27051	Murine hT
Aag58394	Arabidops
Aag59050	Arabidops
Abo64177	Klebsiell
Aar86317	Anti-IL-8
Aaw23784	Monoclona
Aaw31574	Anti IL-8
Aaw42317	Anti IL-8
Aaw33739	Anti IL-8
Aaw69305	Murine an
Aaw40120	Murine mo
Aay29437	Murine 5.
Aay77742	Murine an
Aab30299	Murine an
Abu13776	Mouse ant
Abu59489	Mouse ant
Aae39072	Murine 5.
Adq65796	Novel hum
Aea20996	Novel hum
Abu07056	Maize SSI
Abg02934	Novel hum
Aab93762	Human pro
Adb64748	Human pro
Ado44081	Amino aci
Aea98536	HPV (onco
Abb53776	Lactococc
Aag39746	Arabidops
Aag24830	Arabidops
Abb54740	Lactococc
Aag74676	Human col
Adc87179	Human GPC
Adc86921	Human GPC
Adc87083	Human GPC

536	27	65.9	184	7	ADD25203	Add25203 Fertility
537	27	65.9	184	8	ADN61218	Adn61218 Radish nu
538	27	65.9	186	9	AEB40988	Aeb40988 L. pneumo
539	27	65.9	186	9	AEB37677	Aeb37677 L. pneumo
540	27	65.9	187	2	AAW74826	Aaw74826 Human sec
541	27	65.9	187	5	ABG95277	Abg95277 Human nov
542	27	65.9	187	6	ABU50599	Abu50599 Protein e
543	27	65.9	187	6	ABO34471	Abo34471 Region of
544	27	65.9	187	7	ADI23132	Adi23132 Novel hum
545	27	65.9	187	8	ADH74134	Adh74134 Human sec
546	27	65.9	191	4	AAG92124	Aag92124 C glutami
547	27	65.9	196	8	ADQ66007	Adq66007 Novel hum
548	27	65.9	201	6	ABU47512	Abu47512 Protein e
549	27	65.9	201	6	ABU45503	Abu45503 Protein e
550	27	65.9	205	4	ADM19838	Adm19838 Protein e
551	27	65.9	208	8	ADK90585	Adk90585 Grafted l
552	27	65.9	208	8	ADL13415	Adl13415 Mouse-der
553	27	65.9	209	5	ABB79323	Abb79323 Human ova
554	27	65.9	212	6	ABP70661	Abp70661 Murine in
555	27	65.9	214	5	AAE19696	Aae19696 Antibody
556	27	65.9	214	7	ADE01486	Ade01486 CDP870 li
557	27	65.9	214	8	ADF73140	Adf73140 Humanized
558	27	65.9	214	8	ADH34232	Adh34232 Anti-huma
559	27	65.9	214	8	ADQ07672	Adq07672 Amino aci
560	27	65.9	214	9	ADX27044	Adx27044 Murine hT
561	27	65.9	220	7	ADM04612	Adm04612 Human pro
562	27	65.9	220	9	AEA20005	Aea20005 Novel hum
563	27	65.9	222	3	AAG44306	Aag44306 Arabidops
564	27	65.9	222	8	ADX95336	Adx95336 Plant ful
565	27	65.9	223	8	ADT57875	Adt57875 Plant pol
566	27	65.9	224	3	AAG39745	Aag39745 Arabidops
567	27	65.9	224	3	AAG24829	Aag24829 Arabidops
568	27	65.9	231	2	AAW55421	Aaw55421 H. pylori
569	27	65.9	234	7	ADH87199	Adh87199 Enterococ
570	27	65.9	237	2	AAR86319	Aar86319 Anti-IL-8
571	27	65.9	237	2	AAW23786	Aaw23786 Chimeric
572	27	65.9	237	2	AAW31576	Aaw31576 Chimeric
573	27	65.9	237	2	AAW42319	Aaw42319 Murine va
574	27	65.9	237	2	AAW33741	Aaw33741 Chimeric
575	27	65.9	237	2	AAW69307	Aaw69307 Anti-IL-8
576	27	65.9	237	2	AAW40122	Aaw40122 Mab 5.12.
577	27	65.9	237	2	AAY29446	Aay29446 5.12.14 L
578	27	65.9	237	3	AAY77744	Aay77744 Chimeric
579	27	65.9	237	3	AAB30301	Aab30301 5-12-14 a
580	27	65.9	237	3	AAB01405	Aab01405 Human TAN
581	27	65.9	237	6	ABU13778	Abu13778 Mouse ant
582	27	65.9	237	6	ABU59491	Abu59491 Mouse ant
583	27	65.9	237	7	AAE39074	Aae39074 Murine 5.
584	27	65.9	243	6	ADA54106	Ada54106 Human pro
585	27	65.9	243	7	ADC37297	Adc37297 Nuclear f
586	27	65.9	246	2	AAR45021	Aar45021 Staphyloc
587	27	65.9	246	4	AAB67348	Aab67348 Staphyloc
588	27	65.9	246	5	ABB76244	Abb76244 Staphyloc
589	27	65.9	247	4	ABG03644	Abg03644 Novel hum
590	27	65.9	250	4	AAM39822	Aam39822 Human pol
591	27	65.9	259	5	ABU51104	Abu51104 Helicobac
592	27	65.9	260	5	ABB88997	Abb88997 Babesia m
593	27	65.9	260	7	ADE06125	Ade06125 BMNI-rela
594	27	65.9	260	9	AEB40616	Aeb40616 L. pneumo
595	27	65.9	267	3	AAG44305	Aag44305 Arabidops
596	27	65.9	268	5	ABB88983	Abb88983 Babesia m
597	27	65.9	268	7	ADE06072	Ade06072 BMNI-rela
598	27	65.9	271	9	ABM95103	Abm95103 M. xanthu
599	27	65.9	272	9	AEB37292	Aeb37292 L. pneumo
600	27	65.9	278	4	ABB64991	Abb64991 Drosophil
601	27	65.9	278	6	AAE30104	Aae30104 Drosophil
602	27	65.9	278	9	AEB53785	Aeb53785 Drosophil
603	27	65.9	280	2	AAW55412	Aaw55412 H. pylori
604	27	65.9	281	9	ADZ10391	Adz10391 P. gingiv
605	27	65.9	294	6	ABU16035	Abu16035 Protein e
606	27	65.9	294	6	ABM72932	Abm72932 Staphyloc
607	27	65.9	296	3	AAG24612	Aag24612 Arabidops
608	27	65.9	299	4	AAG81333	Aag81333 Human AFP
609	27	65.9	301	7	ABM85876	Abm85876 Mouse pro
610	27	65.9	302	4	ADM20102	Adm20102 Protein e
611	27	65.9	306	8	ADN23463	Adn23463 Bacterial
612	27	65.9	309	5	ABU51642	Abu51642 Helicobac
613	27	65.9	313	7	ABO79672	Abo79672 Pseudomon
614	27	65.9	317	3	AAG44304	Aag44304 Arabidops
615	27	65.9	321	6	ABU08146	Abu08146 Soluble t
616	27	65.9	328	3	AAG24611	Aag24611 Arabidops
617	27	65.9	328	8	ADO29603	Ado29603 Mouse GPC
618	27	65.9	328	8	ADX97282	Adx97282 Plant ful
619	27	65.9	329	7	ABM85766	Abm85766 Mouse pro
620	27	65.9	330	7	ABO84159	Abo84159 Pseudomon
621	27	65.9	335	2	AAW21007	Aaw21007 H. pylori
622	27	65.9	338	5	ABP64812	Abp64812 Human pro
623	27	65.9	338	8	ADS98773	Ads98773 Protein f
624	27	65.9	338	8	ADS98775	Ads98775 Protein f
625	27	65.9	339	4	AAB64853	Aab64853 Gene 36 h
626	27	65.9	339	4	AAB64854	Aab64854 Human sec
627	27	65.9	339	6	ABP81683	Abp81683 Human pur
628	27	65.9	339	7	ADE36533	Ade36533 Human G-p
629	27	65.9	339	8	ADO29602	Ado29602 Human GPC
630	27	65.9	339	8	ADP44342	Adp44342 Human P2Y
631	27	65.9	339	8	ADR48963	Adr48963 Human G p
632	27	65.9	339	8	ADS98129	Ads98129 Protein f
633	27	65.9	339	8	ADS84361	Ads84361 Human G p
634	27	65.9	339	9	ADY19220	Ady19220 PRO polyp
635	27	65.9	340	7	ADF42450	Adf42450 Human PP5
636	27	65.9	344	2	AAW54370	Aaw54370 G-protein
637	27	65.9	344	8	ADP55122	Adp55122 Human PRO
638	27	65.9	351	5	ABB92218	Abb92218 Herbicida
639	27	65.9	351	8	ADR88992	Adr88992 A. thalia
640	27	65.9	352	7	ADC31412	Adc31412 Human nov
641	27	65.9	353	7	ADF59158	Adf59158 Human pol
642	27	65.9	354	2	AAY35690	Aay35690 Chlamydia
643	27	65.9	354	3	AAG24610	Aag24610 Arabidops
644	27	65.9	356	7	ADC96659	Adc96659 E. faeciu
645	27	65.9	356	8	ADS98128	Ads98128 Protein f
646	27	65.9	356	8	ADX90361	Adx90361 Plant ful
647	27	65.9	358	8	ADP55727	Adp55727 Human PRO
648	27	65.9	360	7	ABM85877	Abm85877 Human pro
649	27	65.9	362	8	ADY12133	Ady12133 Plant ful
650	27	65.9	364	6	ADA34095	Ada34095 Acinetoba
651	27	65.9	366	7	ADE08077	Ade08077 Novel pro
652	27	65.9	366	8	ADS98830	Ads98830 Protein f
653	27	65.9	366	9	ADU40447	Adu40447 Novel hum
654	27	65.9	375	8	ADR09748	Adr09748 Human pro
655	27	65.9	376	2	AAW55644	Aaw55644 H. pylori
656	27	65.9	376	7	ADC97286	Adc97286 E. faeciu
657	27	65.9	377	6	ABO01325	Abo01325 Human pro
658	27	65.9	379	2	AAR53699	Aar53699 Sequence
659	27	65.9	379	5	ABB80029	Abb80029 Soybean m
660	27	65.9	379	9	ADY79698	Ady79698 Soybean m
661	27	65.9	387	4	AAE13429	Aae13429 Soybean m
662	27	65.9	387	6	ABR58240	Abr58240 Protein #
663	27	65.9	388	2	AAY37126	Aay37126 Protein i
664	27	65.9	388	7	ABO66334	Abo66334 Klebsiell
665	27	65.9	390	6	ADA33626	Ada33626 Acinetoba
666	27	65.9	392	8	ADX75311	Adx75311 Plant ful
667	27	65.9	396	3	AAB12144	Aab12144 Hydrophob
668	27	65.9	396	7	ADC37291	Adc37291 Nuclear f
669	27	65.9	396	9	ADY17023	Ady17023 PRO polyp
670	27	65.9	397	4	AAB60502	Aab60502 Human cel
671	27	65.9	398	2	AAR15614	Aar15614 Human typ
672	27	65.9	398	2	AAR42061	Aar42061 Lymphobla
673	27	65.9	398	2	AAR60617	Aar60617 Human typ
674	27	65.9	398	2	AAR85480	Aar85480 Human typ
675	27	65.9	398	2	AAW59267	Aaw59267 Human Typ
676	27	65.9	398	3	AAB51719	Aab51719 Human sec
677	27	65.9	398	3	AAB51720	Aab51720 Human sec
678	27	65.9	398	3	AAB37792	Aab37792 Human int
679	27	65.9	398	3	AAG48142	Aag48142 Arabidops
680	27	65.9	398	4	AAM24185	Aam24185 Human EST
681	27	65.9	398	4	AAB50081	Aab50081 Human IL-

682	27	65.9	398	5	AAU78089	Aau78089 Human int
683	27	65.9	398	5	AAE16581	Aae16581 Human int
684	27	65.9	398	5	ABB08207	Abb08207 Human typ
685	27	65.9	398	6	ABU62118	Abu62118 Human typ
686	27	65.9	398	6	ABR41897	Abr41897 Human typ
687	27	65.9	398	6	ABO01326	Abo01326 Human pro
688	27	65.9	398	6	ABU63658	Abu63658 Human typ
689	27	65.9	398	7	ADB31977	Adb31977 Human int
690	27	65.9	398	7	ADC78815	Adc78815 Human PRO
691	27	65.9	398	7	ADD48331	Add48331 Human Pro
692	27	65.9	398	8	ADF94065	Adf94065 Human IL-
693	27	65.9	398	8	ADG47219	Adg47219 Human typ
694	27	65.9	398	8	ADN96024	Adn96024 Human NOV
695	27	65.9	398	8	ADP12396	Adp12396 Protein e
696	27	65.9	398	8	ADP23857	Adp23857 PRO polyp
697	27	65.9	398	8	ADU06634	Adu06634 Novel bro
698	27	65.9	398	9	ADZ25542	Adz25542 Human IL-
699	27	65.9	398	9	AEA04511	Aea04511 Human pro
700	27	65.9	406	8	ADR09028	Adr09028 Human pro
701	27	65.9	406	9	AEA19966	Aea19966 Novel hum
702	27	65.9	407	2	AAW55290	Aaw55290 H. pylori
703	27	65.9	407	2	AAW20652	Aaw20652 H. pylori
704	27	65.9	409	3	AAG53300	Aag53300 Arabidops
705	27	65.9	409	3	AAG26509	Aag26509 Arabidops
706	27	65.9	410	3	AAG53299	Aag53299 Arabidops
707	27	65.9	410	3	AAG26508	Aag26508 Arabidops
708	27	65.9	422	7	ADH87758	Adh87758 Enterococ
709	27	65.9	426	4	ABB63306	Abb63306 Drosophil
710	27	65.9	426	4	AAU38951	Aau38951 Drosophil
711	27	65.9	426	7	ADC35835	Adc35835 Drosophil
712	27	65.9	427	3	AAG26507	Aag26507 Arabidops
713	27	65.9	427	3	AAG53298	Aag53298 Arabidops
714	27	65.9	429	5	AAM47906	Aam47906 Human cel
715	27	65.9	430	8	ADX76244	Adx76244 Plant ful
716	27	65.9	433	3	AAG48141	Aag48141 Arabidops
717	27	65.9	436	8	ADQ65067	Adq65067 Novel hum
718	27	65.9	442	6	ABU11739	Abu11739 Human MDD
719	27	65.9	442	7	ADD43892	Add43892 Chlamydia
720	27	65.9	442	9	ADW29056	Adw29056 C_trachom
721	27	65.9	442	9	AEA19184	Aea19184 Chlamydia
722	27	65.9	444	8	ADY08784	Ady08784 Plant ful
723	27	65.9	448	3	AAB53201	Aab53201 Macaca mu
724	27	65.9	449	6	ABU02817	Abu02817 S. pneumo
725	27	65.9	449	8	ADK47666	Adk47666 Streptoco
726	27	65.9	450	6	ABB99407	Abb99407 Amino aci
727	27	65.9	451	6	ADA21145	Ada21145 Human sec
728	27	65.9	453	8	ADR95731	Adr95731 Novel S.
729	27	65.9	453	9	AEA59601	Aea59601 Streptoco
730	27	65.9	454	7	ABO66467	Abo66467 Klebsiell
731	27	65.9	466	5	ABP26809	Abp26809 Streptoco
732	27	65.9	466	8	ADV88252	Adv88252 Streptoco
733	27	65.9	466	8	ADV79505	Adv79505 Streptoco
734	27	65.9	466	8	ADV81676	Adv81676 Streptoco
735	27	65.9	467	3	AAY68964	Aay68964 Cps20 pro
736	27	65.9	475	5	AAE28165	Aae28165 Mouse RET
737	27	65.9	477	8	ADN20124	Adn20124 Bacterial
738	27	65.9	478	4	AAM93784	Aam93784 Human pol
739	27	65.9	478	6	ABB99402	Abb99402 Amino aci
740	27	65.9	478	8	ADL31769	Adl31769 Human pro
741	27	65.9	481	2	AAW55465	Aaw55465 H. pylori
742	27	65.9	481	2	AAY36805	Aay36805 Chlamydia
743	27	65.9	481	3	AAY88312	Aay88312 C. parvum
744	27	65.9	483	4	AAB69058	Aab69058 Pseudomon
745	27	65.9	483	4	AAB69059	Aab69059 Pseudomon
746	27	65.9	483	7	ABO77062	Abo77062 Pseudomon
747	27	65.9	483	8	ADS14941	Ads14941 Pseudomon
748	27	65.9	486	2	AAW55242	Aaw55242 H. pylori
749	27	65.9	489	7	ADJ70192	Adj70192 Human hea
750	27	65.9	491	7	ADC96488	Adc96488 E. faeciu
751	27	65.9	506	3	AAY57589	Aay57589 Human pap
752	27	65.9	508	8	ADX95785	Adx95785 Plant ful
753	27	65.9	518	5	AAE20715	Aae20715 Human Mls
754	27	65.9	518	5	AAE21016	Aae21016 Human Icr
755	27	65.9	521	4	ABB10141	Abb10141 Human cDN
756	27	65.9	521	5	ABP66728	Abp66728 Human pol
757	27	65.9	524	5	AAE20716	Aae20716 Human Mls
758	27	65.9	524	5	AAE21017	Aae21017 Human Icr
759	27	65.9	526	8	ADR08797	Adr08797 Human pro
760	27	65.9	527	5	ABB94365	Abb94365 Chlamydia
761	27	65.9	544	2	AAR87014	Aar87014 Xylanase
762	27	65.9	552	7	ABM86987	Abm86987 Rice abio
763	27	65.9	563	2	AAR10330	Aar10330 Gene prod
764	27	65.9	563	2	AAR47577	Aar47577 Lipase of
765	27	65.9	577	7	ADF70492	Adf70492 Orphan re
766	27	65.9	579	8	ADJ49723	Adj49723 Oil-assoc
767	27	65.9	581	8	ADN18371	Adn18371 Bacterial
768	27	65.9	584	8	ADJ49964	Adj49964 Oil-assoc
769	27	65.9	584	8	ADN18531	Adn18531 Bacterial
770	27	65.9	587	8	ADJ49093	Adj49093 Oil-assoc
771	27	65.9	588	4	ABB69947	Abb69947 Drosophil
772	27	65.9	589	8	ADJ49749	Adj49749 Oil-assoc
773	27	65.9	592	7	ADM26411	Adm26411 Hyperther
774	27	65.9	592	8	ADJ49500	Adj49500 Oil-assoc
775	27	65.9	593	8	ADJ50401	Adj50401 Oil-assoc
776	27	65.9	594	8	ADJ49283	Adj49283 Oil-assoc
777	27	65.9	594	8	ADS43017	Ads43017 Bacterial
778	27	65.9	600	7	ADC95980	Adc95980 E. faeciu
779	27	65.9	608	7	ADH87802	Adh87802 Enterococ
780	27	65.9	616	9	AEB36845	Aeb36845 L. pneumo
781	27	65.9	640	6	ABU47632	Abu47632 Protein e
782	27	65.9	640	6	ABU45411	Abu45411 Protein e
783	27	65.9	642	6	ABM70452	Abm70452 Photorhab
784	27	65.9	643	4	ABB71088	Abb71088 Drosophil
785	27	65.9	647	4	ABG02605	Abg02605 Novel hum
786	27	65.9	647	5	AAU76876	Aau76876 Human Eph
787	27	65.9	649	2	AAW12094	Aaw12094 Human pap
788	27	65.9	649	4	AAB98417	Aab98417 Human pap
789	27	65.9	649	7	ADF09513	Adf09513 Human pap
790	27	65.9	654	4	AAB92748	Aab92748 Human pro
791	27	65.9	654	4	AAB94348	Aab94348 Human pro
792	27	65.9	663	2	AAW71542	Aaw71542 Helicobac
793	27	65.9	663	7	ADM05301	Adm05301 Human pro
794	27	65.9	672	6	AAO31022	Aao31022 Actinobac
795	27	65.9	683	7	ABO77875	Abo77875 Pseudomon
796	27	65.9	691	8	ADX91170	Adx91170 Plant ful
797	27	65.9	692	6	ABO07175	Abo07175 Human p53
798	27	65.9	695	5	AAU76877	Aau76877 Human Eph
799	27	65.9	697	2	AAW55639	Aaw55639 H. pylori
800	27	65.9	697	2	AAW55638	Aaw55638 H. pylori
801	27	65.9	697	2	AAY17192	Aay17192 H. pylori
802	27	65.9	697	9	AEB91400	Aeb91400 Microbial
803	27	65.9	701	3	AAY51007	Aay51007 C. vicina
804	27	65.9	701	6	AAE30103	Aae30103 Drosophil
805	27	65.9	727	7	ADE15625	Ade15625 Human str
806	27	65.9	734	2	AAW98740	Aaw98740 H. pylori
807	27	65.9	743	6	ABB98845	Abb98845 Human NEP
808	27	65.9	743	6	ABB98852	Abb98852 Human Eph
809	27	65.9	746	3	AAY82742	Aay82742 DNA repli
810	27	65.9	749	6	ABB98855	Abb98855 Human Eph
811	27	65.9	757	4	AAG85017	Aag85017 Shrimp wh
812	27	65.9	761	8	ADU26323	Adu26323 CheA, a c
813	27	65.9	784	4	ABB71942	Abb71942 Drosophil
814	27	65.9	787	4	AAB96500	Aab96500 Putative
815	27	65.9	790	8	ADN48024	Adn48024 Thermococ
816	27	65.9	795	6	ABU11382	Abu11382 Protein e
817	27	65.9	817	4	AAB95119	Aab95119 Human pro
818	27	65.9	841	9	AEB91392	Aeb91392 Microbial
819	27	65.9	842	6	ABU31064	Abu31064 Protein e
820	27	65.9	843	9	ADW17328	Adw17328 E_grandis
821	27	65.9	847	8	ADR86343	Adr86343 Aspergill
822	27	65.9	852	8	ADJ34904	Adj34904 Xylanase
823	27	65.9	862	6	ABU19348	Abu19348 Protein e
824	27	65.9	871	6	ABU40547	Abu40547 Protein e
825	27	65.9	872	7	ADF05831	Adf05831 Bacterial
826	27	65.9	873	6	ADA55510	Ada55510 Human pro
827	27	65.9	874	9	AEB40795	Aeb40795 L. pneumo

828	27	65.9	877	4	ABB62624	Abb62624 Drosophil
829	27	65.9	877	9	AEB37481	Aeb37481 L. pneumo
830	27	65.9	899	4	ABG27691	Abg27691 Novel hum
831	27	65.9	915	7	ABW02188	Abw02188 Human IL-
832	27	65.9	915	7	ABW02191	Abw02191 Human IL-
833	27	65.9	915	8	ADU23489	Adu23489 Human IL-
834	27	65.9	915	8	ADU23483	Adu23483 Human IL-
835	27	65.9	915	9	AEA29322	Aea29322 Human int
836	27	65.9	915	9	AEA29316	Aea29316 Human int
837	27	65.9	917	7	ABW02193	Abw02193 Human IL-
838	27	65.9	917	7	ABW02192	Abw02192 Human IL-
839	27	65.9	917	7	ABW02190	Abw02190 Human IL-
840	27	65.9	917	7	ABW02189	Abw02189 Human IL-
841	27	65.9	917	8	ADU23491	Adu23491 Human IL-
842	27	65.9	917	8	ADU23485	Adu23485 Human IL-
843	27	65.9	917	8	ADU23493	Adu23493 Human IL-
844	27	65.9	917	8	ADU23487	Adu23487 Human IL-
845	27	65.9	917	9	AEA29318	Aea29318 Human int
846	27	65.9	917	9	AEA29320	Aea29320 Human int
847	27	65.9	917	9	AEA29326	Aea29326 Human int
848	27	65.9	917	9	AEA29324	Aea29324 Human int
849	27	65.9	922	9	AEB91114	Aeb91114 Lacticin
850	27	65.9	922	9	AEB91018	Aeb91018 Lantibiot
851	27	65.9	922	9	AEB90971	Aeb90971 Lantibiot
852	27	65.9	922	9	AEB90992	Aeb90992 Lantibiot
853	27	65.9	927	6	ABB98853	Abb98853 Human Eph
854	27	65.9	928	8	ADN19097	Adn19097 Bacterial
855	27	65.9	968	5	ABP73611	Abp73611 Candida a
856	27	65.9	974	5	AAU76874	Aau76874 Human Eph
857	27	65.9	994	7	ABM88179	Abm88179 Rice abio
858	27	65.9	1000	4	AAM47209	Aam47209 Human NOV
859	27	65.9	1000	8	ADH41721	Adh41721 Novel hum
860	27	65.9	1008	6	ABB98843	Abb98843 Human NEP
861	27	65.9	1008	8	ADM76028	Adm76028 Human bra
862	27	65.9	1009	4	AAU03553	Aau03553 Human pro
863	27	65.9	1009	5	AAE19158	Aae19158 Human kin
864	27	65.9	1018	8	ADH41719	Adh41719 Novel hum
865	27	65.9	1019	7	ADC39170	Adc39170 Novel hum
866	27	65.9	1019	8	ADH42567	Adh42567 Novel hum
867	27	65.9	1022	5	AAU76875	Aau76875 Human Eph
868	27	65.9	1037	4	ABB70288	Abb70288 Drosophil
869	27	65.9	1055	2	AAR70114	Aar70114 IL-1Rtype
870	27	65.9	1114	7	ADB70296	Adb70296 C. neofor
871	27	65.9	1126	4	ABG30229	Abg30229 Novel hum
872	27	65.9	1144	8	ADN25113	Adn25113 Bacterial
873	27	65.9	1150	8	ADN66025	Adn66025 Human 273
874	27	65.9	1248	8	ADN65928	Adn65928 Human 273
875	27	65.9	1250	8	ADN66004	Adn66004 Human 273
876	27	65.9	1250	8	ADN65918	Adn65918 Human 273
877	27	65.9	1250	8	ADN65907	Adn65907 Human 273
878	27	65.9	1250	8	ADN65919	Adn65919 Human 273
879	27	65.9	1250	8	ADN65920	Adn65920 Human 273
880	27	65.9	1250	8	ADN65916	Adn65916 Human 273
881	27	65.9	1263	4	AAB94749	Aab94749 Human pro
882	27	65.9	1287	2	AAR79944	Aar79944 Helicobac
883	27	65.9	1288	2	AAW55547	Aaw55547 H. pylori
884	27	65.9	1288	2	AAW55685	Aaw55685 H. pylori
885	27	65.9	1288	6	ABU31128	Abu31128 Protein e
886	27	65.9	1288	9	AEB91383	Aeb91383 Microbial
887	27	65.9	1313	4	ABB63904	Abb63904 Drosophil
888	27	65.9	1369	9	ADY65554	Ady65554 S. manson
889	27	65.9	1400	6	ABP96237	Abp96237 Human nuc
890	27	65.9	1423	9	AEB41771	Aeb41771 L. pneumo
891	27	65.9	1429	8	ADN23166	Adn23166 Bacterial
892	27	65.9	1438	9	AEB38521	Aeb38521 L. pneumo
893	27	65.9	1466	5	ABP74105	Abp74105 Human TRI
894	27	65.9	1497	2	AAR99390	Aar99390 Human 030
895	27	65.9	1497	2	AAW26666	Aaw26666 Human tum
896	27	65.9	1497	3	AAY76914	Aay76914 Alternati
897	27	65.9	1497	4	AAE05107	Aae05107 Human hom
898	27	65.9	1497	5	AAU96921	Aau96921 Human foh
899	27	65.9	1497	5	AAG66131	Aag66131 Human foh
900	27	65.9	1497	5	AAE13594	Aae13594 Human foh
901	27	65.9	1497	7	ADF13137	Adf13137 Human foh
902	27	65.9	1497	8	ADS64533	Ads64533 Human foh
903	27	65.9	1497	8	ADV09669	Adv09669 Human foh
904	27	65.9	1497	9	ADZ66370	Adz66370 Human foh
905	27	65.9	1502	4	AAM39273	Aam39273 Human pol
906	27	65.9	1533	2	AAR99391	Aar99391 Human 030
907	27	65.9	1533	2	AAW26667	Aaw26667 Human tum
908	27	65.9	1533	3	AAY76913	Aay76913 Human foh
909	27	65.9	1533	3	AAY95438	Aay95438 Mouse mel
910	27	65.9	1533	4	AAE05108	Aae05108 Human hom
911	27	65.9	1533	5	AAU96922	Aau96922 Human foh
912	27	65.9	1533	5	AAG66132	Aag66132 Human foh
913	27	65.9	1533	5	ABU60992	Abu60992 Lung spec
914	27	65.9	1533	5	AAM51862	Aam51862 Human mel
915	27	65.9	1533	5	AAE13595	Aae13595 Splice fo
916	27	65.9	1533	5	ABB07820	Abb07820 Human mel
917	27	65.9	1533	5	AAE20712	Aae20712 Human Mls
918	27	65.9	1533	5	AAE21013	Aae21013 Human Icr
919	27	65.9	1533	7	ADC83409	Adc83409 Human mel
920	27	65.9	1533	7	ADF13139	Adf13139 Human foh
921	27	65.9	1533	8	ADO28691	Ado28691 Human NLS
922	27	65.9	1533	8	ADP18679	Adp18679 Human pro
923	27	65.9	1533	8	ADS64535	Ads64535 Human foh
924	27	65.9	1533	8	ADT93464	Adt93464 Human LTR
925	27	65.9	1533	8	ADU22950	Adu22950 Melastati
926	27	65.9	1533	8	ADV09671	Adv09671 Human foh
927	27	65.9	1533	9	ADV66236	Adv66236 Melastati
928	27	65.9	1533	9	ADZ66372	Adz66372 Human foh
929	27	65.9	1564	8	ADS43994	Ads43994 Bacterial
930	27	65.9	1565	4	AAM41059	Aam41059 Human pol
931	27	65.9	1610	4	ABB63784	Abb63784 Drosophil
932	27	65.9	1626	7	ABM85249	Abm85249 Human pro
933	27	65.9	1662	5	ABB93630	Abb93630 Herbicida
934	27	65.9	1664	8	ADO19404	Ado19404 Human PRO
935	27	65.9	1664	8	ABM81178	Abm81178 Tumour-as
936	27	65.9	1664	9	ADX05747	Adx05747 Cyclin-de
937	27	65.9	1664	9	ADY15167	Ady15167 PRO polyp
938	27	65.9	1840	4	ABB61463	Abb61463 Drosophil
939	27	65.9	1858	5	ABB90859	Abb90859 Herbicida
940	27	65.9	1963	5	ABB93446	Abb93446 Herbicida
941	27	65.9	2000	8	ADL83166	Adl83166 Human PRO
942	27	65.9	2205	8	ADU07874	Adu07874 Amino aci
943	27	65.9	2278	3	AAY53677	Aay53677 Sequence
944	27	65.9	2281	4	AAM40857	Aam40857 Human pol
945	27	65.9	2408	6	ABU70437	Abu70437 Human adi
946	27	65.9	2458	4	AAM39071	Aam39071 Human pol
947	27	65.9	2458	4	AAU28088	Aau28088 Novel hum
948	27	65.9	2541	9	AEB96985	Aeb96985 BtD pepti
949	27	65.9	2870	7	ADN95178	Adn95178 Human BEC
950	27	65.9	2871	6	ABU07402	Abu07402 Protein d
951	27	65.9	2871	7	ADC35075	Adc35075 Human bre
952	27	65.9	2871	8	ADQ17802	Adq17802 Human sof
953	27	65.9	2918	4	ABG27218	Abg27218 Novel hum
954	27	65.9	2918	8	ADR66738	Adr66738 Human pro
955	27	65.9	2918	8	ADR66396	Adr66396 Human pro
956	27	65.9	3006	7	ADE40130	Ade40130 Human NOV
957	27	65.9	3262	3	AAY53675	Aay53675 Mechanica
958	27	65.9	3264	3	AAY53676	Aay53676 Protein 2
959	27	65.9	3843	4	ABB71529	Abb71529 Drosophil
960	27	65.9	5183	6	AAE14793	Aae14793 Human mic
961	27	65.9	5183	8	ADO44006	Ado44006 Amino aci
962	27	65.9	5183	9	ADX06154	Adx06154 Cyclin-de
963	26.5	64.6	814	2	AAY11680	Aay11680 Sulfated
964	26	63.4	8	6	AAE34370	Aae34370 Escherich
965	26	63.4	9	2	AAR58531	Aar58531 Light cha
966	26	63.4	9	2	AAR95304	Aar95304 Light cha
967	26	63.4	9	2	AAY05033	Aay05033 Tumour an
968	26	63.4	9	2	AAY05031	Aay05031 Tumour an
969	26	63.4	9	5	AAE28890	Aae28890 Human KDR
970	26	63.4	9	6	ABJ26783	Abj26783 VEGF bind
971	26	63.4	9	7	ADC82784	Adc82784 CDR regio
972	26	63.4	9	7	ADC82780	Adc82780 CDR regio
973	26	63.4	9	7	ADD24452	Add24452 Human lig

974	26	63.4	9	7	ADD80829	Add80829 Human var
975	26	63.4	9	8	ADK18305	Adk18305 KDR bindi
976	26	63.4	9	8	ADL27479	Adl27479 CDR from
977	26	63.4	9	8	ADT75013	Adt75013 Murine li
978	26	63.4	9	8	ADT75076	Adt75076 Murine li
979	26	63.4	9	8	ADU87723	Adu87723 Anti-CS1
980	26	63.4	9	8	ADU87707	Adu87707 Mouse Luc
981	26	63.4	9	9	AEA45082	Aea45082 Apolipopr
982	26	63.4	9	9	AEC20795	Aec20795 M-CSF spe
983	26	63.4	15	7	ADD26309	Add26309 Staphyloc
984	26	63.4	16	7	ADD26310	Add26310 Staphyloc
985	26	63.4	20	6	ABP82825	Abp82825 G protein
986	26	63.4	22	7	ADM57809	Adm57809 S.hamata
987	26	63.4	28	2	AAW04494	Aaw04494 Staphyloc
988	26	63.4	28	2	AAW73920	Aaw73920 Staphyloc
989	26	63.4	28	4	AAM21041	Aam21041 Peptide #
990	26	63.4	28	4	ABB43224	Abb43224 Peptide #
991	26	63.4	28	4	AAM37064	Aam37064 Peptide #
992	26	63.4	28	4	ABB26305	Abb26305 Protein #
993	26	63.4	28	4	AAM76956	Aam76956 Human bon
994	26	63.4	28	4	AAM64132	Aam64132 Human bra
995	26	63.4	28	4	ABG58618	Abg58618 Human liv
996	26	63.4	28	5	ABG46063	Abg46063 Human pep
997	26	63.4	29	9	ADV25036	Adv25036 IL7_T7 sp
998	26	63.4	30	3	AAY90592	Aay90592 Zinc fing
999	26	63.4	30	3	AAY90590	Aay90590 Zinc fing
1000	26	63.4	30	3	AAY90591	Aay90591 Zinc fing

ALIGNMENTS

RESULT 1
AAR97315
ID AAR97315 standard; peptide; 8 AA.
XX
AC AAR97315;
XX
DT 15-OCT-1996 (first entry)
XX
DE Humanised monoclonal antibody light chain CDR.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Mus musculus.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Claim 5; Page 38; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. This sequence is a murine derived CDR region which corresponds
CC to CDR 3 in the light chain of the humanised MAb. See AAR97313-97333
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 1 QQYSLYRS 8

RESULT 2
ADM95104
ID ADM95104 standard; peptide; 8 AA.
XX
AC ADM95104;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 MAb light chain variable region CDR3.
XX
KW non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW complementarity determining region; pancreatic cancer; breast cancer;
KW ovarian cancer.
XX
OS Mus sp.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-364813/34.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Claim 6; SEQ ID NO 22; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the CDR3 of
CC the murine MN-14 antibody light chain variable region and used to
CC generate the humanised/chimeric antibody of the invention.
XX
SQ Sequence 8 AA;

Query Match 100.0%; Score 41; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 QQYSLYRS 8
              ||||||||
Db          1 QQYSLYRS 8
```

RESULT 3
ADM98313
ID ADM98313 standard; peptide; 8 AA.
XX
AC ADM98313;
XX
DT 15-JUL-2004 (first entry)
XX
DE Humanised murine MN-14 antibody light chain variable region CDR3 peptide.
XX
KW carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; humanised;
KW murine; mouse; antibody; MN-14; non-medullary thyroid carcinoma;
KW medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW hepatocellular carcinoma; breast cancer; lung cancer;
KW antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW apoptosis.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO2004032857-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031801.
XX
PR 08-OCT-2002; 2002US-0416531P.
PR 11-OCT-2002; 2002WO-US032307.
PR 02-MAY-2003; 2003US-0467161P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-340797/31.
XX
PT Treating non-medullary or medullary thyroid carcinoma, involves
PT administering to subject, either concurrently or sequentially, anti-
PT carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS Claim 8; Page 76; 122pp; English.
XX
CC This invention relates to methods for treating cancers that express
CC carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC antibodies that can be used following administration of an agent that
CC will increase antibody effector functions or following administration of
CC an amount of interferon effective to upregulate CEA expression in tumour
CC cells. The present invention describes the anti-CEA antibody as a class
CC III humanised murine monoclonal antibody that retains specificity for CEA
CC binding and is preferably an MN-14 antibody or fragment thereof.
CC Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC composition useful for the treatment of non-medullary or medullary
CC thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC carcinoma, as well as breast or lung cancer. Furthermore, it can
CC stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC cell growth and angiogenesis. This peptide sequence is a CDR region of
CC the humanised murine MN-14 antibody of the invention.
XX
SQ Sequence 8 AA;

```
  Query Match             100.0%;  Score 41;  DB 8;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db          1 QQYSLYRS 8
```

RESULT 4
AAR97337
ID AAR97337 standard; protein; 106 AA.
XX
AC AAR97337;
XX
DT 15-OCT-1996 (first entry)
XX
DE Humanised antibody variable light chain (MN14HuVK).
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Mus musculus.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Binding-site 24. .34
FT /label= CDR 1.
FT Binding-site 50. .56
FT /label= CDR 2.
FT Binding-site 89. .96
FT /label= CDR 3.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
DR N-PSDB; AAT29013.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Disclosure; Fig 8; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. See AAR97313-97333 for the CDR sequence and framework regions
CC of the humanised MAbs
XX
SQ Sequence 106 AA;

```
  Query Match             100.0%;  Score 41;  DB 2;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db         89 QQYSLYRS 96
```

RESULT 5

```
AAR97335
ID   AAR97335 standard; protein; 106 AA.
XX
AC   AAR97335;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Murine NEWM MN-14 variable region light chain.
XX
KW   Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW   complementary determining region; anti-carcinoembryonic antigen; CEA;
KW   diagnosis; imaging; therapy; immune response.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    24. .34
FT                   /label= CDR 1.
FT   Binding-site    50. .56
FT                   /label= CDR 2.
FT   Binding-site    89. .96
FT                   /label= CDR 3.
XX
PN   WO9611013-A1.
XX
PD   18-APR-1996.
XX
PF   28-SEP-1995;   95WO-US011964.
XX
PR   05-OCT-1994;   94US-00318157.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Hansen HJ,  Armour KL;
XX
DR   WPI; 1996-209653/21.
DR   N-PSDB; AAT29011.
XX
PT   New humanised anti-CEA monoclonal antibody - having engrafted murine
PT   CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS   Example 7; Fig 2; 62pp; English.
XX
CC   New humanised monoclonal antibodies (MAbs) comprising the complementary
CC   determining regions (CDRs) of a parental murine class III anti-
CC   carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC   heterologous antibody which can be derived from any species including
CC   human, retain the anti-CEA binding specificity of the parental murine MAb
CC   but are less immunogenic in a human subject than the parental MAb. The
CC   humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC   -producing cancers and patients receiving the humanised antibodies and
CC   conjugates show improved therapeutic results, decreased immune responses
CC   and decreased immune-mediated adverse effects compared to the parent
CC   antibody. See AAR97313-97333 for the CDR sequence and framework regions
CC   of the humanised MAbs
XX
SQ   Sequence 106 AA;

  Query Match             100.0%;  Score 41;  DB 2;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db         89 QQYSLYRS 96


RESULT 6
ADM95097
ID   ADM95097 standard; protein; 106 AA.
XX
AC   ADM95097;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Murine MN-14 MAb light chain variable region.
XX
KW   non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW   complementarity determining region; pancreatic cancer; breast cancer;
KW   ovarian cancer.
XX
OS   Mus sp.
XX
PN   WO2004032962-A1.
XX
PD   22-APR-2004.
XX
PF   11-OCT-2002; 2002WO-US032307.
XX
PR   08-OCT-2002; 2002US-0416531P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-364813/34.
DR   N-PSDB; ADM95096.
XX
PT   Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT   comprises administering, either concurrently or sequentially, Class III
PT   anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT   therapeutic agent(s).
XX
PS   Disclosure; Fig 12A-B; 88pp; English.
XX
CC   The invention relates to a method of treating a non-medullary thyroid
CC   carcinoma or treating medullary thyroid carcinoma involves administering
CC   to a subject, either concurrently or sequentially, a Class III anti-CEA
CC   (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC   least one therapeutic agent. The antibody or its fragment comprises the
CC   complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC   antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC   medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC   ovarian cancer, in a subject. This sequence corresponds to the murine MN-
CC   14 antibody light chain variable region.
XX
SQ   Sequence 106 AA;

  Query Match             100.0%;  Score 41;  DB 8;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db         89 QQYSLYRS 96


RESULT 7
ADM95100
ID   ADM95100 standard; protein; 106 AA.
XX
AC   ADM95100;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 MAb light chain variable region.
XX
KW   non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW   complementarity determining region; pancreatic cancer; breast cancer;
KW   ovarian cancer.
XX
OS   Mus sp.
OS   Homo sapiens.
XX
PN   WO2004032962-A1.
XX
```

PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-364813/34.
DR N-PSDB; ADM95098.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Claim 14; Fig 16A; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the humanised
CC murine MN-14 antibody light chain variable region.
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 41; DB 8; Length 106;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 89 QQYSLYRS 96

RESULT 8
ADM98320
ID ADM98320 standard; protein; 106 AA.
XX
AC ADM98320;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 antibody light chain variable region protein.
XX
KW carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW antibody; MN-14; non-medullary thyroid carcinoma;
KW medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW hepatocellular carcinoma; breast cancer; lung cancer;
KW antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW apoptosis.
XX
OS Mus sp.
XX
PN WO2004032857-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031801.
XX
PR 08-OCT-2002; 2002US-0416531P.
PR 11-OCT-2002; 2002WO-US032307.
PR 02-MAY-2003; 2003US-0467161P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-340797/31.
DR N-PSDB; ADM98319.
XX
PT Treating non-medullary or medullary thyroid carcinoma, involves
PT administering to subject, either concurrently or sequentially, anti-
PT carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS Disclosure; Fig 12; 122pp; English.
XX
CC This invention relates to methods for treating cancers that express
CC carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC antibodies that can be used following administration of an agent that
CC will increase antibody effector functions or following administration of
CC an amount of interferon effective to upregulate CEA expression in tumour
CC cells. The present invention describes the anti-CEA antibody as a class
CC III humanised murine monoclonal antibody that retains specificity for CEA
CC binding and is preferably an MN-14 antibody or fragment thereof.
CC Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC composition useful for the treatment of non-medullary or medullary
CC thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC carcinoma, as well as breast or lung cancer. Furthermore, it can
CC stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC cell growth and angiogenesis. This polypeptide sequence is murine MN-14
CC antibody light chain variable region protein of the invention.
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 41; DB 8; Length 106;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 89 QQYSLYRS 96

RESULT 9
ADM98322
ID ADM98322 standard; protein; 106 AA.
XX
AC ADM98322;
XX
DT 15-JUL-2004 (first entry)
XX
DE Humanised murine MN-14 antibody light chain variable region protein.
XX
KW carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW antibody; MN-14; non-medullary thyroid carcinoma;
KW medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW hepatocellular carcinoma; breast cancer; lung cancer;
KW antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW apoptosis; humanised.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO2004032857-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031801.
XX
PR 08-OCT-2002; 2002US-0416531P.
PR 11-OCT-2002; 2002WO-US032307.
PR 02-MAY-2003; 2003US-0467161P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;

XX
DR WPI; 2004-340797/31.
DR N-PSDB; ADM98321.
XX
PT Treating non-medullary or medullary thyroid carcinoma, involves
PT administering to subject, either concurrently or sequentially, anti-
PT carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS Disclosure; Fig 23a; 122pp; English.
XX
CC This invention relates to methods for treating cancers that express
CC carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC antibodies that can be used following administration of an agent that
CC will increase antibody effector functions or following administration of
CC an amount of interferon effective to upregulate CEA expression in tumour
CC cells. The present invention describes the anti-CEA antibody as a class
CC III humanised murine monoclonal antibody that retains specificity for CEA
CC binding and is preferably an MN-14 antibody or fragment thereof.
CC Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC composition useful for the treatment of non-medullary or medullary
CC thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC carcinoma, as well as breast or lung cancer. Furthermore, it can
CC stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC cell growth and angiogenesis. This polypeptide sequence is the humanised
CC murine MN-14 antibody light chain variable region protein of the
CC invention.
XX
SQ Sequence 106 AA;

Query Match 100.0%; Score 41; DB 8; Length 106;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 89 QQYSLYRS 96

RESULT 10
ABR42756
ID ABR42756 standard; protein; 115 AA.
XX
AC ABR42756;
XX
DT 26-AUG-2003 (first entry)
XX
DE Anti-CEA humanized monoclonal antibody hMN-14 Vkappa region.
XX
KW Humanized; monoclonal antibody; antibody; hMN-14;
KW carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003033654-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032718.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
PR 08-JAN-2002; 2002US-0345641P.
PR 22-AUG-2002; 2002US-0404919P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg DM;
XX
DR WPI; 2003-513460/48.
XX
PT New multivalent, monospecific binding protein comprising two or more
PT binding sites having affinity for the same single target antigen, where
PT each binding site is associated with scFv fragments, useful for
PT diagnosing or treating tumor.
XX
PS Disclosure; Fig 12; 62pp; English.
XX
CC The present sequence is the protein sequence of the light chain variable
CC region of anti-carcinoembryonic antigen (CEA) humanized monoclonal
CC antibody hMN-14. scFv constructs comprising the hMN-14 Vkappa and VH
CC regions are used in novel multivalent, monospecific binding proteins
CC (diabody, triabody and tetrabody) of the invention (see also ABR42754,
CC ABR42757 and ABR42758). Claimed binding proteins are specific for a
CC tumour-associated antigen, and are used in the diagnosis and treatment of
CC a tumour, carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma,
CC lymphoma or myeloma, or a cancer selected from acute lymphoblastic
CC leukaemia, acute myelogenous leukaemia, biliary, breast, cervical,
CC chronic lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC prostate and bladder
XX
SQ Sequence 115 AA;

Query Match 100.0%; Score 41; DB 6; Length 115;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 89 QQYSLYRS 96

RESULT 11
ABG76490
ID ABG76490 standard; protein; 232 AA.
XX
AC ABG76490;
XX
DT 13-MAY-2003 (first entry)
XX
DE Light chain variable, VL, region of antibody hMN14.
XX
KW CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW human; zeta signalling chain; CD8alpha hinge; humanised antibody;
KW light chain variable region; VL.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1. .19
FT /label= Signal_peptide
FT Protein 20. .232
FT /label= Mature_VL_of_hMN14
XX
PN US2002165360-A1.
XX
PD 07-NOV-2002.
XX
PF 10-DEC-2001; 2001US-00006771.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250090P.
XX
PA (JUNG/) JUNGHANS R P.
XX
PI Junghans RP;
XX
DR WPI; 2003-298705/29.

DR N-PSDB; ABX13170.
XX
PT New chimeric molecule from humanized antibody against carcinoembryonic
PT antigen and having signaling molecules of T cells and other effector
PT cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS Disclosure; Page 10-11; 20pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the
CC carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC which the cysteine residues have been mutated, with the IgTCR molecule
CC occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC NK (not defined) or other effector cells are useful in treating patients
CC with cancers expressing the CEA antigen, together with other or with
CC heterologous constructs to engage additional stimulatory and functional
CC properties of the effector cells to enhance the anti-tumour therapeutic
CC efficacy. The cancer disorder includes colorectal, breast and lung
CC cancers. The present sequence represents the light chain variable, VL,
CC region of antibody hMN14. The VL protein is humanised (complementarity
CC determining region-grafted) and has a leader peptide
XX
SQ Sequence 232 AA;

Query Match 100.0%; Score 41; DB 6; Length 232;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 108 QQYSLYRS 115

RESULT 12
ADE64204
ID ADE64204 standard; protein; 232 AA.
XX
AC ADE64204;
XX
DT 29-JAN-2004 (first entry)
XX
DE MN14LC protein related to a novel antibody library.
XX
KW antibody library; retroviral vector; antibody light chain;
KW antibody heavy chain; human therapy; multiplicity of infection; MOI;
KW plasmid; GATEWAY vector; MN14LC.
XX
OS Unidentified.
XX
PN WO2003083077-A2.
XX
PD 09-OCT-2003.
XX
PF 28-MAR-2003; 2003WO-US009662.
XX
PR 28-MAR-2002; 2002US-0368808P.
PR 10-APR-2002; 2002US-0371299P.
PR 28-MAR-2003; 2003US-00371299.
XX
PA (GALA-) GALA DESIGN INC.
XX
PI Bremel RD, Eakle K, Imboden M;
XX
DR WPI; 2003-804051/75.
DR N-PSDB; ADE64208.
XX
PT New antibody library comprising cells comprising at least one integrated
PT retroviral vector expressing an antibody light or heavy chain, useful in
PT preparing a composition for diagnosing or treating disorders.
XX
PS Disclosure; Fig 8; 57pp; English.
XX
CC This invention relates to a new antibody library which comprises at least
CC 100 cells, each of which comprises at least one integrated retroviral
CC vector expressing an antibody light or heavy chain. Antibodies are of
CC increasing importance in human therapy, assay procedures and diagnostic
CC methods and a need exists for efficient methods of generating and
CC screening antibody libraries containing large numbers of antibodies. The
CC antibody library of the invention addresses this need, with the
CC additional advantage of strict control over multiplicity of infection
CC (MOI), and is useful in preparing a composition for diagnosing or
CC treating a wide variety of disorders. The present sequence is the amino
CC acid sequence of the MN14LC protein, which was encoded by the Gateway
CC retroviral vectors used in the exemplification of the invention.
XX
SQ Sequence 232 AA;

Query Match 100.0%; Score 41; DB 7; Length 232;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 108 QQYSLYRS 115

RESULT 13
ADF60817
ID ADF60817 standard; protein; 232 AA.
XX
AC ADF60817;
XX
DT 12-FEB-2004 (first entry)
XX
DE hMN-14 light chain amino acid sequence.
XX
KW Immunomodulatory; antidiabetic; immunosuppressive; cardiovascular;
KW neuroprotective; nootropic; fungicide; virucide; antimalarial;
KW antihelmintic; antiparasitic; haemostatic; muscular; antiinflammatory;
KW dermatological; antipyretic; antirheumatic; cytostatic; mutant;
KW bispecific antibody; immunoglobulin G; IgG; scFvs; Fvs; CH2 domain;
KW immune; autoimmune; disease; organ graft rejection; cardiovascular;
KW neurological; Alzheimer's disease; graft vs host disease;
KW systemic lupus erythematosus; diabetes mellitus.
XX
OS Homo sapiens.
XX
PN WO2003074569-A2.
XX
PD 12-SEP-2003.
XX
PF 03-MAR-2003; 2003WO-GB000871.
XX
PR 01-MAR-2002; 2002US-0361037P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (MCCA/) MCCALL J D.
XX
PI Qu Z, Hansen H, Goldenberg DM;
XX
DR WPI; 2003-902725/82.
DR N-PSDB; ADF60816.
XX
PT Mutant bispecific antibody which is rapidly cleared from a patient's
PT body, useful as a pretargeting agent in methods for diagnosing or
PT treating diseases, such as autoimmune disease, and disease caused by
PT infectious agents.
XX
PS Example; Fig 2; 68pp; English.
XX
CC The invention relates to a mutant bispecific antibody (mbAb1) comprising
CC at least a human hinge constant region from immunoglobulin G (IgG), two
CC single chain variable fragments (scFvs), and two variable fragments
CC (Fvs), where the constant region contains one or more amino acid

```
CC   mutations in the heavy chain 2 (CH2) domain. The methods and antibody of
CC   the invention are used to diagnose or treat an immune dysregulation
CC   disease, an autoimmune disease, organ graft rejection, cardiovascular
CC   disease, neurological disease (Alzheimer's disease) or graft vs. host
CC   disease. The methods are also useful for treating a disease caused by a
CC   fungus, virus, parasite, or bacterium. The methods may also be used for
CC   intraoperative or endoscopic diagnosis to identify diseased tissue. The
CC   autoimmune diseases that may be diagnosed or treated include acute or
CC   chronic idiopathic thrombocytopenic purpura, dermatomyositis, Sydenham's
CC   chorea, myasthenia gravis, systemic lupus erythematosus, lupus nephritis,
CC   rheumatic fever, polyglandular syndromes and diabetes mellitus. The
CC   current sequence represents the hMN-14 light chain amino acid sequence.
XX
SQ   Sequence 232 AA;

  Query Match             100.0%;  Score 41;  DB 7;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 6.7;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        108 QQYSLYRS 115


RESULT 14
ABR42757
ID   ABR42757 standard; protein; 256 AA.
XX
AC   ABR42757;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-0.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-0;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; triabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .256
FT                   /label= hMN-14-0
FT   Region          142. .250
FT                   /label= hMN-14Vkappa
FT   Region          251. .256
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
DR   N-PSDB; ACC58722.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 39; Fig 13; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-0, which is
CC   designed to form an hMN-14 triabody. The hMN-14-0 polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa without a peptide linker. The use of the zero linker enables the
CC   secreted polypeptide to form a triabody, forming 3 binding sites for CEA.
CC   The polypeptide also includes a pelB signal peptide, which precedes the
CC   VH moiety to facilitate synthesis of the polypeptide in the periplasmic
CC   space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific triabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 256 AA;

  Query Match             100.0%;  Score 41;  DB 6;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 7.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        230 QQYSLYRS 237


RESULT 15
ABR42758
ID   ABR42758 standard; protein; 257 AA.
XX
AC   ABR42758;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-1G.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-1G;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; tetrabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .257
FT                   /label= hMN-14-0
FT   Region          142
FT                   /label= 1G_linker
FT   Region          143. .251
FT                   /label= hMN-14Vkappa
FT   Region          252. .257
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
```

```
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 48; Fig 14; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-1G, which is
CC   designed to form an hMN-14 tetrabody. The hMN-14-1G polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa via a single glycine residues. Use of the 1G linker enables some
CC   of the the secreted polypeptide to form a tetrabody with 4 binding sites
CC   for CEA. The polypeptide also includes a pelB signal peptide, which
CC   precedes the VH moiety to facilitate synthesis of the polypeptide in the
CC   periplasmic space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific tetrabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 257 AA;

  Query Match            100.0%;  Score 41;  DB 6;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 7.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        231 QQYSLYRS 238


RESULT 16
ABR42289
ID   ABR42289 standard; protein; 261 AA.
XX
AC   ABR42289;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Diabody 679-scFv-L5 polypeptide (VH-I3Q/C101S mutant).
XX
KW   Diabody; antibody; 679-scFv-L5; histamine-succinyl-glycyl; HSG;
KW   affinity enhancement system; tumour; targeting; mutant; mutein.
XX
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB signal peptide"
FT   Misc-difference 3
FT                   /note= "wild-type Ile substituted by Gln"
FT   Protein         23. .268
FT                   /label= 679-scFv-L5
FT   Region          23. .142
FT                   /label= 679VH(I3Q/C101S)
FT   Misc-difference 101
FT                   /note= "wild-type Cys substituted by Ser"
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .260
FT                   /label= 679Vk
FT   Region          261. .268
FT                   /label= 6His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57803.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Disclosure; Fig 28; 87pp; English.
XX
CC   The present sequence is the protein sequence of a 679 mutant diabody in
CC   which antibody 679 VH has a Gln for Ile amino acid substitution at
CC   position 3 and a Ser for Gln amino acid substitution at position 101.
CC   Murine monoclonal antibody 679 binds with high affinity to molecules
CC   containing the moiety histamine-succinyl-glycyl (HSG). The present
CC   polypeptide comprises: 679 VH(I3Q) linked to 679 Vk via a peptide linker
CC   (enables the secreted polypeptide to dimerise into a diabody, forming 2
CC   sites for HSG); a pelB leader signal peptide (facilitates transport of
CC   the polypeptide into the periplasmic space of Escherichia coli); and 6
CC   His residues (allows purification by IMAC). The 679 diabody was expressed
CC   in E. coli at a level of 10 ug/l of culture, compared with 1 ug/l for the
CC   non-mutant polypeptide. The invention provides a bispecific diabody
CC   comprising an HSG binding site and a carcinoembryonic antigen (CEA)
CC   binding site. The HSG antigen binding site may comprise the VH and Vk
CC   polypeptides of 679 MAb. These diabodies are produced via recombinant DNA
CC   technology and create a novel affinity enhancement system that shows
CC   specific affinity for HSG and CEA. They pre-target CEA positive tumours
CC   for subsequent specific delivery of therapeutic radioisotopes carried by
CC   HSG-carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 261 AA;

  Query Match            100.0%;  Score 41;  DB 6;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        235 QQYSLYRS 242
```

```
RESULT 17
ABR42754
ID   ABR42754 standard; protein; 261 AA.
XX
AC   ABR42754;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-scFv-L5.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-scFv-15;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide          1. .23
FT                    /label= Signal_peptide
FT                    /note= "pelB"
FT   Region           23. .141
FT                    /label= hMN-14VH
FT   Protein          24. .261
FT                    /label= hMN-14-scFv-L5
FT   Region           142. .146
FT                    /label= Linker
FT   Region           147. .255
FT                    /label= hMN-14Vkappa
FT   Region           256. .261
FT                    /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
DR   N-PSDB; ACC58721.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 31; Fig 11; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-scFv-L5, which was
CC   designed to form an hMN-14 diabody. The hMN-14-scFv-L5 polypeptide
CC   comprises the C-terminal end of anti-carcinoembryonic antigen (CEA)
CC   humanized monoclonal antibody hMN-14 VH linked to the N-terminal part of
CC   hMN-14 Vkappa by a peptide linker that enables the secreted polypeptide
CC   to dimerize into a diabody, forming 2 binding sites for CEA. The
CC   polypeptide also includes a pelB signal peptide, which precedes the VH
CC   moiety to facilitate synthesis of the polypeptide in the periplasmic
CC   space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. In the claimed monospecific diabody, each scFv comprises
CC   the present sequence. The diabody is an example of claimed multivalent
CC   binding proteins specific for a tumour-associated antigen. The binding
CC   proteins are used in the diagnosis and treatment of a tumour, carcinoma,
CC   melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma or myeloma,
CC   or a cancer selected from acute lymphoblastic leukaemia, acute
CC   myelogenous leukaemia, biliary, breast, cervical, chronic lymphocytic
CC   leukaemia, chronic myelogenous leukaemia, colorectal, endometrial,
CC   oesophageal, gastric, head and neck, Hodgkin's lymphoma, lung, medullary
CC   thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic, prostate and
CC   bladder
XX
SQ   Sequence 261 AA;

  Query Match             100.0%;  Score 41;  DB 6;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        235 QQYSLYRS 242


RESULT 18
ABR83645
ID   ABR83645 standard; protein; 261 AA.
XX
AC   ABR83645;
XX
DT   16-OCT-2003  (first entry)
XX
DE   hMN14-scFv-L5 amino acid sequence.
XX
KW   Multispecific binding protein; multivalent; target antigen; cytostatic;
KW   immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW   immunotherapy; autoimmune disease; infectious disease;
KW   cardiovascular disease; inflammatory disease.
XX
OS   Escherichia coli.
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003057829-A2.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-US038985.
XX
PR   26-DEC-2001; 2001US-0342103P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg D;
XX
DR   WPI; 2003-607997/57.
DR   N-PSDB; ACF57430.
XX
PT   Novel multivalent, multi-specific binding protein useful for treating
PT   cancer, has first binding site having affinity towards hapten group and
PT   second and third binding sites each having affinity towards target
PT   antigen.
XX
PS   Claim 11; Fig 6; 43pp; English.
XX
CC   The present invention describes a multivalent, multi-specific binding
CC   protein (I) comprising a first binding site having an affinity towards a
CC   hapten group and a second and a third binding sites each having affinity
CC   towards a target antigen, which may be the same or a different target
CC   antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC   and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC   useful for delivering a diagnostic agent, a therapeutic agent, or its
CC   combination to a target, which involves administering (I) to a subject,
CC   waiting for a sufficient amount of time for an amount of the non-binding
CC   protein to clear the subject's blood stream, and administering to the
CC   subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC   agent, or its combination, that binds to a binding site of the binding
CC   protein. (I) is also useful for detecting or treating a human disorder,
CC   preferably cancer, autoimmune diseases, infectious diseases,
```

```
CC   cardiovascular diseases and inflammatory diseases. The present sequence
CC   represents a hMN14-scFv-L5 amino acid sequence, which is used in the
CC   exemplification of the present invention
XX
SQ   Sequence 261 AA;

  Query Match             100.0%;  Score 41;  DB 6;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        235 QQYSLYRS 242


RESULT 19
ABR42295
ID   ABR42295 standard; protein; 262 AA.
XX
AC   ABR42295;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS2 polypeptide #1.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BS2_polypeptide#1
FT   Region          24. .142
FT                   /label= 679_VH(I3Q)
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
FT                   /label= hMN14_VH
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57809.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 34; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #1 of novel
CC   bispecific diabody BS2 comprising the VH region of monoclonal antibody
CC   679 and the Vk region of monoclonal antibody hMN14. The 679VH moiety
CC   includes I3Q and C101S mutations, which improve solubility. Mouse
CC   antibody 679 binds with high affinity to molecules containing the moiety
CC   histamine-succinyl-glycyl (HSG). Humanised antibody hMN14 binds
CC   specifically to carcinoembryonic antigen (CEA). The bispecific diabody
CC   can be produced using recombinant DNA methods, e.g. in Escherichia coli
CC   host cells. It provides a novel affinity enhancement system that shows
CC   specific affinity for HSG and CEA. Such bispecific diabodies pre-target
CC   CEA positive tumours for subsequent specific delivery of therapeutic
CC   radioisotopes carried by HSG-carrying peptides. Cancer, autoimmune
CC   diseases, infectious disease, cardiovascular diseases and inflammatory
CC   diseases can be detected or treated using the methods of the invention
XX
SQ   Sequence 262 AA;

  Query Match             100.0%;  Score 41;  DB 6;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        236 QQYSLYRS 243


RESULT 20
ABR42293
ID   ABR42293 standard; protein; 262 AA.
XX
AC   ABR42293;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS1.5 polypeptide #1.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BS1.5_polypeptide#1
FT   Region          24. .142
FT                   /label= 679_VH(I3Q)
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
FT                   /label= hMN14_VH
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
```

```
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 32; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #1 of a
CC   novel bispecific diabody comprising the VH region of monoclonal antibody
CC   679 and the Vk region of monoclonal antibody hMN14. The 679VH region
CC   includes an I3Q mutation which improves solubility. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen. The bispecific diabody can be produced using
CC   recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC   a novel affinity enhancement system that shows specific affinity for HSG
CC   and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC   subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC   carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 262 AA;

  Query Match             100.0%;  Score 41;  DB 6;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        236 QQYSLYRS 243


RESULT 21
ABR42298
ID   ABR42298 standard; protein; 262 AA.
XX
AC   ABR42298;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS1.5H polypeptide #1.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BS1.5H_polypeptide#1
FT   Region          24. .142
FT                   /label= 679_VH(I3Q)
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
FT                   /label= hMN14_VH
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57812.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 37; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #1 of novel
CC   bispecific diabody BS1.5H comprising the VH region of monoclonal antibody
CC   679 and the Vk region of monoclonal antibody hMN14. The 679VH moiety
CC   includes an I3Q mutation, which improves solubility. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). A humanised version of its VH and Vk sequences
CC   have been used in BS1.5H. Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC   using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC   provides a novel affinity enhancement system that shows specific affinity
CC   for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC   tumours for subsequent specific delivery of therapeutic radioisotopes
CC   carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC   disease, cardiovascular diseases and inflammatory diseases can be
CC   detected or treated using the methods of the invention
XX
SQ   Sequence 262 AA;

  Query Match             100.0%;  Score 41;  DB 6;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        236 QQYSLYRS 243


RESULT 22
ABR42290
ID   ABR42290 standard; protein; 262 AA.
XX
AC   ABR42290;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Diabody hMN14-scFv-L5 polypeptide.
XX
KW   Diabody; antibody; hMN14-scFv-L5; carcinoembryonic antigen; CEA;
KW   affinity enhancement system; tumour; targeting.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB signal peptide"
```

```
FT   Protein         23. .262
FT                   /label= hMN14-scFv-L5
FT   Region          23. .141
FT                   /label= hMN14VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .253
FT                   /label= 679Vk
FT   Region          257. .262
FT                   /label= 6His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 10; Fig 29; 87pp; English.
XX
CC   The present sequence is the protein sequence of a hMN14 diabody,
CC   designated hMN14-scFv-L5. Humanised monoclonal antibody hMN14 binds
CC   specifically to carcinoembryonic antigen (CEA). hMN14-scFv-L5 comprises:
CC   hMN14 VH linked to 679 Vk via a peptide linker (enables the secreted
CC   polypeptide to dimerise into a diabody, forming 2 sites for HSG); a pelB
CC   leader signal peptide (facilitates transport of the polypeptide into the
CC   periplasmic space of Escherichia coli); and 6 His residues (allows
CC   purification by IMAC). The invention provides a bispecific diabody
CC   comprising a histamine-succinyl-glycyl (HSG) binding site and a CEA
CC   binding site. The CEA binding site may comprise the VH and Vk
CC   polypeptides of hMN14 MAb. These diabodies are produced via recombinant
CC   DNA technology and create a novel affinity enhancement system that shows
CC   specific affinity for HSG and CEA. They pre-target CEA positive tumours
CC   for subsequent specific delivery of therapeutic radioisotopes carried by
CC   HSG-carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 262 AA;

  Query Match             100.0%;  Score 41;  DB 6;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        236 QQYSLYRS 243


RESULT 23
ABR42291
ID   ABR42291 standard; protein; 262 AA.
XX
AC   ABR42291;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody polypeptide #1.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BSI_polypeptide#1
FT   Region          24. .142
FT                   /label= 679_VH
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
FT                   /label= hMN14_VH
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57805.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 30; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #1 of a
CC   novel bispecific diabody comprising the VH region of monoclonal antibody
CC   679 and the Vk region of monoclonal antibody hMN14. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen. The bispecific diabody can be produced using
CC   recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC   a novel affinity enhancement system that shows specific affinity for HSG
CC   and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC   subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC   carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 262 AA;

  Query Match             100.0%;  Score 41;  DB 6;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 7.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        236 QQYSLYRS 243
```

RESULT 24
ADU26571
ID ADU26571 standard; protein; 358 AA.
XX
AC ADU26571;
XX
DT 27-JAN-2005 (first entry)
XX
DE Chimeric hBS14 polypeptide 2.
XX
KW cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW neoplasm; fungal infection; viral infection; bacterial infection;
KW mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW autoimmune disease; myocardial infarction; ischemic heart disease;
KW atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
OS Synthetic.
XX
PN WO2004094613-A2.
XX
PD 04-NOV-2004.
XX
PF 22-APR-2004; 2004WO-US012662.
XX
PR 22-APR-2003; 2003US-0464532P.
PR 24-NOV-2003; 2003US-0525391P.
XX
PA (IBCP-) IBC PHARM.
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Rossi EA, Chang C, Mcbride WJ;
XX
DR WPI; 2004-795560/78.
DR N-PSDB; ADU26573.
XX
PT Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT chains having immunoglobulin variable domains, to form complex having
PT three antigen binding sites.
XX
PS Example 2; SEQ ID NO 12; 148pp; English.
XX
CC The invention relates to a polyvalent protein complex (PPC) (I),
CC comprising a first and second polypeptide chains having immunoglobulin
CC variable domains, where the first and second polypeptide chains form a
CC complex having three antigen binding sites, and where each binding site
CC comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC useful in pretargeting method of treating or diagnosing, or treating and
CC diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC also useful for diagnosing a non-neoplastic disease or disorder where the
CC disease or disorder is caused by a fungus, a virus, a bacterium, a
CC mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC infarction, ischemic heart disease, atherosclerotic plaques, graft
CC rejection, Alzheimer's disease or inflammation caused by accretion of
CC activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC site of inflammation (caused by infectious agent). (I) is useful in
CC antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC molecule, and immunostaining technique. This sequence corresponds to the
CC chimeric hBS14 polypeptide 2 containing heavy and light chain variable
CC regions.
XX
SQ Sequence 358 AA;

Query Match 100.0%; Score 41; DB 8; Length 358;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 90 QQYSLYRS 97

RESULT 25
ADU26561
ID ADU26561 standard; protein; 363 AA.
XX
AC ADU26561;
XX
DT 27-JAN-2005 (first entry)
XX
DE Chimeric BS14hp polypeptide 2.
XX
KW cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW neoplasm; fungal infection; viral infection; bacterial infection;
KW mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW autoimmune disease; myocardial infarction; ischemic heart disease;
KW atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1. .6
FT /note= "signal peptide"
FT Protein 7. .363
FT /note= "mature protein"
FT Region 30. .40
FT /note= "CDR1hMN14Vk"
FT Region 56. .62
FT /note= "CDR2hMN14Vk"
FT Region 95. .102
FT /note= "CDR3hMN14Vk"
FT Region 114. .119
FT /note= "linker region"
FT Region 150. .154
FT /note= "CDR1hMN14Vh"
FT Region 169. .185
FT /note= "CDR2hMN14Vh"
FT Region 218. .227
FT /note= "CDR3hMN14Vh"
FT Region 238. .242
FT /note= "linker region"
FT Region 266. .282
FT /note= "CDR1h679Vk"
FT Region 298. .304
FT /note= "CDR2h679Vk"
FT Region 337. .344
FT /note= "CDR3h679Vk"
XX
PN WO2004094613-A2.
XX
PD 04-NOV-2004.

```
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26569.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 1; SEQ ID NO 2; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
CC   activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC   site of inflammation (caused by infectious agent). (I) is useful in
CC   antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric BS14HP polypeptide 2 containing heavy and light chain variable
CC   regions. The encoded polypeptide is designated alpha-factor-hMN-14Vk-
CC   GGGGS-hMN-14Vh-LEGGGS-h679Vk-6-His where the hMN14 is from a humanized
CC   antibody that binds specifically to the carcinoembryonic antigen and the
CC   h679 is a monoclonal antibody that binds the tri-peptide moiety histamine
CC   -succinyl-glycyl (HSG).
XX
SQ   Sequence 363 AA;

  Query Match             100.0%;  Score 41;  DB 8;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db         95 QQYSLYRS 102


RESULT 26
ADU26570
ID   ADU26570 standard; protein; 364 AA.
XX
AC   ADU26570;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric hBS14 polypeptide 1.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26572.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 2; SEQ ID NO 11; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
CC   activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC   site of inflammation (caused by infectious agent). (I) is useful in
CC   antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric hBS14 polypeptide 1 containing heavy and light chain variable
CC   regions.
XX
SQ   Sequence 364 AA;

  Query Match             100.0%;  Score 41;  DB 8;  Length 364;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        214 QQYSLYRS 221


RESULT 27
ADU26560
ID   ADU26560 standard; protein; 370 AA.
XX
```

AC ADU26560;
XX
DT 27-JAN-2005 (first entry)
XX
DE Chimeric BS14HP polypeptide 1.
XX
KW cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW neoplasm; fungal infection; viral infection; bacterial infection;
KW mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW autoimmune disease; myocardial infarction; ischemic heart disease;
KW atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
OS Synthetic.
XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .7
FT		/note= "signal peptide"
FT	Protein	8. .370
FT		/note= "mature protein"
FT	Region	38. .42
FT		/note= "CDR1h679Vh"
FT	Region	57. .68
FT		/note= "CDR2h679Vh"
FT	Region	106. .115
FT		/note= "CDR3h679Vh"
FT	Region	127. .131
FT		/note= "linker region"
FT	Region	155. .165
FT		/note= "CDR1hMN14Vk"
FT	Region	181. .187
FT		/note= "CDR2hMN14Vk"
FT	Region	220. .227
FT		/note= "CDR3hMN14Vk"
FT	Region	239. .244
FT		/note= "linker region"
FT	Region	275. .279
FT		/note= "CDR1hMN14Vh"
FT	Region	294. .310
FT		/note= "CDR2hMN14Vh"
FT	Region	343. .352
FT		/note= "CDR3hMN14Vh"

XX
PN WO2004094613-A2.
XX
PD 04-NOV-2004.
XX
PF 22-APR-2004; 2004WO-US012662.
XX
PR 22-APR-2003; 2003US-0464532P.
PR 24-NOV-2003; 2003US-0525391P.
XX
PA (IBCP-) IBC PHARM.
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Rossi EA, Chang C, Mcbride WJ;
XX
DR WPI; 2004-795560/78.
DR N-PSDB; ADU26568.
XX
PT Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT chains having immunoglobulin variable domains, to form complex having
PT three antigen binding sites.
XX
PS Example 1; SEQ ID NO 1; 148pp; English.
XX
CC The invention relates to a polyvalent protein complex (PPC) (I),
CC comprising a first and second polypeptide chains having immunoglobulin
CC variable domains, where the first and second polypeptide chains form a
CC complex having three antigen binding sites, and where each binding site
CC comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC useful in pretargeting method of treating or diagnosing, or treating and
CC diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC also useful for diagnosing a non-neoplastic disease or disorder where the
CC disease or disorder is caused by a fungus, a virus, a bacterium, a
CC mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC infarction, ischemic heart disease, atherosclerotic plaques, graft
CC rejection, Alzheimer's disease or inflammation caused by accretion of
CC activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC site of inflammation (caused by infectious agent). (I) is useful in
CC antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC molecule, and immunostaining technique. This sequence corresponds to the
CC chimeric BS14HP polypeptide 1 containing heavy and light chain variable
CC regions. The encoded polypeptide is designated alpha-factor-h679Vh-GGGGS-
CC hMN-14Vk-LEGGGS-hMN-14Vh-6-His where the hMN14 is from a humanized
CC antibody that binds specifically to the carcinoembryonic antigen and the
CC h679 is a monoclonal antibody that binds the tri-peptide moiety histamine
CC -succinyl-glycyl (HSG).
XX
SQ Sequence 370 AA;

Query Match 100.0%; Score 41; DB 8; Length 370;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 220 QQYSLYRS 227

RESULT 28
ABR83649
ID ABR83649 standard; protein; 391 AA.
XX
AC ABR83649;
XX
DT 16-OCT-2003 (first entry)
XX
DE TS1 VL chain amino acid sequence.
XX
KW Multispecific binding protein; multivalent; target antigen; cytostatic;
KW immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW immunotherapy; autoimmune disease; infectious disease;
KW cardiovascular disease; inflammatory disease.
XX
OS Escherichia coli.
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003057829-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US038985.
XX
PR 26-DEC-2001; 2001US-0342103P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg D;
XX
DR WPI; 2003-607997/57.
DR N-PSDB; ACF57434.

XX
PT Novel multivalent, multi-specific binding protein useful for treating
PT cancer, has first binding site having affinity towards hapten group and
PT second and third binding sites each having affinity towards target
PT antigen.
XX
PS Claim 48; Fig 9A-B; 43pp; English.
XX
CC The present invention describes a multivalent, multi-specific binding
CC protein (I) comprising a first binding site having an affinity towards a
CC hapten group and a second and a third binding sites each having affinity
CC towards a target antigen, which may be the same or a different target
CC antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC useful for delivering a diagnostic agent, a therapeutic agent, or its
CC combination to a target, which involves administering (I) to a subject,
CC waiting for a sufficient amount of time for an amount of the non-binding
CC protein to clear the subject's blood stream, and administering to the
CC subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC agent, or its combination, that binds to a binding site of the binding
CC protein. (I) is also useful for detecting or treating a human disorder,
CC preferably cancer, autoimmune diseases, infectious diseases,
CC cardiovascular diseases and inflammatory diseases. The present sequence
CC represents the TS1 VL chain amino acid sequence, which is used in the
CC exemplification of the present invention
XX
SQ Sequence 391 AA;

Query Match 100.0%; Score 41; DB 6; Length 391;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 365 QQYSLYRS 372

RESULT 29
ABG76488
ID ABG76488 standard; protein; 443 AA.
XX
AC ABG76488;
XX
DT 13-MAY-2003 (first entry)
XX
DE Humanised anti-CEA antibody, hMN14.
XX
KW CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW human; zeta signalling chain; CD8alpha hinge; humanised antibody.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
PN US2002165360-A1.
XX
PD 07-NOV-2002.
XX
PF 10-DEC-2001; 2001US-00006771.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250090P.
XX
PA (JUNG/) JUNGHANS R P.
XX
PI Junghans RP;
XX
DR WPI; 2003-298705/29.
DR N-PSDB; ABX13168.
XX
PT New chimeric molecule from humanized antibody against carcinoembryonic
PT antigen and having signaling molecules of T cells and other effector
PT cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS Disclosure; Page 7-8; 20pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the
CC carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC which the cysteine residues have been mutated, with the IgTCR molecule
CC occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC NK (not defined) or other effector cells are useful in treating patients
CC with cancers expressing the CEA antigen, together with other or with
CC heterologous constructs to engage additional stimulatory and functional
CC properties of the effector cells to enhance the anti-tumour therapeutic
CC efficacy. The cancer disorder includes colorectal, breast and lung
CC cancers. The present sequence represents the chimaeric molecule of the
CC invention
XX
SQ Sequence 443 AA;

Query Match 100.0%; Score 41; DB 6; Length 443;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 108 QQYSLYRS 115

RESULT 30
ABG74240
ID ABG74240 standard; protein; 443 AA.
XX
AC ABG74240;
XX
DT 23-OCT-2003 (revised)
DT 22-APR-2003 (first entry)
XX
DE Chimaeric hMN14/T-cell receptor.
XX
KW Retroviral vector; T-cell receptor; hMN14; antibody; IgTCR; receptor;
KW cytostatic; dermatological; neuroprotective; immunostimulant; GD3;
KW ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4; 3E11;
KW prostate-specific membrane antigen; zeta signalling chain; human; cancer;
KW melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer;
KW mouse; CD8alpha hinge.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
PN US2002132983-A1.
XX
PD 19-SEP-2002.
XX
PF 10-DEC-2001; 2001US-00006773.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250089P.
XX
PA (JUNG/) JUNGHANS R P.
XX
PI Junghans RP;
XX
DR WPI; 2003-208946/20.
DR N-PSDB; ABX16565.
XX
PT New chimeric molecule useful in treating patients with disorders, such as
PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer
PT comprises GD3 and/or PSMA binding domains of antibody.
XX

PS Disclosure; Page 7-8; 35pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the GD3
CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)
CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC sequences, the zeta signalling chain of the T cell receptor and an
CC intervening CD8alpha hinge in which cysteine residues have been mutated.
CC The chimaeric molecules expressed in T cells or NK cells or other
CC effector cells are useful in treating patients with cancers expressing
CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC and/or together with each other or with heterologous constructs to engage
CC additional stimulatory and functional properties of the effector cells to
CC enhance the antitumour therapeutic efficacy (claimed). They are
CC particularly useful in disorders including melanoma, neuroendocrine
CC tumours and prostate and small cell lung cancer. The present sequence is
CC a hMN14 antibody (specific to CEA antigen) in a fusion protein with the
CC modified CD8alpha hinge and the T-cell receptor zeta chain (IgTCR)
CC encoded by a retroviral vector. The hMN14 antibody coding region is
CC replaced with the MB3.6, 3D8, 4D4 or 3E11 genes of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 443 AA;

Query Match 100.0%; Score 41; DB 6; Length 443;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 108 QQYSLYRS 115

RESULT 31
ADY97271
ID ADY97271 standard; protein; 669 AA.
XX
AC ADY97271;
XX
DT 16-JUN-2005 (first entry)
XX
DE Exemplary antibody fusion protein SEQ ID NO:3.
XX
KW antibody engineering; fusion protein; cytostatic; antimicrobial;
KW virucide; antibacterial; cancer; infection.
XX
OS Synthetic.
XX
PN US2005069552-A1.
XX
PD 31-MAR-2005.
XX
PF 28-JUL-2004; 2004US-00900928.
XX
PR 28-JUL-2003; 2003US-0490569P.
XX
PA (BLEC/) BLECK G T.
PA (YORK/) YORK D.
PA (COLL/) COLLINS I.
XX
PI Bleck GT, York D, Collins I;
XX
DR WPI; 2005-261600/27.
DR N-PSDB; ADY97269.
XX
PT Composition useful as cancer vaccine, comprises polypeptide having
PT antibody heavy chain fused to antibody light chain, or multivalent
PT antibody having two polypeptides with antibody heavy chain fused to
PT antibody light chain.
XX
PS Disclosure; SEQ ID NO 3; 101pp; English.
XX
CC The invention describes a composition (I) comprising: (a) a polypeptide
CC comprising at least one antibody heavy chain fused to at least one
CC antibody light chain; or (b) a multivalent antibody comprising at least
CC two polypeptides, where each of the polypeptides comprises at least one
CC antibody heavy chain fused to at least one antibody light chain. Also
CC described: (1) a composition (II) comprising a nucleic acid comprising at
CC least one antibody heavy chain gene and at least one antibody light chain
CC gene, where the nucleic acid encodes a polypeptide comprising at least
CC one antibody heavy chain fused to at least one antibody light chain; (2)
CC a method (M1) of binding an antigen, involves providing a polypeptide
CC comprising at least one antibody heavy chain fused to at least one
CC antibody light chain, and contacting the polypeptide with a sample having
CC an antigen under conditions such that the polypeptide binds to the
CC antigen; (3) a method (M2), which involves providing a vector comprising
CC a bicistronic expression construct comprising genes encoding an antibody
CC heavy chain gene and an antibody light chain gene, and altering the
CC nucleic acid sequence of a splice acceptor sequence or a splice donor
CC sequence in the antibody light chain gene or the antibody heavy chain
CC gene under conditions such that splicing is prevented at the splice
CC acceptor sequence or donor sequence; (4) a nucleic acid sequence produced
CC by (M2); (5) a vector (III) comprising a modified antibody heavy or light
CC gene, where modification eliminates a splice donor or acceptor sequence
CC in antibody heavy or light chain gene; and (6) a host cell comprising
CC (III). (I) is useful in in vitro binding assays for identifying antigens
CC in a mixture or determining the presence or absence of expression of a
CC particular protein. (I) is also useful as vaccine for treating cancer and
CC infections caused by pathogens e.g. virus or bacteria. The present
CC sequence represents an exemplary antibody fusion protein from the present
CC invention.
XX
SQ Sequence 669 AA;

Query Match 100.0%; Score 41; DB 9; Length 669;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 545 QQYSLYRS 552

RESULT 32
AAB43069
ID AAB43069 standard; protein; 79 AA.
XX
AC AAB43069;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF2833 polypeptide sequence SEQ ID NO:5666.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive.
XX
OS Homo sapiens.
XX
PN WO200058473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US008621.
XX

PR 31-MAR-1999; 99US-0127607P.
PR 02-APR-1999; 99US-0127636P.
PR 05-APR-1999; 99US-0127728P.
PR 30-MAR-2000; 2000US-00540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2000-602362/57.
DR N-PSDB; AAC77278.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease.
XX
PS Claim 11; Page 4840-4841; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
SQ Sequence 79 AA;

Query Match 80.5%; Score 33; DB 3; Length 79;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYSLYR 7
||| |||
Db 19 QQYELYR 25

RESULT 33
AAB43084
ID AAB43084 standard; protein; 368 AA.
XX
AC AAB43084;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORFX ORF2848 polypeptide sequence SEQ ID NO:5696.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive.
XX
OS Homo sapiens.
XX
PN WO200058473-A2.
XX
PD 05-OCT-2000.
XX
PF 31-MAR-2000; 2000WO-US008621.
XX
PR 31-MAR-1999; 99US-0127607P.
PR 02-APR-1999; 99US-0127636P.
PR 05-APR-1999; 99US-0127728P.
PR 30-MAR-2000; 2000US-00540763.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2000-602362/57.
DR N-PSDB; AAC77293.
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease.
XX
PS Claim 11; Page 4859-4860; 5507pp; English.
XX
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;
CC anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
CC cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
CC dermatological; immunosuppressive; antiinflammatory; antibacterial;
CC antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
CC sequences can be used for determining the presence of or predisposition
CC to, or preventing or treating pathological conditions associated with an
CC ORFX-associated disorder. The nucleic acids can be used to express ORFX
CC proteins in gene therapy vectors. The proteins and nucleic acids may be
CC used to treat cancers, proliferative disorders, neurodegenerative
CC disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
CC diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
CC storage, systemic lupus erythematosus, severe combined immunodeficiency
CC (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
CC disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
CC cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
CC enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX
SQ Sequence 368 AA;

Query Match 80.5%; Score 33; DB 3; Length 368;
Best Local Similarity 85.7%; Pred. No. 4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYSLYR 7
||| |||
Db 206 QQYELYR 212

RESULT 34
ADJ70573
ID ADJ70573 standard; protein; 393 AA.
XX
AC ADJ70573;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID2379.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;

KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389987P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 2379; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX
SQ Sequence 393 AA;

Query Match 80.5%; Score 33; DB 7; Length 393;
Best Local Similarity 85.7%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYSLYR 7
|||:|||
Db 231 QQYELYR 237

RESULT 35
AAM93645
ID AAM93645 standard; protein; 640 AA.
XX
AC AAM93645;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide, SEQ ID NO: 3503.
XX
KW Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS Homo sapiens.
XX
PN EP1130094-A2.
XX
PD 05-SEP-2001.
XX
PF 07-JUL-2000; 2000EP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
DR N-PSDB; AAK94579.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
PS Claim 8; SEQ ID NO 3503; 1380pp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesising the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX
SQ Sequence 640 AA;

Query Match 80.5%; Score 33; DB 4; Length 640;
Best Local Similarity 85.7%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYSLYR 7
|||:|||
Db 459 QQYELYR 465

RESULT 36
ADL31470
ID ADL31470 standard; protein; 640 AA.
XX
AC ADL31470;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human protein encoded by a full length cDNA clone SeqID 3503.
XX
KW human; medicine; signal transduction; glycoprotein; transcription;
KW oligo-capping method.
XX
OS Homo sapiens.
XX
PN EP1396543-A2.
XX
PD 10-MAR-2004.
XX
PF 07-JUL-2000; 2003EP-00025638.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183865.
PR 07-JUL-2000; 2000EP-00114089.
XX

```
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2004-204755/20.
DR   N-PSDB; ADL31469.
XX
PT   New oligonucleotide primers (830 cDNAs) useful for synthesizing full
PT   length human cDNAs.
XX
PS   Example 1; SEQ ID NO 3503; 1340pp; English.
XX
CC   This invention relates to a novel primers useful for synthesising full
CC   length cDNA molecules that encode human proteins. Specifically, it refers
CC   to secretory or membrane proteins that are potential therapeutic agents/
CC   target molecules in the field of medicine, and in particular genes
CC   encoding proteins that are associated with signal transduction,
CC   glycoproteins and transcription. The present invention describes a method
CC   for efficiently cloning a full length human cDNA from both the 5' and 3'
CC   ends using the oligo-capping method. This polypeptide sequence is a full
CC   length human protein of the invention.
XX
SQ   Sequence 640 AA;

  Query Match             80.5%;  Score 33;  DB 8;  Length 640;
  Best Local Similarity   85.7%;  Pred. No. 7.2e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              ||| |||
Db        459 QQYELYR 465


RESULT 37
ADR10222
ID   ADR10222 standard; protein; 731 AA.
XX
AC   ADR10222;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Human protein useful for treating neurological disease Seq 3728.
XX
KW   human; oligo-capping method; diagnostic marker; gene therapy;
KW   osteoporosis; neurological disease; Alzheimer's disease;
KW   Parkinson's disease; dementia; short memory; cancer;
KW   sense or motor function; emotional reaction; fear response; panic;
KW   osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW   tranquiliser.
XX
OS   Homo sapiens.
XX
PN   EP1447413-A2.
XX
PD   18-AUG-2004.
XX
PF   12-FEB-2004; 2004EP-00003145.
XX
PR   14-FEB-2003; 2003JP-00102207.
PR   09-MAY-2003; 2003JP-00131452.
XX
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T,  Yamamoto J,  Nishikawa T,  Isono Y,  Sugiyama T,  Otsuki T;
PI   Wakamatsu A,  Ishii S,  Nagai K,  Irie R;
XX
DR   WPI; 2004-583265/57.
DR   N-PSDB; ADR08266.
XX
PT   New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT   Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS   Claim 1; SEQ ID NO 3728; 2686pp; English.
XX
CC   This invention relates to novel, isolated full length human cDNA
CC   molecules and the encoded proteins thereof. Specifically, it refers to
CC   cDNA clones obtained by an oligo-capping method, where none of these
CC   clones are identical to any known human mRNAs. The present invention
CC   describes an immunoassay to identify agonists and antagonists, as well as
CC   antibodies, antisense molecules and siRNAs that can all be used to bind
CC   to and modulate expression of the cDNA molecules. As such, these
CC   molecules are useful for diagnostic markers or therapeutic targets for
CC   the various diseases or morbid states. In particular, they are useful in
CC   gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC   disease, Parkinson's disease, dementia, short memory and various cancers,
CC   as well as for maintaining equilibrium of sense or motor function, and
CC   for treating emotional reaction, fear response and panic. Accordingly,
CC   they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian,
CC   cytostatic and tranquiliser activities. This polypeptide is a protein
CC   encoded by a full length human cDNA sequence of the invention. NOTE: This
CC   sequence is not given in the sequence listing of the specification but
CC   can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
CC   office.
XX
SQ   Sequence 731 AA;

  Query Match             80.5%;  Score 33;  DB 8;  Length 731;
  Best Local Similarity   85.7%;  Pred. No. 8.3e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              ||| |||
Db        569 QQYELYR 575


RESULT 38
AAB93899
ID   AAB93899 standard; protein; 1025 AA.
XX
AC   AAB93899;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human protein sequence SEQ ID NO:13848.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-00116126.
XX
PR   29-JUL-1999;   99JP-00248036.
PR   27-AUG-1999;   99JP-00300253.
PR   11-JAN-2000; 2000JP-00118776.
PR   02-MAY-2000; 2000JP-00183767.
PR   09-JUN-2000; 2000JP-00241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT   length cDNAs defined in the specification, and for the detection and/or
PT   diagnosis of the abnormality of the proteins encoded by the full-length
PT   cDNAs.
XX
PS   Claim 8; SEQ ID NO 13848; 2537pp + Sequence Listing; English.
XX
```

CC The present invention describes primer sets for synthesising 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 1025 AA;

```
  Query Match             80.5%;  Score 33;  DB 4;  Length 1025;
  Best Local Similarity   85.7%;  Pred. No. 1.2e+03;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              ||| |||
Db        863 QQYELYR 869
```

RESULT 39
ABB75711
ID ABB75711 standard; protein; 1025 AA.
XX
AC ABB75711;
XX
DT 24-JUN-2002 (first entry)
XX
DE Human poly(ADP-ribose) polymerase p150.
XX
KW Poly(ADP-ribose) polymerase; PARP; p150; human; enzyme; diabetes;
KW cerebral ischaemia; Alzheimer's disease; Parkinson's disease;
KW systemic lupus erythematosus; arthritis; tumour; therapy; diagnosis;
KW cytostatic; vasotropic; antidiabetic; nootropic; neuroprotective;
KW antiparkinsonian; antiarthritic; dermatological; immunosuppressive;
KW antiinflammatory.
XX
OS Homo sapiens.
XX
PN WO200222792-A2.
XX
PD 21-MAR-2002.
XX
PF 11-SEP-2001; 2001WO-EP010494.
XX
PR 12-SEP-2000; 2000EP-00119849.
PR 13-JUN-2001; 2001EP-00113577.
XX
PA (LUES/) LUESCHER B.
PA (AUST/) AUSTEN M.
XX
PI Luescher B, Austen M;
XX
DR WPI; 2002-339867/37.
DR N-PSDB; ABL53715.
XX
PT New polynucleotide encoding poly(ADP-ribose) polymerase useful as a
PT hybridization probe, and for preparing a pharmaceutical composition for
PT preventing and/or treating tumors.
XX
PS Claim 1; Fig 3; 76pp; English.
XX
CC The present sequence is that of a human protein, termed p150, having
CC poly(ADP-ribose) polymerase (PARP) activity. p150 protein was isolated
CC from a native c-Myc complex. Its C-terminal 250 amino acids shows
CC homology to the catalytic domain of PARPs, and biochemical analysis
CC showed this domain to be function. The remaining portions of p150 show no
CC significant homology to known proteins. The p150 protein may participate
CC in activating Myc/Max-driven transcription. It has the capacity to
CC stimulate Myc-mediated transcriptional activation, and the capacity to
CC inhibit cell growth, especially cell proliferation, and/or to inhibit
CC Myc/Ras-mediated transformation of cells. p150 shows ubiquitous
CC expression, and p150 transcription is elevated in the thymus. The
CC invention provides p150 nucleic acids and polypeptides, expression
CC vectors, host cells, antibodies, agonists, antagonists, pharmaceutical
CC compositions and methods for treating disorders associated with aberrant
CC regulation of cellular behaviour. Use of a p150 antagonist for the
CC treatment of cerebral ischaemia, diabetes, Alzheimer's disease,
CC Parkinson's disease, systemic lupus erythematosus or arthritis, or for
CC the prevention and/or treatment of tumours, is claimed. Also claimed is a
CC diagnostic composition comprising a p150 nucleic acid, protein or
CC antibody
XX
SQ Sequence 1025 AA;

```
  Query Match             80.5%;  Score 33;  DB 5;  Length 1025;
  Best Local Similarity   85.7%;  Pred. No. 1.2e+03;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              ||| |||
Db        863 QQYELYR 869
```

RESULT 40
ADY18562
ID ADY18562 standard; protein; 1025 AA.
XX
AC ADY18562;
XX
DT 05-MAY-2005 (first entry)
XX
DE PRO polypeptide SEQ ID NO 4368.
XX
KW Antiinflammatory; Immune disorder; Dermatological; Immunosuppressive;
KW Antirheumatic; Antiarthritic; Osteopathic; Hemostatic; Antianemic;
KW Antithyroid; Antidiabetic; Nephrotropic; CNS-Gen.; Hepatotropic;
KW Virucide; Gastrointestinal-Gen.; Antipsoriatic; Antiasthmatic;
KW Antiallergic; diagnosis.
XX
OS Homo sapiens.
XX
PN WO2005016962-A2.
XX
PD 24-FEB-2005.
XX
PF 11-AUG-2004; 2004WO-US026249.
XX
PR 11-AUG-2003; 2003US-0493546P.
XX
PA (GETH) GENENTECH INC.
XX
PI Abbas A, Clark H, Ouyang W, Williams MP, Wood WI, Wu TD;
XX
DR WPI; 2005-182330/19.
XX
PT New nucleic acid encoding PRO polypeptide, useful for diagnosing and
PT treating an immune related disorder, e.g. systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, thyroiditis, or diabetes mellitus.
XX
PS Claim 8; SEQ ID NO 4368; 158pp; English.
XX

```
CC   The invention relates to an isolated nucleic acid encoding a PRO
CC   polypeptide. The polypeptide, agonist or an antagonist, antibody,
CC   composition, and method are useful for diagnosing and treating an immune
CC   related disorder, e.g. systemic lupus erythematosus, rheumatoid
CC   arthritis. The present sequence represents a PRO polypeptide.
XX
SQ   Sequence 1025 AA;

  Query Match            80.5%;  Score 33;  DB 9;  Length 1025;
  Best Local Similarity  85.7%;  Pred. No. 1.2e+03;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              ||| |||
Db        863 QQYELYR 869


RESULT 41
ABM91906
ID   ABM91906 standard; protein; 1040 AA.
XX
AC   ABM91906;
XX
DT   02-JUN-2005  (first entry)
XX
DE   M. xanthus protein sequence, seq id 11105.
XX
KW   Transgenic plant; DNA replication; gene regulation; gene expression.
XX
OS   Myxococcus xanthus.
XX
PN   US6833447-B1.
XX
PD   21-DEC-2004.
XX
PF   10-JUL-2001; 2001US-00902540.
XX
PR   10-JUL-2000; 2000US-0217883P.
XX
PA   (MONS ) MONSANTO TECHNOLOGY LLC.
XX
PI   Goldman BS,  Hinkle GJ,  Slater SC,  Wiegand RC;
XX
DR   WPI; 2005-028716/03.
XX
PT   New substantially purified Myxococcus xanthus nucleic acid molecule
PT   encoding a nitrite reductase, useful for determining gene expression,
PT   identifying mutations in a gene of interest, and for constructing
PT   mutations in a gene of interest.
XX
PS   Example 2; SEQ ID NO 11105; 25pp; English.
XX
CC   The invention relates to a substantially purified nucleic acid molecule
CC   encoding a nitrite reductase of SEQ ID NO. 11926. Further disclosed is a
CC   recombinant DNA construct for expression of a nitrite reductase gene in a
CC   plant cell, and a plant cell comprising the recombinant DNA construct.
CC   The nucleic acid is useful for determining gene expression, identifying
CC   mutations in a gene of interest, and for constructing mutations in a gene
CC   of interest. Sequences given in records for SEQ IDs 9692-16825 represent
CC   a group of 7134 Mxyococcus xanthus proteins and peptides. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from USPTO
XX
SQ   Sequence 1040 AA;

  Query Match            80.5%;  Score 33;  DB 9;  Length 1040;
  Best Local Similarity  75.0%;  Pred. No. 1.2e+03;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              | |:||||
Db        813 QHYNLYRS 820


RESULT 42
AAU72808
ID   AAU72808 standard; peptide; 8 AA.
XX
AC   AAU72808;
XX
DT   26-FEB-2002  (first entry)
XX
DE   TRA-8 light chain CDR 3.
XX
KW   Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;
KW   TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;
KW   autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
KW   rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;
KW   Addison disease; scleroderma; Goodpasture's syndrome; sterility;
KW   myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
KW   allergy; arteriosclerosis; myocarditis; cardiomyopathy;
KW   glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.
XX
OS   Mus musculus.
XX
PN   WO200183560-A1.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014151.
XX
PR   02-MAY-2000; 2000US-0201344P.
XX
PA   (UABR-) UAB RES FOUND.
XX
PI   Zhou T,  Ichikawa K,  Kimberly RP,  Koopman WJ;
XX
DR   WPI; 2002-049338/06.
XX
PT   Novel antibody specific for tumor necrosis factor-related apoptosis-
PT   inducing ligand, useful for inhibiting cell proliferation in cancer.
XX
PS   Example 16; Page 202; 229pp; English.
XX
CC   The invention describes a novel antibody which recognizes a tumour
CC   necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC   DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
CC   activity to a cell expressing DR5 in vivo. It is also useful for
CC   preparing a therapeutic for selective apoptosis of abnormal or
CC   dysregulated cells, and for inhibiting cell proliferation in a cell,
CC   preferably a human breast, ovary, colon, haematopoietic, prostate,
CC   lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
CC   also be administered e.g. paclitaxel, taxol or cycloheximide. The
CC   antibody is used to treat an autoimmune disease, systemic lupus
CC   erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-
CC   host disease, Sjogren's syndrome, Chron's disease, pernicious anaemia,
CC   Addison disease, scleroderma, Goodpasture's syndrome, autoimmune
CC   haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,
CC   Basedow's disease, insulin-dependent diabetes mellitus, allergy, atopic
CC   disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC   nephritis, hypoplastic anaemia, rejection after organ transplantation,
CC   and numerous malignancies of lung, prostate, liver, ovary, lymphatic or
CC   breast tissue. Complementarity determining regions of the heavy and light
CC   chains of TRA-8 are shown in AAU72803-AAU72808 and the heavy chain
CC   variable region in AAU72809
XX
SQ   Sequence 8 AA;

  Query Match            78.0%;  Score 32;  DB 5;  Length 8;
  Best Local Similarity  75.0%;  Pred. No. 2e+06;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| ||:
Db          1 QQYSSYRT 8
```

```
RESULT 43
AAO29876
ID   AAO29876 standard; peptide; 8 AA.
XX
AC   AAO29876;
XX
DT   27-AUG-2003  (first entry)
XX
DE   Mouse anti-human DR5 antibody (TRA-8) light chain CDR 3.
XX
KW   Tumour necrosis factor; TNF-related apoptosis-inducing ligand; allergy;
KW   inflammatory disease; TRAIL receptor; systemic lupus erythematosus; DR4;
KW   Hashimoto's disease; rheumatoid arthritis; inflammatory disease; cancer;
KW   multiple sclerosis; graft-versus-host disease; arteriosclerosis; asthma;
KW   Goodpasture's syndrome; autoimmune disease; glomerular nephritis; DR5;
KW   Crohn's disease; diabetes mellitus; complementarity determining region;
KW   CDR; TRA-8 antibody; mouse.
XX
OS   Mus sp.
XX
PN   WO2003037913-A2.
XX
PD   08-MAY-2003.
XX
PF   01-NOV-2002; 2002WO-US035333.
XX
PR   01-NOV-2001; 2001US-0346402P.
XX
PA   (UABR-) UAB RES FOUND.
XX
PI   Zhou T,  Kimberly RP,  Koopman WJ,  Lobuglio AF,  Buchsbaum DJ;
XX
DR   WPI; 2003-441350/41.
XX
PT   New purified antibody that specifically binds a TNF-related apoptosis-
PT   inducing ligand receptor DR4 or DR5, useful for treating cancer,
PT   inflammatory disease or autoimmune disease in a subject, e.g. asthma or
PT   rheumatoid arthritis.
XX
PS   Example 16; Page 227; 251pp; English.
XX
CC   The invention relates to an antibody that specifically binds a tumour
CC   necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC   DR4 or DR5. Antibodies of the invention are useful for selectively
CC   inducing apoptosis in target cells expressing DR4, for inhibiting
CC   proliferation of target cells expressing DR4 or for treating cancer,
CC   inflammatory disease or autoimmune disease in a subject e.g. systemic
CC   lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-
CC   versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple
CC   sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or
CC   glomerular nephritis. The present sequence is mouse anti-human DR5
CC   antibody (TRA-8) light chain complementarity determining region (CDR)
XX
SQ   Sequence 8 AA;

  Query Match             78.0%;  Score 32;  DB 6;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 2e+06;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| ||:
Db          1 QQYSSYRT 8


RESULT 44
ADJ79794
ID   ADJ79794 standard; protein; 8 AA.
XX
AC   ADJ79794;
XX
DT   06-MAY-2004  (first entry)
XX
DE   TRA-8 light chain CDR3.
XX
KW   nephrotropic; antiarteriosclerotic; cardiant; antiasthmatic;
KW   antiallergic; antiinflammatory; antidiabetic; haemostatic;
KW   neuroprotective; antiinfertility; immunosuppressive; dermatological;
KW   antianaemic; antirheumatic; antiarthritic; thyromimetic; apoptosis;
KW   proliferation;
KW   tumor necrosis factor-related apoptosis-inducing ligand receptor; TNF;
KW   TRAIL; synovial cell; lymphocyte; neutrophil;
KW   systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis;
KW   graft-versus-host disease; Sjogren's syndrome; pernicious anemia;
KW   Addison disease; scleroderma; Goodpasture's syndrome; Crohn's disease;
KW   autoimmune hemolytic anemia; sterility; myasthenia gravis;
KW   multiple sclerosis; Basedow's disease; thrombotic; thrombocytopenia;
KW   thrombopenia purpura; insulin dependent diabetes mellitus; allergy;
KW   asthma; atopic disease; arteriosclerosis; myocarditis; cardiomyopathy;
KW   glomerular nephritis; hypoplastic anemia.
XX
OS   Homo sapiens.
XX
PN   WO2003038043-A2.
XX
PD   08-MAY-2003.
XX
PF   25-OCT-2002; 2002WO-US034420.
XX
PR   01-NOV-2001; 2001US-0346402P.
PR   24-JUN-2002; 2002US-0391478P.
XX
PA   (UABR-) UAB RES FOUND.
XX
PI   Zhou T,  Ichikawa K,  Kimberly RP,  Koopman WJ,  Oshumi J;
PI   Lobuglio AF,  Buchsbaum DJ;
XX
DR   WPI; 2003-421518/39.
XX
PT   Inducing apoptosis and inhibiting proliferation of target cells
PT   expressing DR5, by contacting the target cell with an antibody that binds
PT   TNF-related apoptosis-inducing ligand receptor DR5 and with therapeutic
PT   agents.
XX
PS   Example 16; SEQ ID NO 30; 274pp; English.
XX
CC   The invention relates to a method of selectively inducing apoptosis in
CC   and inhibiting (M1) proliferation of target cells expressing DR5,
CC   comprising contacting the cell with an antibody that specifically binds
CC   tumor necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL)
CC   receptor DR5, where the antibody, in its soluble form, has in vivo and in
CC   vitro apoptosis-inducing activity in the cell expressing DR5, and
CC   contacting the cell with one or more therapeutic agents. M1 is useful for
CC   inducing apoptosis in target cell and inhibiting proliferation of target
CC   cell expressing DR5, where the target cell is an abnormally proliferating
CC   synovial cells (e.g. rheumatoid arthritis synovial cell), activated
CC   immune cell (e.g. activated lymphocyte), neutrophil, or virally infected
CC   cell. M2 is useful for treating a subject having inflammatory and
CC   autoimmune diseases. The inflammatory or autoimmune disease are selected
CC   from systemic lupus erythematosus, Hashimoto's disease, rheumatoid
CC   arthritis, graft-versus-host disease, Sjogren's syndrome, pernicious
CC   anemia, Addison disease, scleroderma, Goodpasture's syndrome, Crohn's
CC   disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC   multiple sclerosis, Basedow's disease, thrombotic, thrombocytopenia,
CC   thrombopenia purpura, insulin dependent diabetes mellitus, allergy,
CC   asthma, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,
CC   glomerular nephritis, and hypoplastic anemia. This sequence represents a
CC   protein used in the method of the invention.
XX
SQ   Sequence 8 AA;

  Query Match             78.0%;  Score 32;  DB 7;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 2e+06;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
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                 |||| ||:
Db          1 QQYSSYRT 8
```

RESULT 45
ABP58451
ID ABP58451 standard; protein; 107 AA.
XX
AC ABP58451;
XX
DT 14-APR-2003 (first entry)
XX
DE Humanised antibody light chain variable region VKv7.
XX
KW Humanised antibody; monoclonal antibody; antibody engineering;
KW deimmunisation; mouse; DD-3B6/22; D-dimer; fibrin; blood clot; imaging;
KW anticoagulant; antibody; mutant; mutein.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO2003000736-A1.
XX
PD 03-JAN-2003.
XX
PF 26-JUN-2002; 2002WO-AU000827.
XX
PR 26-JUN-2001; 2001US-0301154P.
PR 27-JUN-2001; 2001US-0300947P.
XX
PA (AGEN-) AGEN BIOMEDICAL LTD.
XX
PI Carr FJ, Hamilton AA;
XX
DR WPI; 2003-184035/18.
DR N-PSDB; ABZ57955.
XX
PT Novel variant of an immunointeractive molecule, especially a murine-
PT derived monoclonal antibody having specificity for cross-linked fibrin
PT derivatives, useful for detecting blood clots in vivo and clot
PT dissolution.
XX
PS Claim 20; Page 79; 87pp; English.
XX
CC The present sequence is the protein sequence for 3B6DIVKv7 (VKv7), a
CC 'deimmunised' light chain variable region based on mouse monoclonal
CC antibody DD-3B6/22 (3B6). 3B6 is specific for human D-dimer, a
CC degradation fragment of crosslinked fibrin polymers. The heavy and light
CC chain variable regions of the 3B6 antibody have been deimmunised by
CC inclusion of one or more amino acid mutations designed to eliminate or
CC reduce recognition by major histocompatibility complex class II
CC molecules. Claimed deimmunised 3B6 antibodies for use in humans comprise
CC heavy and light chain variable regions in the combinations VHv5/VKv1,
CC VHv6/VKv1, VHv7/VKv1, VHv5/VKv7, VHv6/VKv7, VHv6/VKv4, VHv7/VKv4,
CC VHv7/VKv7, and VHv5/VKv4 (see ABP58446-51). The antibodies, labelled with
CC a reporter molecule such as a nuclear tag, are useful for detecting blood
CC clots in vivo. Antibodies further comprising a clot dissolution or clot
CC growth prevention agent fused, bound or attached to it, are useful for
CC the dissolution or removal of a blood clot in a human. The antibodies can
CC also be used to deliver cytotoxic agents, such as an isotope that emits
CC beta or gamma emission, to a subject with a fibrin-associated cancer,
CC especially a fibrin encapsulated tumour. They are useful alone or as
CC carriers of diagnostic and/or therapeutic agents to target sites such as
CC blood clots, and also for determining the kinetics of clot dissolution,
CC dissipation and/or disappearance
XX
SQ Sequence 107 AA;

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  Query Match             78.0%;  Score 32;  DB 6;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
```

```
                 ||||||
Db         89 QQYSLY 94
```

RESULT 46
ABP58449
ID ABP58449 standard; protein; 107 AA.
XX
AC ABP58449;
XX
DT 14-APR-2003 (first entry)
XX
DE Humanised antibody light chain variable region VKv1.
XX
KW Humanised antibody; monoclonal antibody; antibody engineering;
KW deimmunisation; mouse; DD-3B6/22; D-dimer; fibrin; blood clot; imaging;
KW anticoagulant; antibody; mutant; mutein.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO2003000736-A1.
XX
PD 03-JAN-2003.
XX
PF 26-JUN-2002; 2002WO-AU000827.
XX
PR 26-JUN-2001; 2001US-0301154P.
PR 27-JUN-2001; 2001US-0300947P.
XX
PA (AGEN-) AGEN BIOMEDICAL LTD.
XX
PI Carr FJ, Hamilton AA;
XX
DR WPI; 2003-184035/18.
DR N-PSDB; ABZ57953.
XX
PT Novel variant of an immunointeractive molecule, especially a murine-
PT derived monoclonal antibody having specificity for cross-linked fibrin
PT derivatives, useful for detecting blood clots in vivo and clot
PT dissolution.
XX
PS Claim 20; Page 78; 87pp; English.
XX
CC The present sequence is the protein sequence for 3B6DIVKv1 (VKv1), a
CC 'deimmunised' light chain variable region based on mouse monoclonal
CC antibody DD-3B6/22 (3B6). 3B6 is specific for human D-dimer, a
CC degradation fragment of crosslinked fibrin polymers. The heavy and light
CC chain variable regions of the 3B6 antibody have been deimmunised by
CC inclusion of one or more amino acid mutations designed to eliminate or
CC reduce recognition by major histocompatibility complex class II
CC molecules. Claimed deimmunised 3B6 antibodies for use in humans comprise
CC heavy and light chain variable regions in the combinations VHv5/VKv1,
CC VHv6/VKv1, VHv7/VKv1, VHv5/VKv7, VHv6/VKv7, VHv6/VKv4, VHv7/VKv4,
CC VHv7/VKv7, and VHv5/VKv4 (see ABP58446-51). The antibodies, labelled with
CC a reporter molecule such as a nuclear tag, are useful for detecting blood
CC clots in vivo. Antibodies further comprising a clot dissolution or clot
CC growth prevention agent fused, bound or attached to it, are useful for
CC the dissolution or removal of a blood clot in a human. The antibodies can
CC also be used to deliver cytotoxic agents, such as an isotope that emits
CC beta or gamma emission, to a subject with a fibrin-associated cancer,
CC especially a fibrin encapsulated tumour. They are useful alone or as
CC carriers of diagnostic and/or therapeutic agents to target sites such as
CC blood clots, and also for determining the kinetics of clot dissolution,
CC dissipation and/or disappearance
XX
SQ Sequence 107 AA;

```
  Query Match             78.0%;  Score 32;  DB 6;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
```

```
                  ||||||
Db          89 QQYSLY 94
```

RESULT 47
ABP58450
ID ABP58450 standard; protein; 107 AA.
XX
AC ABP58450;
XX
DT 14-APR-2003 (first entry)
XX
DE Humanised antibody light chain variable region VKv4.
XX
KW Humanised antibody; monoclonal antibody; antibody engineering;
KW deimmunisation; mouse; DD-3B6/22; D-dimer; fibrin; blood clot; imaging;
KW anticoagulant; antibody; mutant; mutein.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO2003000736-A1.
XX
PD 03-JAN-2003.
XX
PF 26-JUN-2002; 2002WO-AU000827.
XX
PR 26-JUN-2001; 2001US-0301154P.
PR 27-JUN-2001; 2001US-0300947P.
XX
PA (AGEN-) AGEN BIOMEDICAL LTD.
XX
PI Carr FJ, Hamilton AA;
XX
DR WPI; 2003-184035/18.
DR N-PSDB; ABZ57954.
XX
PT Novel variant of an immunointeractive molecule, especially a murine-
PT derived monoclonal antibody having specificity for cross-linked fibrin
PT derivatives, useful for detecting blood clots in vivo and clot
PT dissolution.
XX
PS Claim 20; Page 78-79; 87pp; English.
XX
CC The present sequence is the protein sequence for 3B6DIVKv4 (VKv4), a
CC 'deimmunised' light chain variable region based on mouse monoclonal
CC antibody DD-3B6/22 (3B6). 3B6 is specific for human D-dimer, a
CC degradation fragment of crosslinked fibrin polymers. The heavy and light
CC chain variable regions of the 3B6 antibody have been deimmunised by
CC inclusion of one or more amino acid mutations designed to eliminate or
CC reduce recognition by major histocompatibility complex class II
CC molecules. Claimed deimmunised 3B6 antibodies for use in humans comprise
CC heavy and light chain variable regions in the combinations VHv5/VKv1,
CC VHv6/VKv1, VHv7/VKv1, VHv5/VKv7, VHv6/VKv7, VHv6/VKv4, VHv7/VKv4,
CC VHv7/VKv7, and VHv5/VKv4 (see ABP58446-51). The antibodies, labelled with
CC a reporter molecule such as a nuclear tag, are useful for detecting blood
CC clots in vivo. Antibodies further comprising a clot dissolution or clot
CC growth prevention agent fused, bound or attached to it, are useful for
CC the dissolution or removal of a blood clot in a human. The antibodies can
CC also be used to deliver cytotoxic agents, such as an isotope that emits
CC beta or gamma emission, to a subject with a fibrin-associated cancer,
CC especially a fibrin encapsulated tumour. They are useful alone or as
CC carriers of diagnostic and/or therapeutic agents to target sites such as
CC blood clots, and also for determining the kinetics of clot dissolution,
CC dissipation and/or disappearance
XX
SQ Sequence 107 AA;

```
  Query Match           78.0%;  Score 32;  DB 6;  Length 107;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
```

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                  ||||||
Db          89 QQYSLY 94
```

RESULT 48
AAU72815
ID AAU72815 standard; protein; 212 AA.
XX
AC AAU72815;
XX
DT 26-FEB-2002 (first entry)
XX
DE DNA encoding TRA-8 light chain/human Ig light chain fusion (LM1).
XX
KW Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;
KW TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;
KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;
KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;
KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;
KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.
XX
OS Mus musculus.
OS Homo sapiens.
XX
PN WO200183560-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014151.
XX
PR 02-MAY-2000; 2000US-0201344P.
XX
PA (UABR-) UAB RES FOUND.
XX
PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;
XX
DR WPI; 2002-049338/06.
XX
PT Novel antibody specific for tumor necrosis factor-related apoptosis-
PT inducing ligand, useful for inhibiting cell proliferation in cancer.
XX
PS Example 26; Page 215-216; 229pp; English.
XX
CC The invention describes a novel antibody which recognizes a tumour
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
CC activity to a cell expressing DR5 in vivo. It is also useful for
CC preparing a therapeutic for selective apoptosis of abnormal or
CC dysregulated cells, and for inhibiting cell proliferation in a cell,
CC preferably a human breast, ovary, colon, haematopoietic, prostate,
CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
CC also be administered e.g. paclitaxel, taxol or cycloheximide. The
CC antibody is used to treat an autoimmune disease, systemic lupus
CC erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-
CC host disease, Sjogren's syndrome, Chron's disease, pernicious anaemia,
CC Addison disease, scleroderma, Goodpasture's syndrome, autoimmune
CC haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,
CC Basedow's disease, insulin-dependent diabetes mellitus, allergy, atopic
CC disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, rejection after organ transplantation,
CC and numerous malignancies of lung, prostate, liver, ovary, lymphatic or
CC breast tissue. Fusions of the TRA-8 light chain variable region with the
CC human Ig constant region are shown in AAU72815-AAU72819 and AAU72810
XX
SQ Sequence 212 AA;

```
  Query Match           78.0%;  Score 32;  DB 5;  Length 212;
  Best Local Similarity  75.0%;  Pred. No. 3.6e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
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                ||||  ||:
Db         89 QQYSSYRT 96


RESULT 49
AAO29883
ID   AAO29883 standard; protein; 212 AA.
XX
AC   AAO29883;
XX
DT   23-OCT-2003  (revised)
DT   27-AUG-2003  (first entry)
XX
DE   LM1 fusion protein.
XX
KW   Tumour necrosis factor; TNF-related apoptosis-inducing ligand; allergy;
KW   inflammatory disease; TRAIL receptor; systemic lupus erythematosus; DR4;
KW   Hashimoto's disease; rheumatoid arthritis; inflammatory disease; cancer;
KW   multiple sclerosis; graft-versus-host disease; arteriosclerosis; asthma;
KW   Goodpasture's syndrome; autoimmune disease; glomerular nephritis; DR5;
KW   Crohn's disease; diabetes mellitus; antibody; mouse; fusion protein;
KW   human; LM1.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Chimeric.
XX
PN   WO2003037913-A2.
XX
PD   08-MAY-2003.
XX
PF   01-NOV-2002; 2002WO-US035333.
XX
PR   01-NOV-2001; 2001US-0346402P.
XX
PA   (UABR-) UAB RES FOUND.
XX
PI   Zhou T,  Kimberly RP,  Koopman WJ,  Lobuglio AF,  Buchsbaum DJ;
XX
DR   WPI; 2003-441350/41.
XX
PT   New purified antibody that specifically binds a TNF-related apoptosis-
PT   inducing ligand receptor DR4 or DR5, useful for treating cancer,
PT   inflammatory disease or autoimmune disease in a subject, e.g. asthma or
PT   rheumatoid arthritis.
XX
PS   Example 26; Page 241; 251pp; English.
XX
CC   The invention relates to an antibody that specifically binds a tumour
CC   necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC   DR4 or DR5. Antibodies of the invention are useful for selectively
CC   inducing apoptosis in target cells expressing DR4, for inhibiting
CC   proliferation of target cells expressing DR4 or for treating cancer,
CC   inflammatory disease or autoimmune disease in a subject e.g. systemic
CC   lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-
CC   versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple
CC   sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or
CC   glomerular nephritis. The present sequence is LM1 fusion protein which
CC   comprises humanised mouse anti-human DR5 antibody (TRA-8) light chain
CC   variable region and human Ig light (kappa) chain constant region.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 212 AA;

  Query Match             78.0%;  Score 32;  DB 6;  Length 212;
  Best Local Similarity   75.0%;  Pred. No. 3.6e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
                ||||  ||:
Db         89 QQYSSYRT 96
```

```
RESULT 50
ADJ79836
ID   ADJ79836 standard; protein; 212 AA.
XX
AC   ADJ79836;
XX
DT   06-MAY-2004  (first entry)
XX
DE   LM1-type humanized TRA-8 heavy chain.
XX
KW   nephrotropic; antiarteriosclerotic; cardiant; antiasthmatic;
KW   antiallergic; antiinflammatory; antidiabetic; haemostatic;
KW   neuroprotective; antiinfertility; immunosuppressive; dermatological;
KW   antianaemic; antirheumatic; antiarthritic; thyromimetic; apoptosis;
KW   proliferation;
KW   tumor necrosis factor-related apoptosis-inducing ligand receptor; TNF;
KW   TRAIL; synovial cell; lymphocyte; neutrophil;
KW   systemic lupus erythematosus; Hashimoto's disease; rheumatoid arthritis;
KW   graft-versus-host disease; Sjogren's syndrome; pernicious anemia;
KW   Addison disease; scleroderma; Goodpasture's syndrome; Crohn's disease;
KW   autoimmune hemolytic anemia; sterility; myasthenia gravis;
KW   multiple sclerosis; Basedow's disease; thrombotic; thrombocytopenia;
KW   thrombopenia purpura; insulin dependent diabetes mellitus; allergy;
KW   asthma; atopic disease; arteriosclerosis; myocarditis; cardiomyopathy;
KW   glomerular nephritis; hypoplastic anemia.
XX
OS   Homo sapiens.
XX
PN   WO2003038043-A2.
XX
PD   08-MAY-2003.
XX
PF   25-OCT-2002; 2002WO-US034420.
XX
PR   01-NOV-2001; 2001US-0346402P.
PR   24-JUN-2002; 2002US-0391478P.
XX
PA   (UABR-) UAB RES FOUND.
XX
PI   Zhou T,  Ichikawa K,  Kimberly RP,  Koopman WJ,  Oshumi J;
PI   Lobuglio AF,  Buchsbaum DJ;
XX
DR   WPI; 2003-421518/39.
XX
PT   Inducing apoptosis and inhibiting proliferation of target cells
PT   expressing DR5, by contacting the target cell with an antibody that binds
PT   TNF-related apoptosis-inducing ligand receptor DR5 and with therapeutic
PT   agents.
XX
PS   Example 26; SEQ ID NO 72; 274pp; English.
XX
CC   The invention relates to a method of selectively inducing apoptosis in
CC   and inhibiting (M1) proliferation of target cells expressing DR5,
CC   comprising contacting the cell with an antibody that specifically binds
CC   tumor necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL)
CC   receptor DR5, where the antibody, in its soluble form, has in vivo and in
CC   vitro apoptosis-inducing activity in the cell expressing DR5, and
CC   contacting the cell with one or more therapeutic agents. M1 is useful for
CC   inducing apoptosis in target cell and inhibiting proliferation of target
CC   cell expressing DR5, where the target cell is an abnormally proliferating
CC   synovial cells (e.g. rheumatoid arthritis synovial cell), activated
CC   immune cell (e.g. activated lymphocyte), neutrophil, or virally infected
CC   cell. M2 is useful for treating a subject having inflammatory and
CC   autoimmune diseases. The inflammatory or autoimmune disease are selected
CC   from systemic lupus erythematosus, Hashimoto's disease, rheumatoid
CC   arthritis, graft-versus-host disease, Sjogren's syndrome, pernicious
CC   anemia, Addison disease, scleroderma, Goodpasture's syndrome, Crohn's
CC   disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
CC   multiple sclerosis, Basedow's disease, thrombotic, thrombocytopenia,
CC   thrombopenia purpura, insulin dependent diabetes mellitus, allergy,
CC   asthma, atopic disease, arteriosclerosis, myocarditis, cardiomyopathy,
CC   glomerular nephritis, and hypoplastic anemia. This sequence represents a
CC   protein used in the method of the invention.
```

```
XX
SQ   Sequence 212 AA;

  Query Match             78.0%;  Score 32;  DB 7;  Length 212;
  Best Local Similarity   75.0%;  Pred. No. 3.6e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| ||:
Db         89 QQYSSYRT 96


Search completed: March 23, 2006, 01:52:29
Job time : 100.589 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:54:26 ; Search time 11.0685 Seconds
(without alignments)
69.543 Million cell updates/sec

Title: US-10-755-382-22
Perfect score: 41
Sequence: 1 QQYSLYRS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	82.9	548	2	S61096	probable membrane
2	32	78.0	198	2	C97475	hypothetical prote
3	32	78.0	358	2	G95353	Probable ABC trans
4	32	78.0	382	2	T29554	hypothetical prote
5	32	78.0	423	2	T16750	hypothetical prote
6	31	75.6	104	2	T41381	Chaperonins 10 Kd
7	31	75.6	447	2	S52437	CDP-diacylglycerol
8	31	75.6	505	2	AE1451	hypothetical prote
9	31	75.6	729	2	T35028	probable glycosyl
10	31	75.6	1083	2	A38919	hypothetical prote
11	31	75.6	1541	1	S71839	canalicular multid
12	30	73.2	282	2	C72355	hypothetical prote
13	30	73.2	602	2	S23991	conjugative transf
14	30	73.2	1290	2	G64630	vacuolating cytoto
15	30	73.2	1489	2	G83771	hypothetical prote
16	29	70.7	145	2	H84559	hypothetical prote
17	29	70.7	146	2	T16468	hypothetical prote
18	29	70.7	180	2	T37857	hypothetical prote
19	29	70.7	221	2	T21117	hypothetical prote
20	29	70.7	225	2	G71533	probable pts iia p
21	29	70.7	228	2	S11473	serum amyloid P-co
22	29	70.7	237	2	S55135	hypothetical prote
23	29	70.7	243	2	AG0665	ABC transporter AT
24	29	70.7	355	2	T05390	probable cysteine
25	29	70.7	366	2	T44665	conserved hypothet
26	29	70.7	384	2	I51267	collagenase (EC 3.
27	29	70.7	409	2	G82522	type I restriction
28	29	70.7	425	2	D71965	apolipoprotein n-a
29	29	70.7	469	1	KCBOI	interstitial colla
30	29	70.7	480	2	E83105	exodeoxyribonuclea
31	29	70.7	530	2	B36921	methyl coenzyme M
32	29	70.7	627	2	T10290	hypothetical prote
33	29	70.7	649	2	B91284	probable integrase
34	29	70.7	649	2	D86125	probable integrase
35	29	70.7	660	2	AD0661	invasin-like prote
36	29	70.7	680	2	H84774	probable homeodoma
37	29	70.7	906	2	E84948	NADH2 dehydrogenas
38	29	70.7	920	2	AD2143	two-component sens
39	29	70.7	1253	2	S62544	hypothetical prote
40	29	70.7	1388	2	T30335	KLP2 protein - Afr
41	29	70.7	1532	2	T18438	hypothetical prote
42	29	70.7	1767	2	H97912	conserved hypothet
43	28	68.3	92	2	E95163	conserved hypothet
44	28	68.3	92	2	D98029	conserved hypothet
45	28	68.3	94	2	A86698	hypothetical prote
46	28	68.3	96	2	B82436	conserved hypothet
47	28	68.3	110	2	H96602	unknown protein F1
48	28	68.3	113	2	AH0397	probable lipoprote
49	28	68.3	122	2	T46207	hypothetical prote
50	28	68.3	141	2	A95226	hypothetical prote
51	28	68.3	141	2	D98090	hypothetical prote
52	28	68.3	141	2	AB3143	hypothetical prote
53	28	68.3	141	2	B98145	hypothetical prote
54	28	68.3	154	2	B97868	hypothetical prote
55	28	68.3	159	1	S42878	H+-exporting ATPas
56	28	68.3	184	2	A45503	41-2 protein antig
57	28	68.3	217	2	H70123	hypothetical prote
58	28	68.3	218	2	D87264	hypothetical prote
59	28	68.3	240	2	T49131	hypothetical prote
60	28	68.3	265	2	T18039	ORF4 protein - Chl
61	28	68.3	270	2	G64603	outer membrane pro
62	28	68.3	270	2	G71909	probable outer mem
63	28	68.3	317	2	C89927	conserved hypothet
64	28	68.3	321	2	E81921	probable DNA-inver
65	28	68.3	343	2	S75435	hypothetical prote
66	28	68.3	354	2	AC0932	uroporphyrinogen d
67	28	68.3	354	2	F86091	uroporphyrinogen d
68	28	68.3	354	2	H65206	uroporphyrinogen d
69	28	68.3	354	2	H91243	uroporphyrinogen d
70	28	68.3	362	2	T41910	hypothetical prote
71	28	68.3	362	2	E69605	spore coat protein
72	28	68.3	371	2	A90044	hypothetical prote
73	28	68.3	379	2	S73517	probable mannitol-
74	28	68.3	381	2	C71680	hypothetical prote
75	28	68.3	381	2	T21849	hypothetical prote
76	28	68.3	392	2	H96516	F16N3.10 [imported
77	28	68.3	393	2	S16846	surface layer 45.4
78	28	68.3	411	2	S11961	hypothetical prote
79	28	68.3	444	2	JC7084	alpha-1,3-mannosyl
80	28	68.3	446	2	D87432	conserved hypothet
81	28	68.3	455	2	AI2409	cytochrome P450 [i
82	28	68.3	457	2	T05651	hypothetical prote
83	28	68.3	458	2	E69528	cobyrinic acid a,c
84	28	68.3	469	2	A83411	hypothetical prote
85	28	68.3	546	2	A69890	hypothetical prote
86	28	68.3	547	2	F83720	2,4-diaminobutyrat
87	28	68.3	558	2	E84324	TRK potassium upta
88	28	68.3	578	2	S55102	PSP2 protein - yea
89	28	68.3	594	2	T39677	transcription regu
90	28	68.3	650	2	AE1992	ABC transporter AT
91	28	68.3	789	2	T42564	ribonucleoside-dip
92	28	68.3	799	2	T02981	1,4-alpha-glucan b
93	28	68.3	799	2	T01663	1,4-alpha-glucan b
94	28	68.3	825	2	A48537	starch branching e
95	28	68.3	861	2	S77086	hypothetical prote
96	28	68.3	1061	2	I49328	retinoblastoma-ass
97	28	68.3	1066	2	AB1228	transporter, (to B
98	28	68.3	1066	2	AD1581	transporter, (to B
99	28	68.3	1068	2	S64015	pleiotropic drug r
100	28	68.3	1099	2	G90546	conserved hypothet
101	28	68.3	1148	2	F86403	probable transposo
102	28	68.3	1166	2	H71609	hypothetical prote

103	28	68.3	1655	2	T13998	gene mastermind pr
104	28	68.3	1744	2	T32228	hypothetical prote
105	28	68.3	2358	2	T39569	probable alpha-glu
106	28	68.3	2371	2	T43432	alpha-glucan synth
107	27	65.9	63	2	H84265	hypothetical prote
108	27	65.9	65	2	C82339	hypothetical prote
109	27	65.9	65	2	C82290	hypothetical prote
110	27	65.9	72	2	F97050	hypothetical prote
111	27	65.9	73	2	H91197	EscF protein [impo
112	27	65.9	73	2	D86044	escF [imported] -
113	27	65.9	79	2	F91093	type III secretion
114	27	65.9	80	2	AE0849	pathogenicity 1 is
115	27	65.9	80	2	S69784	prgI protein - Sal
116	27	65.9	82	2	G69446	hypothetical prote
117	27	65.9	83	2	A45271	invasin secretion
118	27	65.9	100	1	WMWGN3	11K protein - narc
119	27	65.9	100	2	H38601	Ig kappa chain V r
120	27	65.9	107	2	T41393	probable transcrip
121	27	65.9	116	2	T01295	hypothetical prote
122	27	65.9	132	2	C96996	hypothetical prote
123	27	65.9	139	2	C64028	hypothetical prote
124	27	65.9	148	2	A61237	E6 protein - human
125	27	65.9	148	2	S36573	E6 protein - human
126	27	65.9	150	2	D86683	hypothetical prote
127	27	65.9	157	2	H86799	hypothetical prote
128	27	65.9	165	2	H71649	hypothetical prote
129	27	65.9	166	2	H86243	hypothetical prote
130	27	65.9	169	2	D84027	molybdopterin-guan
131	27	65.9	187	2	AF0401	probable regulator
132	27	65.9	201	2	AG0793	Ais protein [impor
133	27	65.9	201	2	S74027	hypothetical prote
134	27	65.9	203	2	S75194	hypothetical prote
135	27	65.9	215	2	AB2141	hypothetical prote
136	27	65.9	227	2	D72508	hypothetical prote
137	27	65.9	240	2	T33755	hypothetical prote
138	27	65.9	249	2	AI3401	arginyltransferase
139	27	65.9	250	2	G69438	conserved hypothet
140	27	65.9	264	2	H83224	phosphonate transp
141	27	65.9	276	1	F35718	phnE protein - Esc
142	27	65.9	276	2	F91264	hypothetical prote
143	27	65.9	276	2	C86105	hypothetical prote
144	27	65.9	277	1	PRSAEB	epidermolytic toxi
145	27	65.9	277	2	E98328	hypothetical prote
146	27	65.9	281	2	S34496	hypothetical prote
147	27	65.9	287	2	G84758	hypothetical prote
148	27	65.9	289	2	A83028	proteinase subunit
149	27	65.9	294	2	G90032	hypothetical prote
150	27	65.9	296	2	H75439	probable antibioti
151	27	65.9	306	2	T20012	hypothetical prote
152	27	65.9	310	2	AH2954	hypothetical prote
153	27	65.9	320	2	B36289	CeMyoD protein - C
154	27	65.9	324	2	A36289	CeMyoD protein 1 -
155	27	65.9	331	2	AF3526	homoprotocatechuat
156	27	65.9	336	2	E69214	GTP-binding protei
157	27	65.9	337	2	C82190	formate dehydrogen
158	27	65.9	358	2	D96722	hypothetical prote
159	27	65.9	359	2	E87447	sulfate ABC transp
160	27	65.9	360	2	T15323	hypothetical prote
161	27	65.9	365	2	T39098	hypothetical prote
162	27	65.9	372	2	F90159	sarcosine oxidase,
163	27	65.9	372	2	T23938	hypothetical prote
164	27	65.9	378	2	T35036	hypothetical prote
165	27	65.9	384	2	T02968	cyclin A-type (clo
166	27	65.9	387	2	T07687	omega-6 desaturase
167	27	65.9	395	2	G75587	hypothetical prote
168	27	65.9	398	2	T02484	hypothetical prote
169	27	65.9	398	2	S17428	interleukin-1 rece
170	27	65.9	399	2	AD0498	conserved hypothet
171	27	65.9	405	2	E64995	hypothetical prote
172	27	65.9	420	2	D69252	L-carnitine dehydr
173	27	65.9	432	2	E96680	hypothetical prote
174	27	65.9	438	2	C72006	conserved hypothet
175	27	65.9	438	2	F86619	CT372 hypothetical
176	27	65.9	442	2	E71523	hypothetical prote
177	27	65.9	448	2	T23263	hypothetical prote
178	27	65.9	449	2	G95004	competence factor
179	27	65.9	449	2	D97877	transport protein
180	27	65.9	465	2	S41084	triacylglycerol li
181	27	65.9	466	2	T44650	capsular polysacch
182	27	65.9	467	2	B90502	hypothetical prote
183	27	65.9	471	2	A81680	conserved hypothet
184	27	65.9	477	2	S76496	hypothetical prote
185	27	65.9	480	2	T34102	hypothetical prote
186	27	65.9	481	2	JC5378	protein disulfide-
187	27	65.9	481	2	D71927	cag island protein
188	27	65.9	481	2	B64585	cag pathogenicity
189	27	65.9	483	2	E83359	chitinase PA2300 [
190	27	65.9	485	2	A84859	probable cytochrom
191	27	65.9	497	2	S31477	finger protein zfp
192	27	65.9	504	2	AG1847	anthranilate synth
193	27	65.9	521	2	S27475	nitrogenase (EC 1.
194	27	65.9	521	2	T15322	hypothetical prote
195	27	65.9	527	2	A81712	4-alpha-glucanotra
196	27	65.9	527	2	G71557	probable glucanotr
197	27	65.9	544	2	S41091	triacylglycerol li
198	27	65.9	544	2	S59958	triacylglycerol li
199	27	65.9	544	2	S41090	triacylglycerol li
200	27	65.9	544	2	S41092	triacylglycerol li
201	27	65.9	544	2	S41096	triacylglycerol li
202	27	65.9	544	2	S41093	triacylglycerol li
203	27	65.9	560	2	S50401	hypothetical prote
204	27	65.9	563	1	ACGUGC	triacylglycerol li
205	27	65.9	563	2	S59957	triacylglycerol li
206	27	65.9	567	2	S58750	NADH2 dehydrogenas
207	27	65.9	580	2	G72202	beta transducin-re
208	27	65.9	581	2	E69395	H+-transporting AT
209	27	65.9	583	2	H69165	hypothetical prote
210	27	65.9	584	2	G69227	ATP synthase, subu
211	27	65.9	593	2	A46733	Na+-transporting A
212	27	65.9	594	2	B64327	H+-transporting tw
213	27	65.9	599	2	G83821	DNA primase dnaG [
214	27	65.9	599	2	AG1964	hypothetical prote
215	27	65.9	622	2	S57684	probable membrane
216	27	65.9	638	2	S36546	E1 protein - human
217	27	65.9	640	2	G96034	conserved hypothet
218	27	65.9	640	2	AC0806	probable lipopolys
219	27	65.9	641	2	T17278	hypothetical prote
220	27	65.9	647	2	T42579	capsid protein 35
221	27	65.9	649	1	W1WLHS	E1 protein - human
222	27	65.9	651	2	A72384	conserved hypothet
223	27	65.9	669	2	S75785	translation elonga
224	27	65.9	678	2	S48412	probable membrane
225	27	65.9	679	2	D69329	conserved hypothet
226	27	65.9	681	2	E64598	hypothetical prote
227	27	65.9	683	2	H71914	hypothetical prote
228	27	65.9	696	2	D64664	outer membrane pro
229	27	65.9	697	2	C71850	probable outer mem
230	27	65.9	699	2	T50457	protein kinase [im
231	27	65.9	700	2	T27364	hypothetical prote
232	27	65.9	733	2	S44254	alpha-galactosidas
233	27	65.9	756	2	AI3275	phosphoenolpyruvat
234	27	65.9	761	2	E82205	chemotaxis protein
235	27	65.9	787	2	C75068	probable beta-gala
236	27	65.9	824	2	S40937	hypothetical prote
237	27	65.9	840	2	E96541	unknown protein [i
238	27	65.9	841	2	E71808	probable iron (III
239	27	65.9	842	2	H64694	iron(III) dicitrat
240	27	65.9	862	2	T29133	hypothetical prote
241	27	65.9	862	2	D70199	DNA mismatch repai
242	27	65.9	879	2	H82192	conserved hypothet
243	27	65.9	918	2	A89221	protein T27F2.2 [i
244	27	65.9	924	2	T21738	hypothetical prote
245	27	65.9	928	2	S50578	hypothetical prote
246	27	65.9	962	2	T05845	hypothetical prote
247	27	65.9	997	2	T15243	hypothetical prote
248	27	65.9	1045	2	F90365	hypothetical prote

249	27	65.9	1077	2	D71660	hypothetical prote
250	27	65.9	1098	1	YGBSG1	phenylalanine race
251	27	65.9	1173	2	B97208	pyruvate ferredoxi
252	27	65.9	1283	2	A47377	multidrug resistan
253	27	65.9	1287	2	B53739	vacuolating cytoto
254	27	65.9	1288	2	E71884	vacuolating cytoto
255	27	65.9	1291	2	S44983	vacuolating cytoto
256	27	65.9	1429	2	S06434	homeotic protein 1
257	27	65.9	1495	2	S27001	alpha-2-macroglobu
258	27	65.9	1520	2	T00273	hypothetical prote
259	27	65.9	1564	2	S55517	probable transport
260	27	65.9	1581	1	VGWJBV	peplomer glycoprot
261	27	65.9	1595	2	T31082	endo-1,4-beta-xyla
262	27	65.9	1878	2	E86189	hypothetical prote
263	27	65.9	1963	2	T49914	callose synthase c
264	27	65.9	1998	2	T13009	hypothetical prote
265	27	65.9	2054	2	T07584	hypothetical prote
266	27	65.9	2276	2	T00076	hypothetical prote
267	27	65.9	2677	2	A38194	desmoplakin I - hu
268	27	65.9	5369	2	T44807	mycosubtilin synth
269	26	63.4	56	2	AH3377	hypothetical cytos
270	26	63.4	72	2	C70241	hypothetical prote
271	26	63.4	92	2	S28564	hypothetical prote
272	26	63.4	101	2	AF0223	hypothetical prote
273	26	63.4	104	2	T45316	hypothetical prote
274	26	63.4	104	2	E90635	CcdB-like protein
275	26	63.4	104	2	E85486	CcdB-like protein
276	26	63.4	106	1	NRASTP	ribonuclease T1 (E
277	26	63.4	108	1	K1HUKU	Ig kappa chain V-I
278	26	63.4	111	2	H84201	hypothetical prote
279	26	63.4	116	2	JC5188	sporulation-specif
280	26	63.4	117	2	S42466	Ig kappa chain V r
281	26	63.4	118	2	G70306	ribosomal protein
282	26	63.4	128	2	F69310	conserved hypothet
283	26	63.4	141	2	A32124	photosystem I chai
284	26	63.4	147	2	S76854	hypothetical prote
285	26	63.4	147	2	F86660	HYPOTETICAL PROTEI
286	26	63.4	149	2	D82068	DNA polymerase III
287	26	63.4	153	2	F70882	hypothetical prote
288	26	63.4	180	2	F70454	hypothetical prote
289	26	63.4	181	2	F75561	hypothetical prote
290	26	63.4	190	2	F72206	hypothetical prote
291	26	63.4	190	2	T37428	membrane glycoprot
292	26	63.4	194	2	I42521	A43R protein - vac
293	26	63.4	194	2	JQ1780	SalF5R protein pre
294	26	63.4	195	2	T28588	18R protein - vari
295	26	63.4	195	2	H72169	A51R protein - var
296	26	63.4	195	2	D36853	A48R protein - var
297	26	63.4	201	2	F83441	hypothetical prote
298	26	63.4	202	2	D84013	hypothetical prote
299	26	63.4	211	2	AH3232	autoinducer synthe
300	26	63.4	216	2	F91064	hypothetical prote
301	26	63.4	216	2	B85909	hypothetical prote
302	26	63.4	224	2	F90606	conserved hypothet
303	26	63.4	225	2	F86498	Pts IIA protein wi
304	26	63.4	225	2	F72124	pts iia protein +
305	26	63.4	229	2	JC5409	platelet-activatin
306	26	63.4	230	2	S64784	hypothetical prote
307	26	63.4	233	1	F69178	conserved hypothet
308	26	63.4	238	2	S62809	type I restriction
309	26	63.4	246	2	T24493	hypothetical prote
310	26	63.4	249	2	S73553	restriction-modifi
311	26	63.4	252	2	S01829	hypothetical prote
312	26	63.4	254	2	F82733	arginine-tRNA-prot
313	26	63.4	257	2	A28664	enterotoxin A prec
314	26	63.4	268	2	S73797	restriction enzyme
315	26	63.4	279	2	A72102	conserved hypothet
316	26	63.4	279	2	G86522	CT142 hypothetical
317	26	63.4	294	2	JT0536	ADP-ribosyl-nitrog
318	26	63.4	296	2	B69678	involved in polyke
319	26	63.4	298	2	B98071	magnesium and coba
320	26	63.4	298	2	A83977	cytochrome caa3 ox
321	26	63.4	302	2	B95204	transporter, CorA
322	26	63.4	306	2	S73876	protein prrB homol
323	26	63.4	308	2	AB3209	hypothetical prote
324	26	63.4	315	2	E83064	hypothetical prote
325	26	63.4	330	2	S73819	restriction enzyme
326	26	63.4	335	2	S73392	type I restriction
327	26	63.4	338	2	A88908	protein Y41E3.7 [i
328	26	63.4	340	2	AD3567	hypothetical prote
329	26	63.4	341	2	D48435	cysteine proteinas
330	26	63.4	344	2	JC5942	chemokine receptor
331	26	63.4	347	2	JC7999	basic helix-loop-h
332	26	63.4	349	2	JC6311	interferon recepto
333	26	63.4	357	2	S18236	omega secalin prec
334	26	63.4	357	2	S18235	omega secalin prec
335	26	63.4	359	2	A41602	transcription fact
336	26	63.4	359	2	T21373	hypothetical prote
337	26	63.4	365	2	T20252	hypothetical prote
338	26	63.4	367	2	A81069	tRNA (5-methylamin
339	26	63.4	375	2	E81442	probable MCP-domai
340	26	63.4	380	2	E88421	protein R74.2 [imp
341	26	63.4	383	2	H81798	tRNA (5-methylamin
342	26	63.4	388	2	E64707	outer membrane pro
343	26	63.4	388	2	C71813	probable outer mem
344	26	63.4	395	2	S64299	probable membrane
345	26	63.4	399	2	T21586	hypothetical prote
346	26	63.4	400	2	T24258	hypothetical prote
347	26	63.4	409	2	T46922	hypothetical prote
348	26	63.4	419	2	T04886	DAG protein homolo
349	26	63.4	421	2	D72677	hypothetical prote
350	26	63.4	423	2	S74278	hypothetical prote
351	26	63.4	425	2	D64542	apolipoprotein N-a
352	26	63.4	426	2	F97022	D-alanyl-D-alanine
353	26	63.4	427	2	I51580	XFKH2 protein - Af
354	26	63.4	429	2	T47717	beta-1,3-glucanase
355	26	63.4	435	2	T26818	hypothetical prote
356	26	63.4	441	2	T42694	hypothetical prote
357	26	63.4	442	2	T18507	hypothetical prote
358	26	63.4	457	2	B82268	conserved hypothet
359	26	63.4	464	2	C40630	GDP-mannose pyroph
360	26	63.4	466	2	JC5897	killer cell inhibi
361	26	63.4	467	2	A43357	pancreatic lipase-
362	26	63.4	475	2	G89587	protein R09F10.4 [
363	26	63.4	481	2	H97054	ribonucleases G/E
364	26	63.4	488	2	G89805	IMP dehydrogenase
365	26	63.4	488	2	E70234	conserved hypothet
366	26	63.4	493	2	JC7205	lysine-tRNA ligase
367	26	63.4	508	2	G47677	hypothetical prote
368	26	63.4	509	2	G95901	probable L-xylulok
369	26	63.4	514	2	E82361	hypothetical prote
370	26	63.4	519	2	H86897	gluconokinase (EC
371	26	63.4	524	2	AH2427	phosphodiesterase/
372	26	63.4	528	2	S14944	regulatory protein
373	26	63.4	532	2	T25807	hypothetical prote
374	26	63.4	538	2	T08640	hypothetical prote
375	26	63.4	539	2	A64455	methyl coenzyme M
376	26	63.4	541	2	B82342	probable transcrip
377	26	63.4	546	1	COBYC1	cyclin 1 - yeast (
378	26	63.4	547	2	T40314	hypothetical coile
379	26	63.4	550	2	H81718	methionyl-tRNA syn
380	26	63.4	553	2	T36441	probable alkaline
381	26	63.4	556	2	A84364	H+-transporting AT
382	26	63.4	556	2	S49754	probable membrane
383	26	63.4	556	2	T39109	probable guanosine
384	26	63.4	558	2	T50595	probable alkaline
385	26	63.4	561	2	AG0720	probable sulphate
386	26	63.4	564	2	AF3553	acetolactate synth
387	26	63.4	580	2	C84526	Mutator-like trans
388	26	63.4	585	1	S14732	H+-transporting tw
389	26	63.4	586	2	T29695	hypothetical prote
390	26	63.4	593	2	T20630	hypothetical prote
391	26	63.4	607	2	A95122	Tn5252, relaxase [
392	26	63.4	607	2	F84525	Mutator-like trans
393	26	63.4	609	2	JC6134	DNA-directed RNA p
394	26	63.4	613	1	A26062	paired box segment

395	26	63.4	631	2	S70908	transferrin-bindin
396	26	63.4	636	2	F90094	hypothetical prote
397	26	63.4	642	2	H81868	probable virulence
398	26	63.4	644	2	S51765	sulfate transport
399	26	63.4	646	2	T02643	hypothetical prote
400	26	63.4	647	2	S61011	hypothetical prote
401	26	63.4	662	2	T33900	hypothetical prote
402	26	63.4	665	2	E84940	transketolase (EC
403	26	63.4	676	2	T32556	hypothetical prote
404	26	63.4	677	2	T50022	sulfate transporte
405	26	63.4	681	2	E70942	hypothetical prote
406	26	63.4	689	2	S74764	hypothetical prote
407	26	63.4	700	2	T41401	spore outgrowth fa
408	26	63.4	718	2	D89845	hypothetical prote
409	26	63.4	730	2	T44313	hypothetical prote
410	26	63.4	730	2	S70954	otnG protein - Vib
411	26	63.4	735	2	T39464	hypothetical prote
412	26	63.4	738	2	S37876	glutamine-rich pro
413	26	63.4	748	2	G83927	alpha-galactosidas
414	26	63.4	767	2	S64571	probable membrane
415	26	63.4	774	2	AI0106	conserved hypothet
416	26	63.4	802	2	A83125	probable TonB-depe
417	26	63.4	806	2	AD0351	probable exported
418	26	63.4	821	2	E95245	penicillin-binding
419	26	63.4	821	2	B99110	peptidoglycan glyc
420	26	63.4	826	2	E96720	probable alpha-amy
421	26	63.4	849	2	T46253	hypothetical prote
422	26	63.4	853	2	D70304	hypothetical prote
423	26	63.4	859	2	T01461	hypothetical prote
424	26	63.4	862	2	T40934	probable integral
425	26	63.4	872	2	H75564	probable ATP-depen
426	26	63.4	877	2	T40413	sulfate permease -
427	26	63.4	883	2	AE0207	conserved hypothet
428	26	63.4	893	2	S64926	probable membrane
429	26	63.4	900	2	E69631	galactosamine-cont
430	26	63.4	911	2	S70911	transferrin-bindin
431	26	63.4	912	2	S70901	transferrin-bindin
432	26	63.4	912	2	C64107	transferrin-bindin
433	26	63.4	1002	2	S62035	isoleucine-tRNA li
434	26	63.4	1009	2	T47327	hypothetical prote
435	26	63.4	1010	2	D72203	hypothetical prote
436	26	63.4	1018	2	E64451	type I restriction
437	26	63.4	1045	2	I51555	recombination acti
438	26	63.4	1068	2	A40265	retinoblastoma-ass
439	26	63.4	1121	2	G64103	exodeoxyribonuclea
440	26	63.4	1130	2	T23104	hypothetical prote
441	26	63.4	1133	2	T23103	hypothetical prote
442	26	63.4	1162	2	T37889	probable nuclear p
443	26	63.4	1180	1	NCECX5	exodeoxyribonuclea
444	26	63.4	1180	2	G85933	DNA helicase RecB
445	26	63.4	1180	2	E91088	DNA helicase RecB
446	26	63.4	1181	2	AB0865	exonuclease V chai
447	26	63.4	1203	2	S27545	pullulanase - Ther
448	26	63.4	1244	2	T49632	hypothetical prote
449	26	63.4	1253	1	A44400	myosin heavy chain
450	26	63.4	1262	2	T33074	hypothetical prote
451	26	63.4	1315	1	BTCLTN	tentoxilysin (EC 3
452	26	63.4	1381	1	QQBE45	major capsid prote
453	26	63.4	1396	2	G70598	hypothetical prote
454	26	63.4	1438	2	AI0093	conserved hypothet
455	26	63.4	1475	2	A44765	alpha-amylase (EC
456	26	63.4	1481	2	S28669	pullulanase (EC 3.
457	26	63.4	1501	2	S57198	multidrug resistan
458	26	63.4	1528	2	T14279	myosin-like protei
459	26	63.4	1593	2	T22028	hypothetical prote
460	26	63.4	1668	1	C69224	cobalamin biosynth
461	26	63.4	1708	2	A05205	hypothetical prote
462	26	63.4	1772	2	A45532	major merozoite su
463	26	63.4	1871	2	D96698	probable DNA polym
464	26	63.4	1894	2	T02155	DNA-directed DNA p
465	26	63.4	1900	2	S45530	probable 1-phospha
466	26	63.4	2052	2	T18290	FYVE finger-contai
467	26	63.4	2095	2	S29529	genome polyprotein
468	26	63.4	2410	2	T43731	cell wall alpha-gl
469	26	63.4	3036	2	T18995	hypothetical prote
470	26	63.4	3068	1	A44062	genome polyprotein
471	25.5	62.2	370	2	S31831	IgA-specific metal
472	25.5	62.2	370	2	S40431	IgA-specific metal
473	25.5	62.2	408	2	AD2473	hypothetical prote
474	25.5	62.2	1532	2	A26039	IgA-specific metal
475	25.5	62.2	1561	2	S61314	IgA-specific metal
476	25.5	62.2	1773	2	A81937	IgA-specific metal
477	25.5	62.2	1815	2	C81169	IgA-specific metal
478	25	61.0	27	2	A48989	chitinase (EC 3.2.
479	25	61.0	69	2	D82933	type I restriction
480	25	61.0	72	2	JC5628	mandibular organ i
481	25	61.0	72	2	B42645	ribosomal protein
482	25	61.0	72	2	G81664	ribosomal protein
483	25	61.0	73	2	F90697	hypothetical prote
484	25	61.0	83	2	AB2558	hypothetical prote
485	25	61.0	85	2	T17882	hypothetical prote
486	25	61.0	93	2	T14766	hypothetical prote
487	25	61.0	105	2	C81394	hypothetical prote
488	25	61.0	107	2	S36264	Ig lambda chain V
489	25	61.0	108	2	B72756	hypothetical prote
490	25	61.0	111	2	T14550	cdc2-related prote
491	25	61.0	115	2	S06809	keratin - chicken
492	25	61.0	118	2	B85686	unknown protein en
493	25	61.0	118	2	E90828	probable terminase
494	25	61.0	118	2	D69837	hypothetical prote
495	25	61.0	127	1	B70022	acyloate catabolis
496	25	61.0	128	2	T49062	hypothetical prote
497	25	61.0	132	2	AB1767	ATP synthase chain
498	25	61.0	135	2	E81433	probable integral
499	25	61.0	136	2	G82480	hypothetical prote
500	25	61.0	137	2	S36303	T-cell receptor de
501	25	61.0	142	1	S06630	hyperglycemic horm
502	25	61.0	153	2	A87732	protein W10C8.4 [i
503	25	61.0	155	2	A82841	hypothetical prote
504	25	61.0	156	2	B70346	hypothetical prote
505	25	61.0	160	2	C72706	hypothetical prote
506	25	61.0	162	2	A84217	hypothetical prote
507	25	61.0	172	2	T40629	hypothetical prote
508	25	61.0	173	2	A82935	type I restriction
509	25	61.0	174	2	E69644	acetolactate synth
510	25	61.0	180	2	B48428	homeotic protein H
511	25	61.0	181	2	AE3600	hypothetical prote
512	25	61.0	186	2	A83887	hypothetical prote
513	25	61.0	188	2	T26741	hypothetical prote
514	25	61.0	188	2	D84149	hypothetical prote
515	25	61.0	189	2	E86707	transcription regu
516	25	61.0	191	2	F72277	hypothetical prote
517	25	61.0	191	2	D70047	hypothetical prote
518	25	61.0	193	1	ASLJSI	vif protein - simi
519	25	61.0	194	2	F64025	hypothetical prote
520	25	61.0	195	2	E89924	conserved hypothet
521	25	61.0	196	2	G69419	phosphate ABC tran
522	25	61.0	197	2	A64484	conserved hypothet
523	25	61.0	197	2	T27159	hypothetical prote
524	25	61.0	202	2	C32132	phosphopyruvate hy
525	25	61.0	205	2	T31046	hypothetical prote
526	25	61.0	213	2	D70430	superoxide dismuta
527	25	61.0	216	2	AH2547	hypothetical prote
528	25	61.0	219	2	T11625	hypothetical prote
529	25	61.0	221	2	B82647	hypothetical prote
530	25	61.0	222	2	JH0488	C-8 sterol isomera
531	25	61.0	229	2	S44217	coat protein - tom
532	25	61.0	237	2	T07820	hypothetical prote
533	25	61.0	237	2	A99103	26S proteasome IOT
534	25	61.0	242	2	AB3523	taurine transport
535	25	61.0	242	2	AD1928	hypothetical prote
536	25	61.0	249	2	C75156	hypothetical prote
537	25	61.0	250	2	S58362	nucleolar protein
538	25	61.0	250	2	F97185	teichoic acid bios
539	25	61.0	251	2	H85649	probable fatty acy
540	25	61.0	251	2	F81947	probable amino aci

541	25	61.0	251	2	B81159	amino acid ABC tra
542	25	61.0	255	2	F97235	probable PHP famil
543	25	61.0	256	2	S22589	hypothetical prote
544	25	61.0	257	2	G64181	ABC-type transport
545	25	61.0	257	2	JQ2332	AR1 protein - cass
546	25	61.0	257	2	S39210	gene V2 protein -
547	25	61.0	257	2	S39234	gene V2 protein -
548	25	61.0	257	2	T03136	hypothetical prote
549	25	61.0	258	2	B82249	uridine phosphoryl
550	25	61.0	259	2	AB1368	amino acid ABC-tra
551	25	61.0	259	2	AC1737	amino acid ABC-tra
552	25	61.0	261	2	D71508	probable glutamine
553	25	61.0	261	2	B81823	DedA-family integr
554	25	61.0	262	2	F88956	protein ZK697.4 [i
555	25	61.0	263	2	C81667	amino acid ABC tra
556	25	61.0	264	2	H64086	glycerol facilitat
557	25	61.0	267	1	UJCH	major prion protei
558	25	61.0	267	2	A37372	prion protein homo
559	25	61.0	273	2	A46280	prion protein - ch
560	25	61.0	273	2	B69480	cobalamin biosynth
561	25	61.0	273	2	B86788	LysR family transc
562	25	61.0	276	2	F84591	hypothetical prote
563	25	61.0	280	2	T34905	probable hydrolase
564	25	61.0	281	2	C69588	L-arabinose transp
565	25	61.0	281	2	H72773	hypothetical prote
566	25	61.0	284	2	S62839	sulfate transport
567	25	61.0	287	2	S64441	prohibitin PHB1 -
568	25	61.0	287	2	A72751	hypothetical prote
569	25	61.0	288	2	D83121	hypothetical prote
570	25	61.0	299	2	S60971	probable membrane
571	25	61.0	299	2	D84337	cation efflux syst
572	25	61.0	301	1	WMVZP4	F4 protein - fowlp
573	25	61.0	302	2	S69725	hypothetical prote
574	25	61.0	305	2	F82370	coproporphyrinogen
575	25	61.0	306	2	S67131	hypothetical prote
576	25	61.0	306	2	AD1482	probable transcrip
577	25	61.0	306	2	AI1121	probable transcrip
578	25	61.0	307	2	B81874	hypothetical prote
579	25	61.0	307	2	C81148	YabO/YceC/SfhB fam
580	25	61.0	307	2	B82394	hypothetical prote
581	25	61.0	308	2	T46338	hypothetical prote
582	25	61.0	309	2	AG0368	coproporphyrinogen
583	25	61.0	312	2	A23705	cysteine proteinas
584	25	61.0	312	2	C86790	2-dehydropantoate
585	25	61.0	314	2	T46279	hypothetical prote
586	25	61.0	315	2	AE0166	probable virulence
587	25	61.0	316	2	S46022	hypothetical prote
588	25	61.0	317	2	T11960	hypothetical prote
589	25	61.0	317	2	C97245	probable phosphohy
590	25	61.0	317	2	C82411	hypothetical prote
591	25	61.0	320	2	A95872	hypothetical prote
592	25	61.0	322	2	S08451	hypothetical prote
593	25	61.0	323	2	G86766	penicillin amidase
594	25	61.0	327	2	G97239	thiamine biosynthe
595	25	61.0	329	2	H83609	sulfate transport
596	25	61.0	333	2	E75368	probable isocitrat
597	25	61.0	337	2	S45360	phytoene synthase
598	25	61.0	338	2	T41448	hypothetical prote
599	25	61.0	338	2	E83688	hypothetical prote
600	25	61.0	339	2	A71473	probable tRNA pyro
601	25	61.0	340	2	H95349	alcohol dehydrogen
602	25	61.0	340	2	S74712	coproporphyrinogen
603	25	61.0	342	2	T22742	hypothetical prote
604	25	61.0	344	2	T19639	hypothetical prote
605	25	61.0	346	2	T24888	hypothetical prote
606	25	61.0	347	2	A95403	probable sulfate/t
607	25	61.0	350	2	E72352	N-acetylglucosamin
608	25	61.0	351	2	AG2677	hypothetical prote
609	25	61.0	351	2	E97459	sulfate ABC transp
610	25	61.0	354	2	S29718	gene nodal protein
611	25	61.0	355	2	T13977	NADH2 dehydrogenas
612	25	61.0	356	2	T33984	hypothetical prote
613	25	61.0	357	2	F81875	sulfate ABC transp
614	25	61.0	357	2	B81147	sulfate ABC transp
615	25	61.0	363	2	AD0366	sulfate transport
616	25	61.0	364	2	AF0811	sulphate transport
617	25	61.0	365	1	QRECSA	sulfate transport
618	25	61.0	365	2	I56197	Fc gamma (IgG) rec
619	25	61.0	365	2	H85884	hypothetical prote
620	25	61.0	365	2	E91040	hypothetical prote
621	25	61.0	365	2	A98088	membrane-bound lyt
622	25	61.0	365	2	A65064	membrane-bound lyt
623	25	61.0	365	2	C85933	membrane-bound lyt
624	25	61.0	366	2	S45915	hypothetical prote
625	25	61.0	366	2	T22544	hypothetical prote
626	25	61.0	366	2	T26449	hypothetical prote
627	25	61.0	367	2	E95930	probable sulfate u
628	25	61.0	369	1	DEBSPF	pyruvate dehydroge
629	25	61.0	375	2	C95106	carboxynorspermidi
630	25	61.0	375	2	E97974	carboxynorspermidi
631	25	61.0	375	2	T20846	hypothetical prote
632	25	61.0	376	2	C82310	sulfate ABC transp
633	25	61.0	376	2	S67085	hypothetical prote
634	25	61.0	378	2	C84442	hypothetical prote
635	25	61.0	382	2	E97742	hypothetical prote
636	25	61.0	384	2	B41500	IgA-specific metal
637	25	61.0	385	2	H69154	hypothetical prote
638	25	61.0	386	2	A81359	probable molybdopt
639	25	61.0	387	2	T25326	hypothetical prote
640	25	61.0	389	2	E96516	F16N3.13 [imported
641	25	61.0	392	2	S52248	nitrate and nitrit
642	25	61.0	400	2	H72119	conserved hypothet
643	25	61.0	400	2	A86504	CT017 hypothetical
644	25	61.0	401	2	S09626	prrB protein - Esc
645	25	61.0	402	2	F83422	conserved hypothet
646	25	61.0	402	2	E83119	probable FAD-depen
647	25	61.0	404	2	G69318	threonine synthase
648	25	61.0	404	2	S46269	synovial sarcoma t
649	25	61.0	404	2	B85466	hypothetical prote
650	25	61.0	404	2	AH3481	sulfate transport
651	25	61.0	405	2	AB0793	probable MR-MLE-fa
652	25	61.0	405	2	G91020	probable racemase
653	25	61.0	405	2	D69142	conserved hypothet
654	25	61.0	405	2	F85864	probable racemase
655	25	61.0	406	2	I41084	type I site-specif
656	25	61.0	407	2	G71414	hydroxymandelonitr
657	25	61.0	407	2	T20078	hypothetical prote
658	25	61.0	410	2	S02167	type I site-specif
659	25	61.0	415	2	I56251	GTP binding protei
660	25	61.0	417	2	T48868	zinc finger protei
661	25	61.0	420	2	S50652	hypothetical prote
662	25	61.0	422	2	T24561	hypothetical prote
663	25	61.0	426	2	AE2635	polysaccharide bio
664	25	61.0	427	2	A84155	hypothetical prote
665	25	61.0	428	2	H96641	hypothetical prote
666	25	61.0	429	2	AC1631	glutamate-1-semial
667	25	61.0	430	2	D97417	hypothetical prote
668	25	61.0	432	2	A69056	hypothetical prote
669	25	61.0	433	2	S63383	POP2 protein - yea
670	25	61.0	444	2	T52034	receiver-like prot
671	25	61.0	445	2	A57400	embryonic TEA doma
672	25	61.0	445	2	F82176	agglutination prot
673	25	61.0	451	2	S49128	twitchin-like prot
674	25	61.0	456	2	AE0164	probable exported
675	25	61.0	457	2	T52074	response regulator
676	25	61.0	458	2	AG3360	trk system potassi
677	25	61.0	458	2	F71698	hypothetical prote
678	25	61.0	461	2	JC4556	alcaligin synthesi
679	25	61.0	461	2	S75711	hypothetical prote
680	25	61.0	462	2	S61332	IgA-specific metal
681	25	61.0	462	2	S54572	hypothetical prote
682	25	61.0	465	2	B85358	SERINE CARBOXYPEPT
683	25	61.0	468	1	KCRBI	interstitial colla
684	25	61.0	468	2	T22287	hypothetical prote
685	25	61.0	469	1	KCPGI	interstitial colla
686	25	61.0	469	2	T20047	hypothetical prote

687	25	61.0	474	2	D84631	probable serine ca
688	25	61.0	476	2	E97769	hypothetical prote
689	25	61.0	478	2	T31955	hypothetical prote
690	25	61.0	478	2	AF1758	chitinase and chit
691	25	61.0	479	2	T26951	hypothetical prote
692	25	61.0	483	2	AB0458	Trk system potassi
693	25	61.0	484	2	T07675	cyclin a2-type, mi
694	25	61.0	484	2	AD0199	sensor protein kin
695	25	61.0	485	1	JC4998	IMP dehydrogenase
696	25	61.0	485	2	E75015	IMP dehydrogenase
697	25	61.0	485	2	C89008	protein W08A12.1 [
698	25	61.0	486	1	E71456	IMP dehydrogenase
699	25	61.0	487	2	S41951	UTP-glucose glucos
700	25	61.0	487	2	G71432	hypothetical prote
701	25	61.0	487	2	T22825	hypothetical prote
702	25	61.0	488	2	JC7995	transient receptor
703	25	61.0	491	2	I49625	testosterone 16a-h
704	25	61.0	495	2	S74210	glucokinase (EC 2.
705	25	61.0	495	2	A48370	nitrogen fixation
706	25	61.0	496	2	JQ2152	mating-type locus
707	25	61.0	496	2	AB0123	enterotoxin-like p
708	25	61.0	497	2	C75618	hypothetical prote
709	25	61.0	499	2	I48741	ryanodine receptor
710	25	61.0	500	2	S57467	probable heme-bind
711	25	61.0	504	2	JQ2151	mating-type locus
712	25	61.0	505	2	F82075	conserved hypothet
713	25	61.0	506	2	B87102	conserved membrane
714	25	61.0	506	2	H70928	hypothetical prote
715	25	61.0	510	2	S53958	hypothetical prote
716	25	61.0	513	2	T33512	hypothetical prote
717	25	61.0	516	2	H70935	hypothetical prote
718	25	61.0	521	2	C96700	protein F12A21.15
719	25	61.0	522	2	S13887	hydroxymethylgluta
720	25	61.0	527	1	S69203	teichoic acid tran
721	25	61.0	527	2	S32430	abrin-b precursor
722	25	61.0	535	2	A41375	cellulase (EC 3.2.
723	25	61.0	536	2	AG1482	hypothetical prote
724	25	61.0	545	2	F71932	type II DNA modifi
725	25	61.0	551	2	S66701	probable membrane
726	25	61.0	557	2	AF3091	hypothetical prote
727	25	61.0	557	2	D98195	hypothetical prote
728	25	61.0	558	2	F64235	Na+ ATPase chain J
729	25	61.0	560	2	D71913	lytic murein trans
730	25	61.0	560	2	E64600	soluble lytic mure
731	25	61.0	572	1	DEMSMX	malate dehydrogena
732	25	61.0	572	1	DERTMX	malate dehydrogena
733	25	61.0	572	2	S44415	malate dehydrogena
734	25	61.0	572	2	JC4160	malate dehydrogena
735	25	61.0	579	2	JC7896	corazonin receptor
736	25	61.0	580	2	T02596	hypothetical prote
737	25	61.0	582	2	S57722	sli-1 protein - Ca
738	25	61.0	585	2	T29654	hypothetical prote
739	25	61.0	586	1	TVVPBP	large T antigen -
740	25	61.0	586	2	S45144	H+-transporting tw
741	25	61.0	603	2	S47917	rab geranylgeranyl
742	25	61.0	607	2	S53387	hypothetical prote
743	25	61.0	611	2	S09142	ND5 intron 1 prote
744	25	61.0	612	2	T13616	hypothetical prote
745	25	61.0	613	2	S74611	hypothetical prote
746	25	61.0	617	2	T52499	ferredoxin oxidore
747	25	61.0	617	2	G70366	glucose inhibited
748	25	61.0	617	2	T00601	hypothetical prote
749	25	61.0	617	2	AF3571	acyl-CoA dehydroge
750	25	61.0	620	2	T11221	DNA polymerase hom
751	25	61.0	629	2	A46500	Ly-9.2 antigen - m
752	25	61.0	645	2	T39614	kinase-binding pro
753	25	61.0	646	2	T48644	negative regulator
754	25	61.0	653	2	F70383	organic solvent to
755	25	61.0	656	2	I49299	receptor interacti
756	25	61.0	658	2	C82512	hypothetical prote
757	25	61.0	663	2	T24881	hypothetical prote
758	25	61.0	669	2	D82739	excinuclease ABC s
759	25	61.0	677	2	T26574	hypothetical prote
760	25	61.0	677	2	AE1861	serine/threonine k
761	25	61.0	692	2	H70362	glycogen phosphory
762	25	61.0	693	2	F82245	conserved hypothet
763	25	61.0	695	2	E82783	hypothetical prote
764	25	61.0	698	2	I60218	hypothetical prote
765	25	61.0	703	2	A49994	sulfate transporte
766	25	61.0	711	2	E85098	hypothetical prote
767	25	61.0	721	1	S77015	cadmium-transporti
768	25	61.0	726	2	T16356	hypothetical prote
769	25	61.0	728	2	B83805	GTP pyrophosphokin
770	25	61.0	729	2	A89946	GTP pyrophosphokin
771	25	61.0	734	2	C69691	GTP pyrophosphokin
772	25	61.0	738	2	AC1265	(p)ppGpp synthetas
773	25	61.0	738	2	AE1627	(p)ppGpp synthetas
774	25	61.0	739	2	S39975	stringent response
775	25	61.0	739	2	E97245	beta-lactamase cla
776	25	61.0	740	2	B86638	GTP diphosphokinas
777	25	61.0	740	2	D97180	relA/SpoT protein,
778	25	61.0	743	2	T15062	hypothetical prote
779	25	61.0	750	1	D69403	conserved hypothet
780	25	61.0	773	2	D90099	hypothetical prote
781	25	61.0	779	2	S64993	hypothetical prote
782	25	61.0	780	2	T50315	hypothetical prote
783	25	61.0	781	2	T51433	probable cation tr
784	25	61.0	797	2	T22294	hypothetical prote
785	25	61.0	811	2	T00036	capsid protein pre
786	25	61.0	815	2	G97266	mannose-1-phosphat
787	25	61.0	835	1	P3XRSR	minor inner core p
788	25	61.0	837	2	D69171	intracellular prot
789	25	61.0	851	2	D90216	hypothetical prote
790	25	61.0	860	2	A43920	nucleolar 100K pol
791	25	61.0	877	2	T03098	p97 protein - Toxo
792	25	61.0	878	2	AE0478	phosphoenolpyruvat
793	25	61.0	883	1	QYEC	phosphoenolpyruvat
794	25	61.0	883	2	B86087	phosphoenolpyruvat
795	25	61.0	883	2	AD0936	phosphoenolpyruvat
796	25	61.0	883	2	E91239	phosphoenolpyruvat
797	25	61.0	883	2	I58181	glutamate receptor
798	25	61.0	883	2	S47031	glutamate receptor
799	25	61.0	883	2	S13677	glutamate receptor
800	25	61.0	885	2	JH0796	nucleolar 100K pol
801	25	61.0	893	2	AH1867	hypothetical prote
802	25	61.0	904	2	C83030	exoribonuclease RN
803	25	61.0	906	2	A43817	transforming prote
804	25	61.0	912	2	B44450	ubiquitin-specific
805	25	61.0	913	1	A42543	DNA-directed DNA p
806	25	61.0	913	2	T17675	DNA-directed DNA p
807	25	61.0	916	2	I55441	vp165 - rat
808	25	61.0	917	2	S26365	surface-layer prot
809	25	61.0	918	2	E90542	lipoprotein [impor
810	25	61.0	921	2	I49695	glutamate receptor
811	25	61.0	921	2	E86764	conserved hypothet
812	25	61.0	933	2	A59250	myosin - Acetabula
813	25	61.0	939	2	I49696	glutamate receptor
814	25	61.0	964	2	S25855	DNA-directed DNA p
815	25	61.0	971	2	C75503	hypothetical prote
816	25	61.0	1006	2	S76892	hypothetical prote
817	25	61.0	1008	2	T33672	hypothetical prote
818	25	61.0	1008	2	AE2304	hypothetical prote
819	25	61.0	1010	2	T33372	hypothetical prote
820	25	61.0	1016	2	T30943	aminopeptidase (EC
821	25	61.0	1016	2	T30942	aminopeptidase (EC
822	25	61.0	1025	2	T18376	multidrug resistan
823	25	61.0	1041	2	T33699	hypothetical prote
824	25	61.0	1043	2	B33754	recombination-acti
825	25	61.0	1058	2	T30178	mitotic checkpoint
826	25	61.0	1080	2	T19048	probable Pro-X car
827	25	61.0	1082	1	P1XRPC	inner layer protei
828	25	61.0	1102	2	T31004	probable mitotic c
829	25	61.0	1113	2	T26954	hypothetical prote
830	25	61.0	1117	2	C91286	hypothetical prote
831	25	61.0	1117	2	G86127	hypothetical prote
832	25	61.0	1121	2	T21303	hypothetical prote

833	25	61.0	1171	2	F83110	exodeoxyribonuclea
834	25	61.0	1185	2	T46428	hypothetical prote
835	25	61.0	1200	2	T35599	probable DNA methy
836	25	61.0	1237	2	T46609	calcium-activated
837	25	61.0	1249	2	T14150	vesicle associated
838	25	61.0	1252	2	S02004	phospholipase C (E
839	25	61.0	1266	2	T27024	hypothetical prote
840	25	61.0	1277	2	E70224	hypothetical prote
841	25	61.0	1296	2	S55511	valine-tRNA ligase
842	25	61.0	1426	2	T30817	homeotic protein C
843	25	61.0	1433	2	B83952	DNA polymerase III
844	25	61.0	1436	2	B81704	conserved hypothet
845	25	61.0	1437	2	F69680	DNA-directed DNA p
846	25	61.0	1512	2	AH0439	probable membrane
847	25	61.0	1541	2	A37023	IgA-specific metal
848	25	61.0	1548	2	S34583	serine proteinase
849	25	61.0	1689	2	JS0080	DNA-directed RNA p
850	25	61.0	1711	2	T21432	hypothetical prote
851	25	61.0	1768	2	T27023	hypothetical prote
852	25	61.0	1819	2	D97033	uncharacterized pr
853	25	61.0	1938	2	A37361	probable integral
854	25	61.0	2100	2	T38128	t7i23.15 protein -
855	25	61.0	2194	1	JQ1977	glutamate synthase
856	25	61.0	2225	1	A23443	pyrimidine synthes
857	25	61.0	2338	2	T25810	hypothetical prote
858	25	61.0	2352	2	T43431	alpha-glucan synth
859	25	61.0	2357	2	A59249	class VII unconven
860	25	61.0	2399	2	H71879	toxin-like outer m
861	25	61.0	2413	2	S34670	splicing factor PR
862	25	61.0	2440	2	S39162	transcription coac
863	25	61.0	2441	2	S39161	CREB-binding prote
864	25	61.0	2529	2	B64635	toxin-like outer m
865	25	61.0	2899	2	T21546	hypothetical prote
866	25	61.0	2915	2	G87867	protein F36A2.13 [
867	25	61.0	3092	2	S46009	GTPase-activating
868	25	61.0	3305	2	T18358	apolipophorin prec
869	25	61.0	3329	2	T42205	breast cancer susc
870	25	61.0	3329	2	T30904	breast cancer tumo
871	25	61.0	3345	2	T13423	hypothetical prote
872	25	61.0	3421	1	WZBEB6	367K tegument prot
873	25	61.0	4563	1	LPHUB	apolipoprotein B-1
874	25	61.0	5032	1	A35041	ryanodine receptor
875	25	61.0	5035	1	I46646	ryanodine receptor
876	25	61.0	5037	1	A54161	ryanodine-binding
877	25	61.0	5037	2	B35041	ryanodine receptor
878	24.5	59.8	398	2	T15758	hypothetical prote
879	24	58.5	20	2	S78760	ribosomal protein
880	24	58.5	31	2	S14615	hypothetical prote
881	24	58.5	38	2	A60216	hyperglycemic horm
882	24	58.5	55	2	AH1443	phage protein homo
883	24	58.5	59	2	S31306	ribosomal protein
884	24	58.5	63	1	R5RZ32	ribosomal protein
885	24	58.5	69	2	AH0170	cold shock-like pr
886	24	58.5	73	2	S29776	hyperglycemic neur
887	24	58.5	77	2	T09829	fungus resistance
888	24	58.5	78	2	S36313	T-cell receptor de
889	24	58.5	79	2	H87655	transcription regu
890	24	58.5	82	2	AD2287	hypothetical prote
891	24	58.5	86	2	S78488	Ig kappa chain V r
892	24	58.5	88	2	S53088	NADH2 dehydrogenas
893	24	58.5	89	2	H69774	conserved hypothet
894	24	58.5	91	2	T28444	hypothetical prote
895	24	58.5	91	2	C83804	hypothetical prote
896	24	58.5	92	2	S38622	Ig kappa chain V r
897	24	58.5	93	2	S17642	Ig kappa chain V r
898	24	58.5	93	2	S17643	Ig kappa chain V r
899	24	58.5	93	2	S17640	Ig kappa chain V r
900	24	58.5	93	2	S17623	Ig kappa chain V r
901	24	58.5	94	2	D49039	T-cell receptor be
902	24	58.5	96	2	B75134	hypothetical prote
903	24	58.5	97	2	A42575	Ig kappa chain V r
904	24	58.5	97	2	F84155	bltD operon transc
905	24	58.5	98	2	A72151	B9L protein - vari
906	24	58.5	100	2	S70048	hypothetical prote
907	24	58.5	100	2	H81310	probable periplasm
908	24	58.5	103	2	PH1047	Ig light chain V r
909	24	58.5	103	2	PH1052	Ig light chain V r
910	24	58.5	104	2	S53118	protamine p2 - com
911	24	58.5	104	2	T10351	hypothetical prote
912	24	58.5	106	2	A55121	transcription fact
913	24	58.5	109	2	S17381	T-cell receptor be
914	24	58.5	109	2	I38952	transcription init
915	24	58.5	112	2	T28965	hypothetical prote
916	24	58.5	113	2	PT0408	Ig light chain V r
917	24	58.5	113	2	PT0407	Ig light chain V r
918	24	58.5	114	2	S45800	probable membrane
919	24	58.5	114	2	T50166	homolog to yeast g
920	24	58.5	116	2	S71438	probable glutamate
921	24	58.5	116	2	A72263	response regulator
922	24	58.5	117	2	F87086	hypothetical prote
923	24	58.5	122	2	AD1085	transcription regu
924	24	58.5	123	2	I38311	T-cell receptor be
925	24	58.5	123	2	S26264	T-cell receptor be
926	24	58.5	126	2	AC2652	hypothetical prote
927	24	58.5	128	2	AF2143	hypothetical prote
928	24	58.5	130	2	A32513	Ig kappa chain pre
929	24	58.5	130	2	B32456	Ig kappa chain pre
930	24	58.5	133	2	T34864	hypothetical prote
931	24	58.5	134	2	S52118	hyperglycemic horm
932	24	58.5	134	2	S52117	hyperglycemic horm
933	24	58.5	135	2	S48141	hypoglycemic hormo
934	24	58.5	135	2	S48142	hypoglycemic hormo
935	24	58.5	136	2	S36320	T-cell receptor de
936	24	58.5	136	2	B90443	hypothetical prote
937	24	58.5	137	2	AC1817	hypothetical prote
938	24	58.5	138	2	S37773	ankyrin, erythrocy
939	24	58.5	145	2	C64447	hypothetical prote
940	24	58.5	146	2	C42520	A28L 16.3K protein
941	24	58.5	146	2	JQ1834	3L protein - vario
942	24	58.5	146	2	S46858	A31L protein - var
943	24	58.5	146	2	E72167	A32L protein - var
944	24	58.5	146	2	G83943	hypothetical prote
945	24	58.5	148	2	S38660	finger protein ZFX
946	24	58.5	150	1	H64057	biopolymer transpo
947	24	58.5	150	2	JH0220	prolamin precursor
948	24	58.5	150	2	T37513	probable acetyltra
949	24	58.5	151	2	H90420	hypothetical prote
950	24	58.5	151	2	JS0672	prolamin 13K precu
951	24	58.5	155	1	PXBOV6	H+-exporting ATPas
952	24	58.5	156	1	JN0456	H+-exporting ATPas
953	24	58.5	157	2	T28383	ORF MSV222 hypothe
954	24	58.5	158	2	AH1985	hypothetical prote
955	24	58.5	159	2	I40564	hypothetical DNA-b
956	24	58.5	159	2	S48970	hypothetical prote
957	24	58.5	159	2	AH1899	hypothetical prote
958	24	58.5	162	2	H70212	hypothetical prote
959	24	58.5	163	2	D65068	hypothetical prote
960	24	58.5	163	2	H85937	hypothetical prote
961	24	58.5	163	2	D91092	hypothetical prote
962	24	58.5	163	2	F84059	hypothetical prote
963	24	58.5	166	2	D86026	hypothetical prote
964	24	58.5	166	2	S61859	hrpD protein - Pse
965	24	58.5	167	2	AH1106	hypothetical prote
966	24	58.5	170	2	T43779	ribosomal protein
967	24	58.5	171	2	H64107	signal peptidase I
968	24	58.5	171	2	T39247	hypothetical prote
969	24	58.5	171	2	C65187	yigL protein - Esc
970	24	58.5	172	2	S23768	hypothetical prote
971	24	58.5	172	2	S26684	hypothetical prote
972	24	58.5	173	2	I39569	hypothetical prote
973	24	58.5	176	2	H72201	conserved hypothet
974	24	58.5	179	2	H81682	conserved hypothet
975	24	58.5	180	2	T41102	probable n-termina
976	24	58.5	180	2	H82480	probable acetyltra
977	24	58.5	181	2	T08670	cell division cont
978	24	58.5	183	2	T48689	hypothetical prote

979	24	58.5	185	1	S60942	hypothetical prote
980	24	58.5	187	2	S56494	gluconokinase (EC
981	24	58.5	187	2	AD3627	maltose/maltodextr
982	24	58.5	188	2	AG2484	hypothetical prote
983	24	58.5	190	2	F97857	hypothetical prote
984	24	58.5	190	2	G97832	RP691 protein homo
985	24	58.5	191	2	I37904	c-myc promoter-bin
986	24	58.5	195	2	S44260	hypothetical prote
987	24	58.5	197	2	T33661	hypothetical prote
988	24	58.5	197	2	C86523	CT142 hypothetical
989	24	58.5	197	2	B95309	probable ABC sugar
990	24	58.5	197	2	S62984	hypothetical prote
991	24	58.5	198	2	F82241	outer membrane lip
992	24	58.5	199	2	E46449	hypothetical prote
993	24	58.5	200	2	B82738	conserved hypothet
994	24	58.5	200	2	S75359	hypothetical prote
995	24	58.5	203	2	AG2120	hypothetical prote
996	24	58.5	204	2	AI1215	hypothetical prote
997	24	58.5	205	2	C81665	conserved hypothet
998	24	58.5	206	2	AB1021	NrfG protein [impo
999	24	58.5	207	2	F64309	hypothetical prote
1000	24	58.5	207	2	D71886	type I restriction

ALIGNMENTS

RESULT 1
S61096
probable membrane protein YNL048w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N2510
C;Species: Saccharomyces cerevisiae
C;Date: 23-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S61096; S62153; S62973; S62976; S65103
R;Nasr, F.; Becam, A.M.; Herbert, C.J.
submitted to the EMBL Data Library, December 1995
A;Description: The sequence of 12.8kb from the left arm of chromosome XIV reveals a sigm
ne A4 hydrolase.
A;Reference number: S61095
A;Accession: S61096
A;Molecule type: DNA
A;Residues: 1-548 <NAS>
A;Cross-references: UNIPROT:P53954; UNIPARC:UPI0000125849; EMBL:X94547; NID:g1149538; PI
R;Bergez, P.; Doignon, F.; Crouzet, M.
Yeast 11, 967-974, 1995
A;Title: The sequence of a 44 420 bp fragment located on the left arm of chromosome XIV
A;Reference number: S58711; MUID:96021608; PMID:8533472
A;Accession: S62153
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-548 <BER>
A;Cross-references: UNIPARC:UPI0000125849; EMBL:U12141; NID:g1314216; PIDN:AAA99664.1; P
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
R;Nasr, F.; Becam, A.M.; Herbert, C.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62967
A;Accession: S62973
A;Molecule type: DNA
A;Residues: 1-548 <NAF>
A;Cross-references: UNIPARC:UPI0000125849; EMBL:Z71324; NID:g1301906; PID:e239888; PID:g
A;Experimental source: strain S288C
R;Bergez, P.; Doignon, F.; Crouzet, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S62975
A;Accession: S62976
A;Molecule type: DNA
A;Residues: 1-548 <BEW>
A;Cross-references: UNIPARC:UPI0000125849; EMBL:Z71324; NID:g1301906; PID:e239888; PID:g
A;Experimental source: strain S288C
R;Nasr, F.; Becam, A.M.; Herbert, C.J.
Yeast 12, 493-499, 1996
A;Title: The sequence of 12.8 kb from the left arm of chromosome XIV reveals a sigma ele
otriene A(4) hydrolase.
A;Reference number: S65102; MUID:96310629; PMID:8740423
A;Accession: S65103
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-548 <NAW>
A;Cross-references: UNIPARC:UPI0000125849; EMBL:X94547; NID:g1149538; PIDN:CAA64234.1; PI
C;Genetics:
A;Gene: SGD:ALG11
A;Cross-references: SGD:S0004993; MIPS:YNL048w
A;Map position: 14L
C;Keywords: transmembrane protein
F;24-40/Domain: transmembrane #status predicted <TM1>
F;163-179/Domain: transmembrane #status predicted <TM2>
F;407-423/Domain: transmembrane #status predicted <TM3>

Query Match 82.9%; Score 34; DB 2; Length 548;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 QQYSLYR 7
              ||||||:
Db        514 QQYSLYK 520
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RESULT 2
C97475
hypothetical protein AGR_C_1733 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97475
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C97475
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-198 <KUR>
A;Cross-references: UNIPROT:Q8U5G9; UNIPARC:UPI00000D2868; GB:AE007869; PIDN:AAK86756.1;
C;Genetics:
A;Gene: AGR_C_1733
A;Map position: circular chromosome

Query Match 78.0%; Score 32; DB 2; Length 198;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 QQYSLYRS 8
              ||:|:||:
Db         88 QQFSMYRN 95
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RESULT 3
G95353
Probable ABC transporter ATP-binding protein SMa1345 [imported] - Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: G95353
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bowse
.; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilotı
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: G95353
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-358 <KUR>
A;Cross-references: UNIPROT:Q92YX7; UNIPARC:UPI00000CB1B3; GB:AE006469; PIDN:AAK65393.1;
A;Experimental source: strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMa1345
A;Genome: plasmid

Query Match 78.0%; Score 32; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLY 6
||||||
Db 82 QQYSLY 87

RESULT 4
T29554
hypothetical protein C16D9.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C;Accession: T29554
R;Gattung, S.; Le, T.T.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid C16D9.
A;Reference number: Z20640
A;Accession: T29554
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-382 <GAT>
A;Cross-references: UNIPROT:Q22899; UNIPARC:UPI000007C5BD; EMBL:U64858; PIDN:AAB18283.1;
A;Experimental source: strain Bristol N2; clone C16D9
C;Genetics:
A;Gene: CESP:C16D9.5
A;Map position: 5
A;Introns: 33/3; 113/1; 256/3; 277/1; 318/2; 354/2

Query Match 78.0%; Score 32; DB 2; Length 382;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
| | ||||
Db 369 QDYKLYRS 376

RESULT 5
T16750
hypothetical protein R13F6.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C;Accession: T16750
R;Miller, N.
submitted to the EMBL Data Library, April 1994
A;Description: The sequence of C. elegans cosmid R13F6.
A;Reference number: Z18570
A;Accession: T16750
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-423 <MIL>
A;Cross-references: UNIPARC:UPI0000179149; EMBL:U00046; NID:g470358; PID:g470367; PIDN:A
A;Experimental source: strain Bristol N2; clone R13F6
C;Genetics:
A;Gene: CESP:R13F6.9
A;Map position: 3
A;Introns: 47/1; 77/3; 102/3; 132/2; 154/1; 182/3; 214/3; 234/2; 318/3; 345/3; 372/3; 39

Query Match 78.0%; Score 32; DB 2; Length 423;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QYSLYRS 8
|:|||||
Db 396 QFSLYRS 402

RESULT 6
T41381
Chaperonins 10 Kd subunit - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41381
R;Murphy, L.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, May 1998
A;Reference number: Z21990
A;Accession: T41381
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-104 <MUR>
A;Cross-references: UNIPROT:O59804; UNIPARC:UPI0000127649; EMBL:AL023592; PIDN:CAA19110.1
A;Experimental source: strain 972h-; cosmid c550
C;Genetics:
A;Gene: hsp10; SPDB:SPCC550.06c
A;Map position: 3
C;Superfamily: chaperonin groES

Query Match 75.6%; Score 31; DB 2; Length 104;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYR 7
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Db 88 EEYSLYR 94

RESULT 7
S52437
CDP-diacylglycerol synthase - fruit fly (Drosophila sp.)
C;Species: Drosophila sp.
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
C;Accession: S52437
R;Wu, L.; Niemeyer, B.; Colley, N.; Socolich, M.; Zuker, C.S.
Nature 373, 216-222, 1995
A;Title: Regulation of PLC-mediated signalling in vivo by CDP-diacylglycerol synthase.
A;Reference number: S52437; MUID:95115794; PMID:7816135
A;Accession: S52437
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-447 <WUL>
A;Cross-references: UNIPARC:UPI0000179A38

Query Match 75.6%; Score 31; DB 2; Length 447;
Best Local Similarity 62.5%; Pred. No. 85;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||| :|:|
Db 430 QQYQIYQS 437

RESULT 8
AE1451
hypothetical protein homolog lin0148 [imported] - Listeria innocua (strain Clip11262)
C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE1451
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.

```
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1451
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-505 <GLA>
A;Cross-references: UNIPROT:Q92FF8; UNIPARC:UPI00000CC12F; GB:AL592022; PIDN:CAC95381.1;
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin0148

  Query Match             75.6%;  Score 31;  DB 2;  Length 505;
  Best Local Similarity   71.4%;  Pred. No. 96;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              |||:||:
Db         28 QYSIYRT 34


RESULT 9
T35028
probable glycosyl hydrolase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35028
R;Seeger, S.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A;Reference number: Z21565
A;Accession: T35028
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-729 <SEE>
A;Cross-references: UNIPROT:Q9XAM0; UNIPARC:UPI00000DB17F; EMBL:AL079355; PIDN:CAB45584.
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC4C6.20c

  Query Match             75.6%;  Score 31;  DB 2;  Length 729;
  Best Local Similarity   62.5%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              | ||:||:
Db        666 QHYSIYRN 673


RESULT 10
A38919
hypothetical protein 1 - human
C;Species: Homo sapiens (man)
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C;Accession: A38919
R;Nomura, N.; Miyajima, N.; Kawarabayashi, Y.; Tabata, S.
submitted to the EMBL Data Library, May 1994
A;Description: Prediction of new human genes by entire sequencing of randomly sampled cD
A;Reference number: A38919
A;Accession: A38919
A;Molecule type: mRNA
A;Residues: 1-1083 <NOM>
A;Cross-references: UNIPROT:Q15386; UNIPARC:UPI0000071402; EMBL:D13635; NID:g285982; PID

  Query Match             75.6%;  Score 31;  DB 2;  Length 1083;
  Best Local Similarity   75.0%;  Pred. No. 2.1e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||: ||
Db         64 QQYSIQRS 71


RESULT 11
S71839
canalicular multidrug resistance protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S71839
R;Buechler, M.; Koenig, J.; Brom, M.; Kartenbeck, J.; Spring, H.; Horie, T.; Keppler, D.
J. Biol. Chem. 271, 15091-15098, 1996
A;Title: cDNA cloning of the hepatocyte canalicular isoform of the multidrug resistance p
A;Reference number: S71839; MUID:96279006; PMID:8662992
A;Accession: S71839
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-1541 <BUE>
A;Cross-references: UNIPROT:Q63120; UNIPARC:UPI000012F578; EMBL:X96393; NID:g1292881; PII
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
C;Keywords: ATP; glycoprotein; nucleotide binding; P-loop; transmembrane protein
F;100-124/Domain: transmembrane #status predicted <TM01>
F;127-151/Domain: transmembrane #status predicted <TM02>
F;160-187/Domain: transmembrane #status predicted <TM03>
F;305-329/Domain: transmembrane #status predicted <TM04>
F;354-381/Domain: transmembrane #status predicted <TM05>
F;431-451/Domain: transmembrane #status predicted <TM06>
F;456-476/Domain: transmembrane #status predicted <TM07>
F;536-564/Domain: transmembrane #status predicted <TM08>
F;574-602/Domain: transmembrane #status predicted <TM09>
F;650-833/Domain: ATP-binding cassette homology <ABC1>
F;667-674/Region: nucleotide-binding motif A (P-loop)
F;966-994/Domain: transmembrane #status predicted <TM10>
F;1018-1046/Domain: transmembrane #status predicted <TM11>
F;1104-1132/Domain: transmembrane #status predicted <TM12>
F;1203-1228/Domain: transmembrane #status predicted <TM13>
F;1313-1506/Domain: ATP-binding cassette homology <ABC2>
F;1330-1337/Region: nucleotide-binding motif A (P-loop)
F;6,1007,1010,1011/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             75.6%;  Score 31;  DB 1;  Length 1541;
  Best Local Similarity   75.0%;  Pred. No. 2.9e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              | ||:|||
Db         46 QLYSVYRS 53


RESULT 12
C72355
hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: C72355
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequ
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: C72355
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-282 <ARN>
A;Cross-references: UNIPROT:Q9WZ76; UNIPARC:UPI00000C13DE; GB:AE001735; GB:AE000512; NID
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM0607

  Query Match             73.2%;  Score 30;  DB 2;  Length 282;
  Best Local Similarity   85.7%;  Pred. No. 87;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              || ||||
Db        247 QYILYRS 253


RESULT 13
```

S23991
conjugative transfer protein traN precursor - Escherichia coli plasmid F
C;Species: Escherichia coli
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C;Accession: S23991; B39442; S17095
R;Maneewannakul, S.; Kathir, P.; Ippen-Ihler, K.
J. Mol. Biol. 225, 299-311, 1992
A;Title: Characterization of the F plasmid mating aggregation gene traN and of a new F t
A;Reference number: S23990; MUID:92277643; PMID:1593622
A;Accession: S23991
A;Molecule type: DNA
A;Residues: 1-602 <MAN>
A;Cross-references: UNIPROT:P24082; UNIPARC:UPI00001372F4; EMBL:X61575; NID:g43125; PIDN
R;Maneewannakul, S.; Maneewannakul, K.; Ippen-Ihler, K.
J. Bacteriol. 173, 3872-3878, 1991
A;Title: Characterization of trbC, a new F plasmid tra operon gene that is essential to
A;Reference number: A39442; MUID:91267954; PMID:2050638
A;Accession: B39442
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-19 <MA2>
A;Cross-references: UNIPARC:UPI000017AA35; GB:M60427
C;Genetics:
A;Gene: traN
A;Genome: plasmid
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-602/Product: conjugative transfer protein traN #status predicted <MAT>

 Query Match 73.2%; Score 30; DB 2; Length 602;
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
Db 326 QSYSMYQS 333

RESULT 14
G64630
vacuolating cytotoxin precursor - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: G64630
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: G64630
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1290 <TOM>
A;Cross-references: UNIPROT:P55981; UNIPARC:UPI00001380B8; GB:AE000598; GB:AE000511; NID
F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-1290/Product: vacuolating cytotoxin #status predicted <MAT>

 Query Match 73.2%; Score 30; DB 2; Length 1290;
 Best Local Similarity 62.5%; Pred. No. 4e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
Db 96 KEYDLYRS 103

RESULT 15
G83771
hypothetical protein BH0975 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83771
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83771
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1489 <STO>
A;Cross-references: UNIPROT:Q9KE81; UNIPARC:UPI00000C3A5A; GB:AP001510; GB:BA000004; NID:
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0975

 Query Match 73.2%; Score 30; DB 2; Length 1489;
 Best Local Similarity 71.4%; Pred. No. 4.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYSLYR 7
Db 198 QQYPIYR 204

RESULT 16
H84559
hypothetical protein At2g18070 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84559
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84559
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-145 <STO>
A;Cross-references: UNIPROT:Q9SL40; UNIPARC:UPI00000A8138; GB:AE002093; NID:g4406811; PII
C;Genetics:
A;Gene: At2g18070
A;Map position: 2

 Query Match 70.7%; Score 29; DB 2; Length 145;
 Best Local Similarity 62.5%; Pred. No. 73;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
Db 85 EAYSVYRS 92

RESULT 17
T16468
hypothetical protein F56C9.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16468
R;Du, Z.
submitted to the EMBL Data Library, May 1994
A;Description: The sequence of C. elegans cosmid F56C9.
A;Reference number: S46729
A;Accession: T16468
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-146 <DUZ>
A;Cross-references: UNIPROT:Q20862; UNIPARC:UPI000007E71C; EMBL:U00063; NID:g488186; PID:
A;Experimental source: strain Bristol N2
C;Genetics:
A;Gene: CESP:F56C9.5
A;Introns: 23/1; 88/3

 Query Match 70.7%; Score 29; DB 2; Length 146;

```
  Best Local Similarity   71.4%;  Pred. No. 74;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              | ||||:
Db         34 QMYSLYK 40


RESULT 18
T37857
hypothetical protein SPAC17G8.05 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37857
R;Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z21750
A;Accession: T37857
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-180 <DEV>
A;Cross-references: UNIPROT:Q10317; UNIPARC:UPI000013A886; EMBL:Z69795; PIDN:CAA93688.1;
A;Experimental source: strain 972h-; cosmid c17G8
C;Genetics:
A;Gene: SPDB:SPAC17G8.05
A;Map position: 1
A;Introns: 22/1

  Query Match             70.7%;  Score 29;  DB 2;  Length 180;
  Best Local Similarity   71.4%;  Pred. No. 91;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              || |||:
Db         27 QYKLYRN 33


RESULT 19
T21117
hypothetical protein F19D8.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21117
R;Swinburne, J.; Ainscough, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19377
A;Accession: T21117
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-221 <WIL>
A;Cross-references: UNIPROT:Q93530; UNIPARC:UPI00000815EE; EMBL:Z78541; PIDN:CAB01739.1;
A;Experimental source: clone F19D8
C;Genetics:
A;Gene: CESP:F19D8.2
A;Map position: X
A;Introns: 91/3; 116/1; 188/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F19D8.2

  Query Match             70.7%;  Score 29;  DB 2;  Length 221;
  Best Local Similarity   83.3%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYR 7
              :|||||
Db        132 EYSLYR 137


RESULT 20
G71533
probable pts iia protein + hth dna-binding domain - Chlamydia trachomatis (serotype D, s
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: G71533
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trach
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: G71533
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-225 <ARN>
A;Cross-references: UNIPROT:O84292; UNIPARC:UPI00000D3325; GB:AE001301; GB:AE001273; NID:
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: ptsN_1

  Query Match             70.7%;  Score 29;  DB 2;  Length 225;
  Best Local Similarity   71.4%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              :|||||:
Db         72 RYSLYRA 78


RESULT 21
S11473
serum amyloid P-component - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S11473
R;Dowton, S.B.; McGrew, S.D.
Biochem. J. 270, 553-556, 1990
A;Title: Rat serum amyloid P component. Analysis of cDNA sequence and gene expression.
A;Reference number: S11473; MUID:90380060; PMID:2400402
A;Accession: S11473
A;Molecule type: mRNA
A;Residues: 1-228 <DOW>
A;Cross-references: UNIPROT:P23680; UNIPARC:UPI0000167A6D; EMBL:X55761; NID:g57179; PIDN:
C;Superfamily: C-reactive protein

  Query Match             70.7%;  Score 29;  DB 2;  Length 228;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              :|||||
Db         89 EQYSLY 94


RESULT 22
S55135
hypothetical protein YMR188c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YM8010.18c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S55135; S59809; S70897
R;Churcher, C.M.
submitted to the EMBL Data Library, June 1995
A;Reference number: S55118
A;Accession: S55135
A;Molecule type: DNA
A;Residues: 1-237 <CHU>
A;Cross-references: UNIPROT:Q03246; UNIPARC:UPI00000530A2; EMBL:Z49808; NID:g854440; PIDN
A;Experimental source: strain AB972
R;Sinclair, D.A.; Dawes, I.W.
submitted to the EMBL Data Library, February 1995
A;Description: Cloning and expression of glycine decarboxylase from Saccharomyces cerevis
A;Reference number: S59809
A;Accession: S59809
A;Molecule type: DNA
A;Residues: 1-47 <SIN>
A;Cross-references: UNIPARC:UPI0000168A07; EMBL:U20641; NID:g676869; PIDN:AAB18932.1; PID
R;Sinclair, D.A.; Hong, S.P.; Dawes, I.W.
Mol. Microbiol. 19, 611-623, 1996
A;Title: Specific induction by glycine of the gene for the P-subunit of glycine decarboxy
```

```
A;Reference number: S70896; MUID:96228709; PMID:8830251
A;Accession: S70897
A;Molecule type: DNA
A;Residues: 1-47 <SIW>
A;Cross-references: UNIPARC:UPI0000168A07; EMBL:U20641; NID:g676869; PIDN:AAB18932.1; PI
C;Genetics:
A;Cross-references: SGD:S0004800
A;Map position: 13R
A;Note: YMR188c

  Query Match             70.7%;  Score 29;  DB 2;  Length 237;
  Best Local Similarity   62.5%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||::|| |
Db         83 QQFALYES 90


RESULT 23
AG0665
ABC transporter ATP-binding chain STY1436 [imported] - Salmonella enterica subsp. enteri
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AG0665
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AG0665
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-243 <PAR>
A;Cross-references: UNIPARC:UPI0000059EED; GB:AL513382; PIDN:CAD01696.1; PID:g16502547;
C;Genetics:
A;Gene: STY1436

  Query Match             70.7%;  Score 29;  DB 2;  Length 243;
  Best Local Similarity   71.4%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              | |:|||
Db         86 QNYALYR 92


RESULT 24
T05390
probable cysteine proteinase (EC 3.4.22.-) F16G20.220 - Arabidopsis thaliana
N;Alternate names: protein F16G20.220
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05390
R;Bevan, M.; Watson, M.D.; Gibbons, T.; Bartley, J.; Bancroft, I.; Mewes, H.W.; Mayer, K
submitted to the Protein Sequence Database, August 1998
A;Reference number: Z15413
A;Accession: T05390
A;Molecule type: DNA
A;Residues: 1-355 <BEV>
A;Cross-references: UNIPROT:O81748; UNIPARC:UPI00000A2EA9; EMBL:AL031326; GSPDB:GN00062;
A;Experimental source: cultivar Columbia; BAC clone F16G20
C;Genetics:
A;Gene: ATSP:F16G20.220
A;Map position: 4
A;Introns: 155/1; 237/3; 280/3
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase
F;157,293,313/Active site: Cys, His, Asn #status predicted

  Query Match             70.7%;  Score 29;  DB 2;  Length 355;
  Best Local Similarity   62.5%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |:: ||||
Db        273 QEFMLYRS 280


RESULT 25
T44665
conserved hypothetical protein nosX [imported] - Bradyrhizobium japonicum
C;Species: Bradyrhizobium japonicum
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44665
R;Bedmar, E.J.; Velasco, L.; Xu, C.A.; Delgado, M.J.
submitted to the EMBL Data Library, March 1998
A;Description: Bradyrhizobium japonicum nosRZDFYLX gene cluster.
A;Reference number: Z22825
A;Accession: T44665
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-366 <BED>
A;Cross-references: UNIPROT:Q9ZF33; UNIPARC:UPI00000B0053; EMBL:AJ002531; PIDN:CAA05524.1
A;Experimental source: strain USDA110
C;Genetics:
A;Note: nosX

  Query Match             70.7%;  Score 29;  DB 2;  Length 366;
  Best Local Similarity   71.4%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              |:||||:
Db         76 QFSLYRA 82


RESULT 26
I51267
collagenase (EC 3.4.24.-) - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51267
R;Oofusa, K.; Yomori, S.; Yoshizato, K.
Int. J. Dev. Biol. 38, 345-350, 1994
A;Title: Regionally and hormonally regulated expression of genes of collagen and collager
A;Reference number: I51267; MUID:95071832; PMID:7981043
A;Accession: I51267
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-384 <OOF>
A;Cross-references: UNIPROT:Q11133; UNIPARC:UPI000012F23C; GB:S75623; NID:g913070; PIDN:A
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteir
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
F;53-231/Domain: matrix metalloproteinase homology <MMP>
F;236-381/Domain: hemopexin repeat homology <PXN>
F;81,189,193,199/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status p
F;189,193,199/Binding site: zinc, catalytic (His) (active) #status predicted
F;190/Active site: Glu #status predicted

  Query Match             70.7%;  Score 29;  DB 2;  Length 384;
  Best Local Similarity   71.4%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              | |:|||
Db        179 QDYNLYR 185


RESULT 27
G82522
type I restriction-modification system specificity determinant XF2726 [imported] - Xylell
C;Species: Xylella fastidiosa
```

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: G82522
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: G82522
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-409 <SIM>
A;Cross-references: UNIPROT:Q9P9Z4; UNIPARC:UPI00000C2B24; GB:AE004079; GB:AE003849; NID
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2726

 Query Match 70.7%; Score 29; DB 2; Length 409;
 Best Local Similarity 71.4%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYSLYR 7
Db 393 QQYAYYR 399

RESULT 28
D71965
apolipoprotein n-acyltransferase - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: D71965
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: D71965
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-425 <ARN>
A;Cross-references: UNIPROT:Q9ZMQ0; UNIPARC:UPI00000D35E5; GB:AE001455; GB:AE001439; NID
A;Experimental source: strain J99
C;Genetics:
A;Gene: lnt

 Query Match 70.7%; Score 29; DB 2; Length 425;
 Best Local Similarity 75.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
Db 275 QGYSLYNS 282

RESULT 29
KCBOI
interstitial collagenase (EC 3.4.24.7) precursor - bovine
N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col
C;Species: Bos primigenius taurus (cattle)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: S14654; S20336; S14655
R;Tamura, M.; Shimokawa, H.; Sasaki, S.
submitted to the EMBL Data Library, March 1991
A;Reference number: S14654
A;Accession: S14654
A;Molecule type: mRNA
A;Residues: 1-469 <TAM>
A;Cross-references: UNIPROT:P28053; UNIPARC:UPI000012F238; EMBL:X58256; NID:g259; PIDN:C
R;Sudbeck, B.D.; Jeffrey, J.J.; Welgus, H.G.; Mecham, R.P.; McCourt, D.; Parks, W.C.
Arch. Biochem. Biophys. 293, 370-376, 1992
A;Title: Purification and characterization of bovine interstitial collagenase and tissue
A;Reference number: S20336; MUID:92161820; PMID:1311165
A;Accession: S20336
A;Molecule type: protein
A;Residues: 19-21,'FP',24-29,'L',31-34,'LL',37-39,'F';86-105,'NPR',109-112,'D',114-125 <S
A;Cross-references: UNIPARC:UPI0000172CC8; UNIPARC:UPI0000172CC9
C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in the
C;Comment: Procollagenase can be activated without removal of the activation peptide. Str
tion peptide by other proteinases.
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whic
C;Function:
A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteir
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallop
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-469/Product: procollagenase #status predicted <PRO>
F;19-99/Domain: activation peptide #status predicted <ACT>
F;60-261/Domain: matrix metalloproteinase homology <MMP>
F;90-97/Region: autoinhibitory
F;100-469/Product: interstitial collagenase #status predicted <MAT>
F;272-466/Domain: hemopexin repeat homology <PXN>
F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status p
F;120,143/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F;219/Active site: Glu #status predicted
F;278-466/Disulfide bonds: #status predicted

 Query Match 70.7%; Score 29; DB 1; Length 469;
 Best Local Similarity 71.4%; Pred. No. 2.4e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYSLYR 7
Db 208 QDYNLYR 214

RESULT 30
E83105
exodeoxyribonuclease I PA4316 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: E83105
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83105
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-480 <STO>
A;Cross-references: UNIPROT:Q9HW85; UNIPARC:UPI00000C5CB4; GB:AE004848; GB:AE004091; NID:
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: sbcB; PA4316
C;Superfamily: exodeoxyribonuclease I

 Query Match 70.7%; Score 29; DB 2; Length 480;
 Best Local Similarity 71.4%; Pred. No. 2.4e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 QYSLYRS 8
              :|||||:
Db        109 RYSLYRN 115
```

RESULT 31
B36921
methyl coenzyme M reductase (EC 1.8.-.-) component A2 - Methanobacterium thermoautotroph
C;Species: Methanobacterium thermoautotrophicum
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C;Accession: B36921; D69002
R;Kuhner, C.H.; Lindenbach, B.D.; Wolfe, R.S.
J. Bacteriol. 175, 3195-3203, 1993
A;Title: Component A2 of methylcoenzyme M reductase system from Methanobacterium thermoa
A;Reference number: A36921; MUID:93259970; PMID:8491734
A;Contents: delta H
A;Accession: B36921
A;Status: preliminary
A;Molecule type: DNA; protein
A;Residues: 1-530 <KUH>
A;Cross-references: UNIPROT:O27095; UNIPARC:UPI000016FFAE; GB:S61233; NID:g385922; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBIN:132019, NCBIP:132021)
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: D69002
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 'MLILVTEGED',1-155,'T',157-530 <MTH>
A;Cross-references: UNIPARC:UPI0000066744; GB:AE000874; GB:AE000666; NID:g2622110; PIDN:
A;Experimental source: strain Delta H
A;Note: an incorrect initiation codon was used
C;Genetics:
A;Gene: MTH1015
C;Keywords: ATP; methanogenesis; nucleotide binding; oxidoreductase; P-loop
F;19-245/Domain: ATP-binding cassette homology <ABC1>
F;36-43/Region: nucleotide-binding motif A (P-loop)
F;300-504/Domain: ATP-binding cassette homology <ABC2>
F;317-324/Region: nucleotide-binding motif A (P-loop)

 Query Match 70.7%; Score 29; DB 2; Length 530;
 Best Local Similarity 83.3%; Pred. No. 2.7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 QQYSLY 6
              |:||||
Db        372 QEYSLY 377
```

RESULT 32
T10290
hypothetical protein 21 - Orgyia pseudotsugata nuclear polyhedrosis virus
C;Species: Orgyia pseudotsugata nuclear polyhedrosis virus, OpMNPV
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T10290
R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
Virology 229, 381-399, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
A;Reference number: Z17011; MUID:97271300; PMID:9126251
A;Accession: T10290
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-627 <AHR>
A;Cross-references: UNIPARC:UPI0000179742; EMBL:U75930; NID:g2934903; PIDN:AAC59020.1; P

 Query Match 70.7%; Score 29; DB 2; Length 627;
 Best Local Similarity 83.3%; Pred. No. 3.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 QYSLYR 7
              |||||:
Db        318 QYSLYK 323
```

RESULT 33
B91284
probable integrase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: B91284
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genor
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B91284
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-649 <HAY>
A;Cross-references: UNIPROT:Q8XC99; UNIPARC:UPI00000D04D4; GB:BA000007; PIDN:BAB38665.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs5242

 Query Match 70.7%; Score 29; DB 2; Length 649;
 Best Local Similarity 71.4%; Pred. No. 3.3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 QQYSLYR 7
              |:| |||
Db          3 QRYKLYR 9
```

RESULT 34
D86125
probable integrase Z5878 [imported] - Escherichia coli (strain O157:H7, substrain EDL933
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D86125
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: D86125
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-649 <STO>
A;Cross-references: UNIPROT:Q8XC99; UNIPARC:UPI00001659FD; GB:AE005174; NID:g12519277; PI
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z5878

 Query Match 70.7%; Score 29; DB 2; Length 649;
 Best Local Similarity 71.4%; Pred. No. 3.3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 QQYSLYR 7
              |:| |||
Db          3 QRYKLYR 9
```

RESULT 35
AD0661
invasin-like protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (str
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AD0661
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.

```
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AD0661
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-660 <PAR>
A;Cross-references: UNIPARC:UPI00000CDB2E; GB:AL513382; PIDN:CAD01661.1; PID:g16502513;
C;Genetics:
A;Gene: STY1395

  Query Match             70.7%;  Score 29;  DB 2;  Length 660;
  Best Local Similarity   83.3%;  Pred. No. 3.3e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              |:||||
Db        399 QEYSLY 404


RESULT 36
H84774
probable homeodomain transcription factor [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84774
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84774
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-680 <STO>
A;Cross-references: UNIPROT:Q9SJ56; UNIPARC:UPI000009E071; GB:AE002093; NID:g4510375; PI
C;Genetics:
A;Gene: At2g35940
A;Map position: 2

  Query Match             70.7%;  Score 29;  DB 2;  Length 680;
  Best Local Similarity   85.7%;  Pred. No. 3.4e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              ||||| |
Db        112 QYSLYGS 118


RESULT 37
E84948
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain G [imported] - Buchnera sp. (strain
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 03-Jun-2002
C;Accession: E84948
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: E84948
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-906 <STO>
A;Cross-references: UNIPARC:UPI000005E4A0; GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: nuoG; BU159
C;Keywords: NAD; oxidoreductase

  Query Match             70.7%;  Score 29;  DB 2;  Length 906;
  Best Local Similarity   71.4%;  Pred. No. 4.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              :| ||||
Db        571 EYDLYRS 577


RESULT 38
AD2143
two-component sensor histidine kinase all2699 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AD2143
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2143
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-920 <KUR>
A;Cross-references: UNIPROT:Q8YTL8; UNIPARC:UPI00000CE51D; GB:BA000019; PIDN:BAB74398.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all2699

  Query Match             70.7%;  Score 29;  DB 2;  Length 920;
  Best Local Similarity   71.4%;  Pred. No. 4.7e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              ||| ||:
Db        417 QQYELYQ 423


RESULT 39
S62544
hypothetical protein SPAC12G12.13c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 05-Oct-2004
C;Accession: S62544; T37588
R;Devlin, K.; Odell, C.; Churcher, C.M.
submitted to the EMBL Data Library, November 1995
A;Reference number: S62532
A;Accession: S62544
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1253 <DEV>
A;Cross-references: UNIPROT:Q9UTN3; UNIPARC:UPI000017A4B8; EMBL:Z66568; NID:g1052518; PII
R;Devlin, K.; Odell, C.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, November 1995
A;Reference number: Z21727
A;Accession: T37588
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 638-1253 <DE2>
A;Cross-references: UNIPARC:UPI000013A0A2; EMBL:Z66568; PIDN:CAA91508.1; GSPDB:GN00066; S
A;Experimental source: strain 972h-; cosmid c12G12
C;Genetics:
A;Gene: SPDB:SPAC12G12.13c
A;Map position: 1L
A;Introns: 473/1; 554/1
F;160-193/Domain: WD repeat homology <WD1>
F;244-279/Domain: WD repeat homology <WD3>

  Query Match             70.7%;  Score 29;  DB 2;  Length 1253;
  Best Local Similarity   62.5%;  Pred. No. 6.3e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||::|| |
```

```
Db        508 QQFTLYHS 515


RESULT 40
T30335
KLP2 protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 05-Oct-2004
C;Accession: T30335
R;Boleti, H.; Karsenti, E.; Vernos, I.
Cell 84, 49-59, 1996
A;Title: Xklp2, a new Xenopus centrosomal kinesin-like protein required for centrosome s
A;Reference number: Z20827; MUID:96140639; PMID:8548825
A;Accession: T30335
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1388 <BOL>
A;Cross-references: UNIPROT:Q91785; UNIPARC:UPI00000FD639; EMBL:X94082; NID:g1129172; PI
C;Genetics:
A;Gene: klp2

  Query Match             70.7%;  Score 29;  DB 2;  Length 1388;
  Best Local Similarity   83.3%;  Pred. No. 7e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYR 7
              :|||||
Db        826 EYSLYR 831


RESULT 41
T18438
hypothetical protein C0415c - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18438
R;Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z18935
A;Accession: T18438
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1532 <LAW>
A;Cross-references: UNIPROT:O77332; UNIPARC:UPI000017CC26; EMBL:Z98547; NID:e1325376; PI
C;Genetics:
A;Map position: 3
A;Note: C0415c

  Query Match             70.7%;  Score 29;  DB 2;  Length 1532;
  Best Local Similarity   50.0%;  Pred. No. 7.8e+02;
  Matches    4;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              :||::|:|
Db       1445 KQYNIYKS 1452


RESULT 42
H97912
conserved hypothetical protein spr0328 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: H97912
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: H97912
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1767 <KUR>
A;Cross-references: UNIPROT:Q8DR60; UNIPARC:UPI00000E340E; GB:AE007317; PIDN:AAK99132.1;
C;Genetics:
A;Gene: spr0328

  Query Match             70.7%;  Score 29;  DB 2;  Length 1767;
  Best Local Similarity   75.0%;  Pred. No. 9e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              | | ||||
Db       1037 QPYVLYRS 1044


RESULT 43
E95163
conserved hypothetical protein SP1404 [imported] - Streptococcus pneumoniae (strain TIGR4
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: E95163
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: E95163
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-92 <KUR>
A;Cross-references: UNIPROT:Q97Q27; UNIPARC:UPI000005182B; GB:AE005672; PIDN:AAK75502.1;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1404

  Query Match             68.3%;  Score 28;  DB 2;  Length 92;
  Best Local Similarity   83.3%;  Pred. No. 75;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YSLYRS 8
              |||||:
Db         71 YSLYRA 76


RESULT 44
D98029
conserved hypothetical protein spr1261 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: D98029
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; Mc
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: D98029
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-92 <KUR>
A;Cross-references: UNIPROT:Q97Q27; UNIPARC:UPI000005182B; GB:AE007317; PIDN:AAL00065.1;
C;Genetics:
A;Gene: spr1261

  Query Match             68.3%;  Score 28;  DB 2;  Length 92;
  Best Local Similarity   83.3%;  Pred. No. 75;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YSLYRS 8
              |||||:
Db         71 YSLYRA 76
```

RESULT 45
A86698
hypothetical protein yfhK [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C;Species: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86698
R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: A86698
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-94 <STO>
A;Cross-references: UNIPROT:Q9CHY3; UNIPARC:UPI00000C6873; GB:AE005176; PID:g12723477; P
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yfhK

 Query Match 68.3%; Score 28; DB 2; Length 94;
 Best Local Similarity 71.4%; Pred. No. 77;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYSLYRS 8
:|||| |
Db 37 EYSLYES 43

RESULT 46
B82436
conserved hypothetical protein VCA0636 [imported] - Vibrio cholerae (strain N16961 serog
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82436
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82436
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-96 <HEI>
A;Cross-references: UNIPROT:Q9KLV5; UNIPARC:UPI00000C35C3; GB:AE004393; GB:AE003853; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0636
A;Map position: 2

 Query Match 68.3%; Score 28; DB 2; Length 96;
 Best Local Similarity 83.3%; Pred. No. 79;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYSLYR 7
|| |||
Db 37 QYELYR 42

RESULT 47
H96602
unknown protein F14G9.23 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H96602
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96602
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 <STO>
A;Cross-references: UNIPROT:Q9SGU2; UNIPARC:UPI000000C434; GB:AE005173; NID:g11094716; PI
C;Genetics:
A;Gene: F14G9.23
A;Map position: 1
C;Superfamily: auxin-induced protein 10A

 Query Match 68.3%; Score 28; DB 2; Length 110;
 Best Local Similarity 85.7%; Pred. No. 90;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYSLYRS 8
|||| ||
Db 16 QYSLLRS 22

RESULT 48
AH0397
probable lipoprotein YPO3274 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 31-Dec-2004
C;Accession: AH0397
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; P
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, P
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AH0397
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <KUR>
A;Cross-references: UNIPROT:Q8ZBW0; UNIPARC:UPI00000DCD20; GB:AL590842; PIDN:CAC92508.1;
C;Genetics:
A;Gene: YPO3274
C;Superfamily: periplasmic lipoprotein

 Query Match 68.3%; Score 28; DB 2; Length 113;
 Best Local Similarity 83.3%; Pred. No. 93;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 YSLYRS 8
|||||:
Db 106 YSLYRA 111

RESULT 49
T46207
hypothetical protein T8P19.140 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T46207
R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sau
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23008
A;Accession: T46207
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-122 <CHO>
A;Cross-references: UNIPROT:Q9SMN6; UNIPARC:UPI00000A626D; EMBL:AL133315
A;Experimental source: cultivar Columbia; BAC clone T8P19
C;Genetics:
A;Map position: 3
A;Note: T8P19.140

Query Match 68.3%; Score 28; DB 2; Length 122;
Best Local Similarity 83.3%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 QQYSLY 6
              :|||||
Db         99 KQYSLY 104
```

RESULT 50
A95226
hypothetical protein SP1934 [imported] - Streptococcus pneumoniae (strain TIGR4)
C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: A95226
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: A95226
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-141 <KUR>
A;Cross-references: UNIPROT:Q97NS9; UNIPARC:UPI0000051A53; GB:AE005672; PIDN:AAK76002.1;
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1934

Query Match 68.3%; Score 28; DB 2; Length 141;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 QQYSLYR 7
              ::|:|||
Db         73 EEYALYR 79
```

Search completed: March 23, 2006, 02:04:33
Job time : 28.0685 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:40:40 ; Search time 68.8219 Seconds
(without alignments)
82.012 Million cell updates/sec

Title: US-10-755-382-22
Perfect score: 41
Sequence: 1 QQYSLYRS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	37	90.2	310	2	Q4NNX7_9DELT	Q4nnx7 anaeromyxob
2	35	85.4	452	2	Q4S5J9_TETNG	Q4s5j9 tetraodon n
3	35	85.4	655	2	Q8STS4_ENCCU	Q8sts4 encephalito
4	34	82.9	254	1	ATE_RHILO	Q983e4 rhizobium l
5	34	82.9	315	2	Q88NF4_PSEPK	Q88nf4 pseudomonas
6	34	82.9	548	1	ALG11_YEAST	P53954 saccharomyc
7	33	80.5	132	2	Q4YP95_PLABE	Q4yp95 plasmodium
8	33	80.5	347	2	Q91ER5_GVCP	Q91er5 cydia pomon
9	33	80.5	368	2	Q802V1_BRARE	Q802v1 brachydanio
10	33	80.5	390	2	Q96CH7_HUMAN	Q96ch7 homo sapien
11	33	80.5	405	2	Q4IDE6_GIBZE	Q4ide6 gibberella
12	33	80.5	640	2	Q8N2I0_HUMAN	Q8n2i0 homo sapien
13	33	80.5	659	2	Q7RL96_PLAYO	Q7rl96 plasmodium
14	33	80.5	669	2	Q8WV05_HUMAN	Q8wv05 homo sapien
15	33	80.5	1025	2	Q53GL7_HUMAN	Q53gl7 homo sapien
16	33	80.5	1025	2	Q96K72_HUMAN	Q96k72 homo sapien
17	33	80.5	1576	2	Q70KN5_9NIDO	Q70kn5 porcine tor
18	32	78.0	198	2	Q8U5G9_AGRT5	Q8u5g9 agrobacteri
19	32	78.0	201	2	Q7PYZ5_ANOGA	Q7pyz5 anopheles g
20	32	78.0	237	2	Q7V3C7_PROMP	Q7v3c7 prochloroco
21	32	78.0	304	2	Q83AP7_COXBU	Q83ap7 coxiella bu
22	32	78.0	328	2	Q8MSM4_DROME	Q8msm4 drosophila
23	32	78.0	335	2	Q6W1N7_RHISN	Q6w1n7 rhizobium s
24	32	78.0	337	2	Q98C49_RHILO	Q98c49 rhizobium l
25	32	78.0	342	2	Q89PB1_BRAJA	Q89pb1 bradyrhizob
26	32	78.0	348	2	Q7Q6R9_ANOGA	Q7q6r9 anopheles g
27	32	78.0	348	2	Q63NB3_BURPS	Q63nb3 burkholderi
28	32	78.0	355	2	Q58AE7_9BURK	Q58ae7 ralstonia m
29	32	78.0	358	2	Q92YX7_RHIME	Q92yx7 rhizobium m
30	32	78.0	364	2	Q9VFE1_DROME	Q9vfe1 drosophila
31	32	78.0	392	2	Q22899_CAEEL	Q22899 caenorhabdi
32	32	78.0	415	2	Q5WYA9_LEGPL	Q5wya9 legionella
33	32	78.0	700	2	Q8ECU0_SHEON	Q8ecu0 shewanella
34	32	78.0	722	1	DYRK2_DROME	Q9v3d5 drosophila
35	32	78.0	785	2	Q7Q3B4_ANOGA	Q7q3b4 anopheles g
36	32	78.0	1749	2	Q4I1F1_GIBZE	Q4i1f1 gibberella
37	32	78.0	2913	2	Q4WZM5_ASPFU	Q4wzm5 aspergillus
38	32	78.0	2941	2	Q520T8_MAGGR	Q520t8 magnaporthe
39	32	78.0	3043	2	Q5AWI2_EMENI	Q5awi2 aspergillus
40	32	78.0	3054	2	Q7RXY5_NEUCR	Q7rxy5 neurospora
41	31	75.6	66	2	Q6H8C9_ORYSA	Q6h8c9 oryza sativ
42	31	75.6	68	2	Q8XS41_RALSO	Q8xs41 ralstonia s
43	31	75.6	72	2	Q8GGS3_STRAZ	Q8ggs3 streptomyce
44	31	75.6	104	1	CH10_SCHPO	O59804 schizosacch
45	31	75.6	120	2	Q55D69_DICDI	Q55d69 dictyosteli
46	31	75.6	120	2	Q55D70_DICDI	Q55d70 dictyosteli
47	31	75.6	134	2	Q7RQK6_PLAYO	Q7rqk6 plasmodium
48	31	75.6	157	2	Q6E6C8_ANTLO	Q6e6c8 antonospora
49	31	75.6	161	2	Q6RKG9_GIBZE	Q6rkg9 gibberella
50	31	75.6	196	2	Q5IXM2_MONPV	Q5ixm2 monkeypox v
51	31	75.6	197	2	Q8V4T6_MONPV	Q8v4t6 monkeypox v
52	31	75.6	255	2	Q9VK15_DROME	Q9vk15 drosophila
53	31	75.6	294	2	Q7YY70_CRYPV	Q7yy70 cryptospori
54	31	75.6	311	2	Q9HKK5_THEAC	Q9hkk5 thermoplasm
55	31	75.6	318	2	Q5LKW2_SILPO	Q5lkw2 silicibacte
56	31	75.6	339	2	Q61B67_CAEBR	Q61b67 caenorhabdi
57	31	75.6	375	2	Q52EP8_MAGGR	Q52ep8 magnaporthe
58	31	75.6	447	1	CDSA_DROME	P56079 d phosphati
59	31	75.6	475	2	Q9RFN4_RHIET	Q9rfn4 rhizobium e
60	31	75.6	505	2	Q724V5_LISMF	Q724v5 listeria mo
61	31	75.6	505	2	Q92FF8_LISIN	Q92ff8 listeria in
62	31	75.6	510	2	Q8SRR6_ENCCU	Q8srr6 encephalito
63	31	75.6	541	2	Q5B6M9_EMENI	Q5b6m9 aspergillus
64	31	75.6	546	2	Q5AWY5_EMENI	Q5awy5 aspergillus
65	31	75.6	587	2	Q8XSL1_RALSO	Q8xsl1 ralstonia s
66	31	75.6	627	2	Q746Q4_GEOSL	Q746q4 geobacter s
67	31	75.6	664	2	Q55V64_CRYNE	Q55v64 cryptococcu
68	31	75.6	664	2	Q5KL18_CRYNE	Q5kl18 cryptococcu
69	31	75.6	680	2	Q4WBT0_ASPFU	Q4wbt0 aspergillus
70	31	75.6	729	2	Q9XAM0_STRCO	Q9xam0 streptomyce
71	31	75.6	761	2	Q4I909_GIBZE	Q4i909 gibberella
72	31	75.6	845	2	Q6FKN0_CANGA	Q6fkn0 candida gla
73	31	75.6	956	1	UVH1_ARATH	Q91ki5 arabidopsis
74	31	75.6	966	2	Q55GK4_DICDI	Q55gk4 dictyosteli
75	31	75.6	1033	1	SA190_YEAST	P36123 saccharomyc
76	31	75.6	1061	1	EX5C_BUCAP	Q8k9b0 buchnera ap
77	31	75.6	1083	1	UBE3C_HUMAN	Q15386 homo sapien
78	31	75.6	1110	2	Q54L20_DICDI	Q54l20 dictyosteli
79	31	75.6	1541	1	MRP2_RAT	Q63120 rattus norv
80	31	75.6	2317	2	Q4PE93_USTMA	Q4pe93 ustilago ma
81	31	75.6	2465	2	Q4ILW8_GIBZE	Q4ilw8 gibberella
82	31	75.6	2674	2	Q7T6T6_9VIRU	Q7t6t6 ectropis ob
83	31	75.6	2986	2	Q91BL4_9VIRU	Q91bl4 perina nuda
84	31	75.6	2987	2	Q6UP17_9VIRU	Q6up17 ectropis ob
85	30	73.2	103	2	Q6ZDT2_ORYSA	Q6zdt2 oryza sativ
86	30	73.2	109	2	Q84FS3_HELPY	Q84fs3 helicobacte
87	30	73.2	113	2	Q84FS4_HELPY	Q84fs4 helicobacte
88	30	73.2	141	2	Q72VF9_LEPIC	Q72vf9 leptospira
89	30	73.2	141	2	Q8F907_LEPIN	Q8f907 leptospira
90	30	73.2	148	2	O87750_HELPY	O87750 helicobacte
91	30	73.2	148	2	Q9R3I3_HELPY	Q9r3i3 helicobacte
92	30	73.2	148	2	Q9R3R9_HELPY	Q9r3r9 helicobacte
93	30	73.2	148	2	Q9R456_HELPY	Q9r456 helicobacte
94	30	73.2	148	2	Q9R835_HELPY	Q9r835 helicobacte
95	30	73.2	148	2	Q9R836_HELPY	Q9r836 helicobacte
96	30	73.2	148	2	Q9R837_HELPY	Q9r837 helicobacte
97	30	73.2	148	2	Q9R838_HELPY	Q9r838 helicobacte
98	30	73.2	148	2	Q9R839_HELPY	Q9r839 helicobacte
99	30	73.2	148	2	Q9R840_HELPY	Q9r840 helicobacte
100	30	73.2	148	2	Q9R841_HELPY	Q9r841 helicobacte
101	30	73.2	148	2	Q9R842_HELPY	Q9r842 helicobacte
102	30	73.2	148	2	Q9R844_HELPY	Q9r844 helicobacte
103	30	73.2	148	2	Q9R845_HELPY	Q9r845 helicobacte
104	30	73.2	148	2	Q9R848_HELPY	Q9r848 helicobacte

105	30	73.2	148	2	Q9R851_HELPY	Q9r851 helicobacte
106	30	73.2	148	2	Q9S3H8_HELPY	Q9s3h8 helicobacte
107	30	73.2	148	2	Q9S3I1_HELPY	Q9s3i1 helicobacte
108	30	73.2	148	2	Q9S3I4_HELPY	Q9s3i4 helicobacte
109	30	73.2	148	2	Q9S3I6_HELPY	Q9s3i6 helicobacte
110	30	73.2	148	2	Q8VNB7_HELPY	Q8vnb7 helicobacte
111	30	73.2	148	2	Q8VNC0_HELPY	Q8vnc0 helicobacte
112	30	73.2	148	2	Q8VNC1_HELPY	Q8vnc1 helicobacte
113	30	73.2	148	2	Q8VNC5_HELPY	Q8vnc5 helicobacte
114	30	73.2	148	2	Q8VNC7_HELPY	Q8vnc7 helicobacte
115	30	73.2	160	2	O32659_HELPY	O32659 helicobacte
116	30	73.2	160	2	O32660_HELPY	O32660 helicobacte
117	30	73.2	160	2	O32673_HELPY	O32673 helicobacte
118	30	73.2	160	2	O32677_HELPY	O32677 helicobacte
119	30	73.2	160	2	O32681_HELPY	O32681 helicobacte
120	30	73.2	160	2	O32682_HELPY	O32682 helicobacte
121	30	73.2	160	2	O32684_HELPY	O32684 helicobacte
122	30	73.2	160	2	Q6LCF2_HELPY	Q6lcf2 helicobacte
123	30	73.2	203	2	Q7YWY6_CAEEL	Q7ywy6 caenorhabdi
124	30	73.2	204	2	Q6ZDK6_ORYSA	Q6zdk6 oryza sativ
125	30	73.2	208	2	Q4RKH6_TETNG	Q4rkh6 tetraodon n
126	30	73.2	214	2	Q50EI6_LACRE	Q50ei6 lactobacill
127	30	73.2	216	2	Q8KSP6_HELPY	Q8ksp6 helicobacte
128	30	73.2	217	2	Q938Q3_HELPY	Q938q3 helicobacte
129	30	73.2	225	2	Q8VN40_HELPY	Q8vn40 helicobacte
130	30	73.2	225	2	Q8VN41_HELPY	Q8vn41 helicobacte
131	30	73.2	254	2	Q6RIA5_LEIME	Q6ria5 leishmania
132	30	73.2	259	2	Q5ID30_HELPY	Q5id30 helicobacte
133	30	73.2	267	2	Q4JCC1_SULAC	Q4jcc1 sulfolobus
134	30	73.2	282	2	Q9WZ76_THEMA	Q9wz76 thermotoga
135	30	73.2	287	2	Q7T5G6_GVCL	Q7t5g6 cryptophleb
136	30	73.2	305	2	Q6C3H9_YARLI	Q6c3h9 yarrowia li
137	30	73.2	314	2	Q54IS1_DICDI	Q54is1 dictyosteli
138	30	73.2	324	2	Q9HIZ7_THEAC	Q9hiz7 thermoplasm
139	30	73.2	334	2	Q5YRD1_NOCFA	Q5yrd1 nocardia fa
140	30	73.2	340	2	Q6AE21_LEIXX	Q6ae21 leifsonia x
141	30	73.2	343	2	Q9SNV1_ANTMA	Q9snv1 antirrhinum
142	30	73.2	363	1	TAGH_LACPL	Q88zh4 lactobacill
143	30	73.2	369	2	Q8EAK6_SHEON	Q8eak6 shewanella
144	30	73.2	373	2	Q8U201_PYRFU	Q8u201 pyrococcus
145	30	73.2	390	2	Q55XC7_CRYNE	Q55xc7 cryptococcu
146	30	73.2	426	2	Q75N74_ACHTE	Q75n74 achaearanea
147	30	73.2	433	2	Q7S6W9_NEUCR	Q7s6w9 neurospora
148	30	73.2	445	2	Q6R4V3_9VIRU	Q6r4v3 bacteriopha
149	30	73.2	497	2	Q7PTK1_ANOGA	Q7ptk1 anopheles g
150	30	73.2	542	2	Q8ECL0_SHEON	Q8ecl0 shewanella
151	30	73.2	555	2	Q7REM0_PLAYO	Q7rem0 plasmodium
152	30	73.2	575	2	Q9APR6_9BACT	Q9apr6 uncultured
153	30	73.2	576	2	Q8TQK0_METAC	Q8tqk0 methanosarc
154	30	73.2	596	2	Q58TW4_9HETE	Q58tw4 cryptococcu
155	30	73.2	602	1	TRAN_ECOLI	P24082 escherichia
156	30	73.2	602	2	Q84A27_ECOLI	Q84a27 escherichia
157	30	73.2	695	2	Q5AVH8_EMENI	Q5avh8 aspergillus
158	30	73.2	722	2	Q87YV0_PSESM	Q87yv0 pseudomonas
159	30	73.2	751	2	Q5F449_CHICK	Q5f449 gallus gall
160	30	73.2	761	2	Q4WGC7_ASPFU	Q4wgc7 aspergillus
161	30	73.2	803	2	Q4LIW3_9BURK	Q4liw3 burkholderi
162	30	73.2	816	2	Q86HD8_DICDI	Q86hd8 dictyosteli
163	30	73.2	841	2	Q847M6_HELPY	Q847m6 helicobacte
164	30	73.2	908	2	Q8LTQ0_9CAUD	Q8ltq0 lactococcus
165	30	73.2	918	2	Q9AZ57_9CAUD	Q9az57 lactococcus
166	30	73.2	931	2	Q5LHQ2_BACFN	Q5lhq2 bacteroides
167	30	73.2	931	2	Q64YQ3_BACFR	Q64yq3 bacteroides
168	30	73.2	941	2	Q6DLS7_HELPY	Q6dls7 helicobacte
169	30	73.2	1194	2	Q6BN52_DEBHA	Q6bn52 debaryomyce
170	30	73.2	1290	1	VACA_HELPY	P55981 helicobacte
171	30	73.2	1290	2	O34111_HELPY	O34111 helicobacte
172	30	73.2	1295	2	O34110_HELPY	O34110 helicobacte
173	30	73.2	1295	2	Q60FM9_HELPY	Q60fm9 helicobacte
174	30	73.2	1296	1	VACA1_HELPY	Q48247 helicobacte
175	30	73.2	1302	2	Q60FL5_HELPY	Q60fl5 helicobacte
176	30	73.2	1303	2	Q60FL1_HELPY	Q60fl1 helicobacte
177	30	73.2	1303	2	Q60FM7_HELPY	Q60fm7 helicobacte
178	30	73.2	1310	1	VACA3_HELPY	Q48253 helicobacte
179	30	73.2	1313	2	Q93UN0_HELPY	Q93un0 helicobacte
180	30	73.2	1323	2	O87018_HELPY	O87018 helicobacte
181	30	73.2	1327	2	Q60FL9_HELPY	Q60fl9 helicobacte
182	30	73.2	1489	2	Q9KE81_BACHD	Q9ke81 bacillus ha
183	30	73.2	1499	2	Q6BL45_DEBHA	Q6bl45 debaryomyce
184	30	73.2	1501	2	Q6BL46_DEBHA	Q6bl46 debaryomyce
185	30	73.2	2367	1	POL1_RRVC	Q6w8w4 r rna1 poly
186	30	73.2	5222	2	Q54L33_DICDI	Q54l33 dictyosteli
187	30	73.2	8348	2	Q4S6Y5_TETNG	Q4s6y5 tetraodon n
188	29	70.7	62	2	Q81MA1_BACAN	Q81ma1 bacillus an
189	29	70.7	66	2	Q635F6_BACCZ	Q635f6 bacillus ce
190	29	70.7	68	2	Q4MMX7_BACCE	Q4mmx7 bacillus ce
191	29	70.7	68	2	Q6HE40_BACHK	Q6he40 bacillus th
192	29	70.7	83	2	Q5F8K4_NEIG1	Q5f8k4 neisseria g
193	29	70.7	86	2	Q95JZ7_MACFA	Q95jz7 macaca fasc
194	29	70.7	94	2	Q4X6S2_PLACH	Q4x6s2 plasmodium
195	29	70.7	95	2	Q8NHJ5_HUMAN	Q8nhj5 homo sapien
196	29	70.7	99	2	Q637B3_BACCZ	Q637b3 bacillus ce
197	29	70.7	99	2	Q81XY3_BACAN	Q81xy3 bacillus an
198	29	70.7	114	2	Q4Z626_PLABE	Q4z626 plasmodium
199	29	70.7	116	2	Q9QD51_9GEMI	Q9qd51 tomato leaf
200	29	70.7	121	2	Q9BGL7_SHEEP	Q9bgl7 ovis aries
201	29	70.7	122	2	Q8R3X3_MOUSE	Q8r3x3 mus musculu
202	29	70.7	125	1	Y1708_HAEDU	Q7vkz5 haemophilus
203	29	70.7	130	2	Q98P66_RHILO	Q98p66 rhizobium l
204	29	70.7	134	2	Q7PUC2_ANOGA	Q7puc2 anopheles g
205	29	70.7	134	2	Q4N1H6_THEPA	Q4n1h6 theileria p
206	29	70.7	134	2	Q4FP48_9RICK	Q4fp48 candidatus
207	29	70.7	145	2	Q9SL40_ARATH	Q9sl40 arabidopsis
208	29	70.7	146	2	Q20862_CAEEL	Q20862 caenorhabdi
209	29	70.7	150	2	Q4UJM7_RICFE	Q4ujm7 rickettsia
210	29	70.7	169	2	Q5ANM9_CANAL	Q5anm9 candida alb
211	29	70.7	171	2	Q58TX2_CRYNV	Q58tx2 cryptococcu
212	29	70.7	171	2	Q58TX4_CRYNV	Q58tx4 cryptococcu
213	29	70.7	172	2	Q58TX5_CRYNE	Q58tx5 cryptococcu
214	29	70.7	174	2	Q9TVA5_BOVIN	Q9tva5 bos taurus
215	29	70.7	180	1	YD65_SCHPO	Q10317 schizosacch
216	29	70.7	181	2	Q6QXF4_GVAS	Q6qxf4 agrotis seg
217	29	70.7	184	2	Q96GI7_HUMAN	Q96gi7 homo sapien
218	29	70.7	184	2	Q555N6_DICDI	Q555n6 dictyosteli
219	29	70.7	185	2	Q5KTK2_9MAGN	Q5ktk2 illicium an
220	29	70.7	189	2	Q648D2_9ARCH	Q648d2 uncultured
221	29	70.7	192	2	Q74NW6_BACC1	Q74nw6 bacillus ce
222	29	70.7	202	2	Q6T4T2_9MAGN	Q6t4t2 illicium he
223	29	70.7	202	2	Q6T4T3_9MAGN	Q6t4t3 illicium he
224	29	70.7	215	2	Q6TER0_CRYNV	Q6ter0 cryptococcu
225	29	70.7	219	2	Q6TER1_CRYNE	Q6ter1 cryptococcu
226	29	70.7	223	2	Q9PKA4_CHLMU	Q9pka4 chlamydia m
227	29	70.7	225	2	O84292_CHLTR	O84292 chlamydia t
228	29	70.7	227	2	Q93530_CAEEL	Q93530 caenorhabdi
229	29	70.7	233	2	Q4NF73_9MICC	Q4nf73 arthrobacte
230	29	70.7	236	2	Q8X1J5_CRYNE	Q8x1j5 cryptococcu
231	29	70.7	236	2	Q86AU3_DICDI	Q86au3 dictyosteli
232	29	70.7	237	1	RTS17_YEAST	Q03246 saccharomyc
233	29	70.7	243	2	Q57P25_SALCH	Q57p25 salmonella
234	29	70.7	243	2	Q8ZPA1_SALTY	Q8zpa1 salmonella
235	29	70.7	243	2	Q8Z770_SALTI	Q8z770 salmonella
236	29	70.7	244	2	Q6BMF9_DEBHA	Q6bmf9 debaryomyce
237	29	70.7	251	2	Q8GF12_EDWTA	Q8gf12 edwardsiell
238	29	70.7	251	2	Q7VUY9_BORPE	Q7vuy9 bordetella
239	29	70.7	251	2	Q7WBD1_BORPA	Q7wbd1 bordetella
240	29	70.7	251	2	Q7WMV0_BORBR	Q7wmv0 bordetella
241	29	70.7	252	2	Q5X5B7_LEGPA	Q5x5b7 legionella
242	29	70.7	253	2	Q7MAC3_WOLSU	Q7mac3 wolinella s
243	29	70.7	260	2	Q54UR0_DICDI	Q54ur0 dictyosteli
244	29	70.7	260	2	Q8SSU2_DICDI	Q8ssu2 dictyosteli
245	29	70.7	261	2	Q70G16_LEGPN	Q70g16 legionella
246	29	70.7	261	2	Q5ZVJ2_LEGPH	Q5zvj2 legionella
247	29	70.7	262	2	Q60WI9_CAEBR	Q60wi9 caenorhabdi
248	29	70.7	262	2	Q7MZP2_PHOLL	Q7mzp2 photorhabdu
249	29	70.7	277	2	Q5L966_BACFN	Q5l966 bacteroides
250	29	70.7	293	2	Q7MZP0_PHOLL	Q7mzp0 photorhabdu

251	29	70.7	297	2	Q937N2_PHOLU	Q937n2	photorhabdu
252	29	70.7	311	2	Q95V93_CULQU	Q95v93	culex quinq
253	29	70.7	313	2	Q5VNI9_ORYSA	Q5vni9	oryza sativ
254	29	70.7	321	2	Q5UR48_MIMIV	Q5ur48	mimivirus.
255	29	70.7	327	2	Q8EQ29_OCEIH	Q8eq29	oceanobacil
256	29	70.7	332	2	Q89XJ4_BRAJA	Q89xj4	bradyrhizob
257	29	70.7	335	2	Q5ASW2_EMENI	Q5asw2	aspergillus
258	29	70.7	336	2	Q6D2L8_ERWCT	Q6d2l8	erwinia car
259	29	70.7	352	2	Q4S6B4_TETNG	Q4s6b4	tetraodon n
260	29	70.7	354	2	Q61R75_CAEBR	Q61r75	caenorhabdi
261	29	70.7	355	2	O81748_ARATH	O81748	arabidopsis
262	29	70.7	358	2	Q67N10_SYMTH	Q67n10	symbiobacte
263	29	70.7	361	2	Q57ZR9_9TRYP	Q57zr9	trypanosoma
264	29	70.7	366	2	Q9ZF33_BRAJA	Q9zf33	bradyrhizob
265	29	70.7	371	2	Q90YI8_FUGRU	Q90yi8	fugu rubrip
266	29	70.7	372	2	Q6BWI0_DEBHA	Q6bwi0	debaryomyce
267	29	70.7	372	2	Q63QH7_BURPS	Q63qh7	burkholderi
268	29	70.7	372	2	Q62DC2_BURMA	Q62dc2	burkholderi
269	29	70.7	374	2	Q6P4E2_HUMAN	Q6p4e2	homo sapien
270	29	70.7	375	2	Q96J85_HUMAN	Q96j85	homo sapien
271	29	70.7	378	2	Q4WXV8_ASPFU	Q4wxv8	aspergillus
272	29	70.7	381	2	Q82ZU2_ENTFA	Q82zu2	enterococcu
273	29	70.7	384	1	MMP1_RANCA	Q11133	rana catesb
274	29	70.7	386	2	Q5WHN5_BACSK	Q5whn5	bacillus cl
275	29	70.7	389	2	Q8A4Z0_BACTN	Q8a4z0	bacteroides
276	29	70.7	403	2	Q6DDK1_XENLA	Q6ddk1	xenopus lae
277	29	70.7	405	2	Q879W5_XYLFT	Q879w5	xylella fas
278	29	70.7	409	2	Q9P9Z4_XYLFA	Q9p9z4	xylella fas
279	29	70.7	410	2	Q4LL06_9BURK	Q4ll06	burkholderi
280	29	70.7	416	2	Q5WS23_LEGPA	Q5ws23	legionella
281	29	70.7	419	2	Q5X6V8_LEGPA	Q5x6v8	legionella
282	29	70.7	420	2	Q7YEU8_SACSE	Q7yeu8	saccharomyc
283	29	70.7	423	2	Q5ZXD9_LEGPH	Q5zxd9	legionella
284	29	70.7	425	1	LNT_HELPJ	Q9zmq0	helicobacte
285	29	70.7	435	2	Q4KH06_PSEP5	Q4kh06	pseudomonas
286	29	70.7	437	2	Q87HK9_VIBPA	Q87hk9	vibrio para
287	29	70.7	439	1	LIRA3_HUMAN	Q8n6c8	homo sapien
288	29	70.7	442	2	Q4P2I8_USTMA	Q4p2i8	ustilago ma
289	29	70.7	449	2	Q8IEM8_PLAF7	Q8iem8	plasmodium
290	29	70.7	460	2	Q8MJZ4_PANTR	Q8mjz4	pan troglod
291	29	70.7	469	1	MMP1_BOVIN	P28053	bos taurus
292	29	70.7	472	2	Q6PIZ7_HUMAN	Q6piz7	homo sapien
293	29	70.7	474	2	Q84ME2_ARATH	Q84me2	arabidopsis
294	29	70.7	477	2	Q88N51_PSEPK	Q88n51	pseudomonas
295	29	70.7	478	2	Q5B3T5_EMENI	Q5b3t5	aspergillus
296	29	70.7	480	2	Q9HW85_PSEAE	Q9hw85	pseudomonas
297	29	70.7	485	2	Q20139_CAEEL	Q20139	caenorhabdi
298	29	70.7	489	1	LIRA1_HUMAN	O75019	homo sapien
299	29	70.7	489	2	Q51DV5_ENTHI	Q51dv5	entamoeba h
300	29	70.7	491	2	Q503H6_BRARE	Q503h6	brachydanio
301	29	70.7	492	2	Q585D7_9TRYP	Q585d7	trypanosoma
302	29	70.7	493	2	Q604R4_METCA	Q604r4	methylococc
303	29	70.7	497	2	Q4K7B4_PSEF5	Q4k7b4	pseudomonas
304	29	70.7	530	2	Q7LYR5_METTF	Q7lyr5	methanobact
305	29	70.7	531	2	Q6LZK7_METMP	Q6lzk7	methanococc
306	29	70.7	532	2	Q8TVF6_METKA	Q8tvf6	methanopyru
307	29	70.7	534	2	Q6VUB3_9ARCH	Q6vub3	uncultured
308	29	70.7	534	2	Q64E10_9ARCH	Q64e10	uncultured
309	29	70.7	535	2	Q647L0_9ARCH	Q647l0	uncultured
310	29	70.7	540	2	Q50576_METTF	Q50576	methanobact
311	29	70.7	540	2	O27095_METTH	O27095	methanobact
312	29	70.7	541	2	Q64EG8_9ARCH	Q64eg8	uncultured
313	29	70.7	542	2	Q64AQ0_9ARCH	Q64aq0	uncultured
314	29	70.7	542	2	Q64A16_9ARCH	Q64a16	uncultured
315	29	70.7	545	2	Q8G3N6_BIFLO	Q8g3n6	bifidobacte
316	29	70.7	580	2	Q5A2A8_CANAL	Q5a2a8	candida alb
317	29	70.7	580	2	Q5A2G0_CANAL	Q5a2g0	candida alb
318	29	70.7	586	2	Q5UXY8_HALMA	Q5uxy8	haloarcula
319	29	70.7	588	2	Q6BKV4_DEBHA	Q6bkv4	debaryomyce
320	29	70.7	594	2	Q4WZB9_ASPFU	Q4wzb9	aspergillus
321	29	70.7	598	1	LIRB2_HUMAN	Q8n423	h leukocyte
322	29	70.7	602	2	Q9HEM4_NEUCR	Q9hem4	neurospora
323	29	70.7	603	2	Q8DUM6_STRMU	Q8dum6	streptococc
324	29	70.7	607	2	Q9SKN1_ARATH	Q9skn1	a expressed
325	29	70.7	617	2	Q72HA4_THET2	Q72ha4	thermus the
326	29	70.7	627	2	Q4N3H0_THEPA	Q4n3h0	theileria p
327	29	70.7	634	2	Q5U2S6_RAT	Q5u2s6	rattus norv
328	29	70.7	634	2	Q8K0L0_MOUSE	Q8k0l0	mus musculu
329	29	70.7	649	2	Q7A8Q6_ECO57	Q7a8q6	escherichia
330	29	70.7	649	2	Q8XC99_ECO57	Q8xc99	escherichia
331	29	70.7	650	1	LIRB1_HUMAN	Q8nhl6	h leukocyte
332	29	70.7	654	2	Q6ZV14_HUMAN	Q6zv14	homo sapien
333	29	70.7	654	2	Q7TLW5_NPVCF	Q7tlw5	choristoneu
334	29	70.7	657	1	Y023_NPVOP	O10282	orgyia pseu
335	29	70.7	657	2	Q53KJ6_ORYSA	Q53kj6	oryza sativ
336	29	70.7	660	2	Q83T27_SALTI	Q83t27	salmonella
337	29	70.7	660	2	Q8Z795_SALTI	Q8z795	salmonella
338	29	70.7	660	2	Q8ZP78_SALTY	Q8zp78	salmonella
339	29	70.7	662	2	Q8MJZ6_PANTR	Q8mjz6	pan troglod
340	29	70.7	680	2	Q94KL4_ARATH	Q94kl4	arabidopsis
341	29	70.7	680	2	Q9SJ56_ARATH	Q9sj56	arabidopsis
342	29	70.7	684	2	Q518I4_ENTHI	Q518i4	entamoeba h
343	29	70.7	691	2	Q5CY15_CRYPV	Q5cy15	cryptospori
344	29	70.7	691	2	Q5CNY6_CRYHO	Q5cny6	cryptospori
345	29	70.7	699	2	Q9VVV4_DROME	Q9vvv4	drosophila
346	29	70.7	702	2	Q5A2A7_CANAL	Q5a2a7	candida alb
347	29	70.7	703	2	Q6XM38_9PHYC	Q6xm38	feldmannia
348	29	70.7	717	1	LARP4_MOUSE	Q8bww4	mus musculu
349	29	70.7	719	1	TOP1_MYCGA	Q9jn65	mycoplasma
350	29	70.7	719	2	Q6BPL3_DEBHA	Q6bpl3	debaryomyce
351	29	70.7	719	2	Q9R6Q0_MYCGA	Q9r6q0	mycoplasma
352	29	70.7	720	2	Q7UYB2_RHOBA	Q7uyb2	rhodopirell
353	29	70.7	723	1	LARP4_HUMAN	Q71rc2	homo sapien
354	29	70.7	723	2	Q758H4_ASHGO	Q758h4	ashbya goss
355	29	70.7	724	2	Q9H6S7_HUMAN	Q9h6s7	homo sapien
356	29	70.7	735	2	Q9NDE8_APLCA	Q9nde8	aplysia cal
357	29	70.7	754	2	Q8DHS2_SYNEL	Q8dhs2	synechococc
358	29	70.7	813	2	Q4XS52_PLACH	Q4xs52	plasmodium
359	29	70.7	831	2	Q4FY46_LEIMA	Q4fy46	leishmania
360	29	70.7	832	2	Q86H63_DICDI	Q86h63	dictyosteli
361	29	70.7	843	2	Q553E3_DICDI	Q553e3	dictyosteli
362	29	70.7	845	2	Q8TUI8_METAC	Q8tui8	methanosarc
363	29	70.7	849	2	Q7XK56_ORYSA	Q7xk56	oryza sativ
364	29	70.7	893	2	Q659I9_SPHGR	Q659i9	sphaerechin
365	29	70.7	906	1	NUOG_BUCAI	P57257	buchnera ap
366	29	70.7	907	1	NUOG_BUCBP	Q89au1	buchnera ap
367	29	70.7	920	2	Q8YTL8_ANASP	Q8ytl8	anabaena sp
368	29	70.7	936	2	O97272_PLAF7	O97272	plasmodium
369	29	70.7	959	2	Q511Y9_ENTHI	Q511y9	entamoeba h
370	29	70.7	978	2	Q8IB83_PLAF7	Q8ib83	plasmodium
371	29	70.7	982	2	Q9VLI0_DROME	Q9vli0	drosophila
372	29	70.7	986	2	Q6H6D6_ORYSA	Q6h6d6	oryza sativ
373	29	70.7	1003	2	Q7RTD2_PLAYO	Q7rtd2	plasmodium
374	29	70.7	1016	2	Q4YSG2_PLABE	Q4ysg2	plasmodium
375	29	70.7	1047	2	Q6DRG7_BRARE	Q6drg7	brachydanio
376	29	70.7	1052	2	Q5WXP7_LEGPL	Q5wxp7	legionella
377	29	70.7	1107	1	ALA2_ARATH	P98205	arabidopsis
378	29	70.7	1117	2	Q5TZI3_BRARE	Q5tz13	brachydanio
379	29	70.7	1201	2	Q7R4Q5_GIALA	Q7r4q5	giardia lam
380	29	70.7	1287	2	Q93UM9_HELPY	Q93um9	helicobacte
381	29	70.7	1343	2	Q7MW22_PORGI	Q7mw22	porphyromon
382	29	70.7	1381	2	Q5F989_NEIG1	Q5f989	neisseria g
383	29	70.7	1388	2	Q4XPH9_PLACH	Q4xph9	plasmodium
384	29	70.7	1388	2	Q91785_XENLA	Q91785	xenopus lae
385	29	70.7	1431	2	Q51RC9_MAGGR	Q51rc9	magnaporthe
386	29	70.7	1609	2	Q51DL9_ENTHI	Q51dl9	entamoeba h
387	29	70.7	1638	2	Q7R0U5_GIALA	Q7r0u5	giardia lam
388	29	70.7	1672	2	Q6P7Y1_BRARE	Q6p7y1	brachydanio
389	29	70.7	1673	2	O77332_PLAF7	O77332	plasmodium
390	29	70.7	1680	2	Q5TZ97_BRARE	Q5tz97	brachydanio
391	29	70.7	1680	2	Q7T163_BRARE	Q7t163	brachydanio
392	29	70.7	1767	2	Q8DR60_STRR6	Q8dr60	streptococc
393	29	70.7	1872	2	Q55UK7_CRYNE	Q55uk7	cryptococcu
394	29	70.7	1872	2	Q5KHT7_CRYNE	Q5kht7	cryptococcu
395	29	70.7	1899	2	Q54YJ1_DICDI	Q54yj1	dictyosteli
396	29	70.7	1901	2	Q4I1B9_GIBZE	Q4i1b9	gibberella

397	29	70.7	1905	2	Q9XTP6_PLABE	Q9xtp6 plasmodium
398	29	70.7	2387	2	Q5B0P5_EMENI	Q5b0p5 aspergillus
399	29	70.7	2420	2	Q5VJG3_CRYNE	Q5vjg3 cryptococcu
400	29	70.7	2426	2	Q96UR0_ASPFU	Q96ur0 aspergillus
401	29	70.7	2426	2	Q4X143_ASPFU	Q4x143 aspergillus
402	29	70.7	2430	2	Q55Q36_CRYNE	Q55q36 cryptococcu
403	29	70.7	2430	2	Q5KDD1_CRYNE	Q5kdd1 cryptococcu
404	29	70.7	2532	2	Q560W1_CRYNE	Q560w1 cryptococcu
405	29	70.7	2532	2	Q5KPW2_CRYNE	Q5kpw2 cryptococcu
406	29	70.7	3892	2	Q9VU08_DROME	Q9vu08 drosophila
407	29	70.7	4492	2	Q518T8_ENTHI	Q518t8 entamoeba h
408	28	68.3	25	2	Q4TAI5_TETNG	Q4tai5 tetraodon n
409	28	68.3	43	2	Q878F2_STRP3	Q878f2 streptococc
410	28	68.3	58	2	Q7RLR5_PLAYO	Q7rlr5 plasmodium
411	28	68.3	64	2	Q9W4L1_DROME	Q9w4l1 drosophila
412	28	68.3	65	2	Q5NG67_FRATT	Q5ng67 francisella
413	28	68.3	70	2	Q72TR6_LEPIC	Q72tr6 leptospira
414	28	68.3	70	2	Q8F1G7_LEPIN	Q8f1g7 leptospira
415	28	68.3	73	2	Q50RA1_ENTHI	Q50ra1 entamoeba h
416	28	68.3	87	2	Q4Z3U8_PLABE	Q4z3u8 plasmodium
417	28	68.3	90	2	Q9A0Y6_STRPY	Q9a0y6 streptococc
418	28	68.3	92	1	Y1261_STRR6	P67362 streptococc
419	28	68.3	92	1	Y1404_STRPN	P67361 streptococc
420	28	68.3	92	1	Y2462_ENTFA	Q831n9 enterococcu
421	28	68.3	94	2	Q9CHY3_LACLA	Q9chy3 lactococcus
422	28	68.3	96	2	Q9KLV5_VIBCH	Q9klv5 vibrio chol
423	28	68.3	97	2	Q4XUM5_PLACH	Q4xum5 plasmodium
424	28	68.3	107	2	Q98SN0_BRARE	Q98sn0 brachydanio
425	28	68.3	110	2	Q9SGU2_ARATH	Q9sgu2 arabidopsis
426	28	68.3	111	2	Q9VAW7_DROME	Q9vaw7 drosophila
427	28	68.3	112	2	Q75D32_ASHGO	Q75d32 ashbya goss
428	28	68.3	112	2	Q4QPY3_DROME	Q4qpy3 drosophila
429	28	68.3	113	2	Q8ZBW0_YERPE	Q8zbw0 yersinia pe
430	28	68.3	113	2	Q66E44_YERPS	Q66e44 yersinia ps
431	28	68.3	117	2	O18540_9PULM	O18540 bulinus tru
432	28	68.3	122	2	Q9SMN6_ARATH	Q9smn6 arabidopsis
433	28	68.3	127	2	Q86EC0_SCHJA	Q86ec0 schistosoma
434	28	68.3	127	2	Q9SF18_ARATH	Q9sf18 arabidopsis
435	28	68.3	131	2	Q600Q6_MYCHY	Q600q6 mycoplasma
436	28	68.3	132	2	Q9LTV3_ARATH	Q9ltv3 arabidopsis
437	28	68.3	132	2	Q6G3Q8_BARHE	Q6g3q8 bartonella
438	28	68.3	136	2	Q8IEQ4_PLAF7	Q8ieq4 plasmodium
439	28	68.3	136	2	Q8I1P5_PLAF7	Q8i1p5 plasmodium
440	28	68.3	136	2	Q4MUB8_BACCE	Q4mub8 bacillus ce
441	28	68.3	141	2	Q8CYA7_STRR6	Q8cya7 streptococc
442	28	68.3	141	2	Q97NS9_STRPN	Q97ns9 streptococc
443	28	68.3	141	2	Q8U6P1_AGRT5	Q8u6p1 agrobacteri
444	28	68.3	148	2	Q8VND0_HELPY	Q8vnd0 helicobacte
445	28	68.3	150	2	Q7QWI7_GIALA	Q7qwi7 giardia lam
446	28	68.3	152	2	Q4Z5S1_PLABE	Q4z5s1 plasmodium
447	28	68.3	152	2	Q4FP71_9RICK	Q4fp71 candidatus
448	28	68.3	154	2	Q5BWI4_SCHJA	Q5bwi4 schistosoma
449	28	68.3	154	2	Q7PA84_RICSI	Q7pa84 rickettsia
450	28	68.3	154	2	Q4UJR3_RICFE	Q4ujr3 rickettsia
451	28	68.3	154	2	Q92FY1_RICCN	Q92fy1 rickettsia
452	28	68.3	159	1	VATL_DROME	P23380 drosophila
453	28	68.3	159	2	Q53XD4_DROME	Q53xd4 drosophila
454	28	68.3	159	2	Q6XI23_DROYA	Q6xi23 drosophila
455	28	68.3	160	2	Q88PS1_PSEPK	Q88ps1 pseudomonas
456	28	68.3	164	2	Q734B6_BACC1	Q734b6 bacillus ce
457	28	68.3	170	2	Q8TPH0_METAC	Q8tph0 methanosarc
458	28	68.3	170	2	Q58TW5_9HETE	Q58tw5 cryptococcu
459	28	68.3	170	2	Q58TW6_9HETE	Q58tw6 cryptococcu
460	28	68.3	170	2	Q58TW7_9HETE	Q58tw7 cryptococcu
461	28	68.3	170	2	Q58TW9_9HETE	Q58tw9 cryptococcu
462	28	68.3	170	2	Q58TX0_9HETE	Q58tx0 cryptococcu
463	28	68.3	171	2	Q7UJ01_RHOBA	Q7uj01 rhodopirell
464	28	68.3	175	2	Q8RBI9_THETN	Q8rbi9 thermoanaer
465	28	68.3	183	2	Q4Y963_PLACH	Q4y963 plasmodium
466	28	68.3	184	1	TPPC5_PLAF7	Q7kqm2 plasmodium
467	28	68.3	184	1	TPPC5_PLAFA	P15847 plasmodium
468	28	68.3	184	2	Q549B9_PLAFA	Q549b9 plasmodium
469	28	68.3	185	2	Q81RF9_BACAN	Q81rf9 bacillus an
470	28	68.3	189	2	Q6UUE8_ORYSA	Q6uue8 oryza sativ
471	28	68.3	189	2	Q7XZK8_SORBI	Q7xzk8 sorghum bic
472	28	68.3	199	2	Q8EEQ1_SHEON	Q8eeq1 shewanella
473	28	68.3	204	2	Q4U8T1_THEAN	Q4u8t1 theileria a
474	28	68.3	208	2	Q72AK8_DESVH	Q72ak8 desulfovibr
475	28	68.3	213	2	Q8EI66_SHEON	Q8ei66 shewanella
476	28	68.3	215	2	Q7G0S2_HORVU	Q7g0s2 hordeum vul
477	28	68.3	217	2	O51210_BORBU	O51210 borrelia bu
478	28	68.3	218	2	Q6J2B5_PSEYM	Q6j2b5 pseudomonas
479	28	68.3	218	2	Q9ABU5_CAUCR	Q9abu5 caulobacter
480	28	68.3	219	2	Q6TEQ9_9HETE	Q6teq9 cryptococcu
481	28	68.3	223	2	Q83EK8_COXBU	Q83ek8 coxiella bu
482	28	68.3	228	2	Q6J2H7_PSEYM	Q6j2h7 pseudomonas
483	28	68.3	228	2	Q6VE85_PSESY	Q6ve85 pseudomonas
484	28	68.3	229	2	Q5C0K2_SCHJA	Q5c0k2 schistosoma
485	28	68.3	240	2	Q9LXP8_ARATH	Q9lxp8 arabidopsis
486	28	68.3	241	2	Q586A2_9TRYP	Q586a2 trypanosoma
487	28	68.3	245	2	Q4XQ35_PLACH	Q4xq35 plasmodium
488	28	68.3	246	2	Q8VZ18_ARATH	Q8vz18 arabidopsis
489	28	68.3	246	2	Q94AI8_ARATH	Q94ai8 arabidopsis
490	28	68.3	251	2	Q7U6C1_SYNPX	Q7u6c1 synechococc
491	28	68.3	252	2	Q841J3_COXBU	Q841j3 coxiella bu
492	28	68.3	252	2	Q841J4_COXBU	Q841j4 coxiella bu
493	28	68.3	252	2	Q8KQK0_COXBU	Q8kqk0 coxiella bu
494	28	68.3	252	2	Q8DAX1_VIBVU	Q8dax1 vibrio vuln
495	28	68.3	252	2	Q87R38_VIBPA	Q87r38 vibrio para
496	28	68.3	252	2	Q7MIY6_VIBVY	Q7miy6 vibrio vuln
497	28	68.3	253	2	Q6XQD7_9CAUD	Q6xqd7 enterobacte
498	28	68.3	257	2	Q4YW81_PLABE	Q4yw81 plasmodium
499	28	68.3	258	1	ATE_BRAJA	Q89k72 bradyrhizob
500	28	68.3	258	1	ATE_RHOPA	Q6n6a7 rhodopseudo
501	28	68.3	263	2	Q8PX62_METMA	Q8px62 methanosarc
502	28	68.3	264	2	Q8ETF1_OCEIH	Q8etf1 oceanobacil
503	28	68.3	265	2	Q66212_PBCV1	Q66212 paramecium
504	28	68.3	267	2	Q5ADM8_CANAL	Q5adm8 candida alb
505	28	68.3	268	2	Q8TUK4_METAC	Q8tuk4 methanosarc
506	28	68.3	269	1	UPPP_GEOSL	P60938 geobacter s
507	28	68.3	270	2	O49023_GRACH	O49023 gracilaria
508	28	68.3	270	2	Q4NDY3_9MICC	Q4ndy3 arthrobacte
509	28	68.3	270	2	O25382_HELPY	O25382 helicobacte
510	28	68.3	270	2	Q9ZLG6_HELPJ	Q9zlg6 helicobacte
511	28	68.3	270	2	Q4T447_TETNG	Q4t447 tetraodon n
512	28	68.3	273	2	Q8VUP0_STRSU	Q8vup0 streptococc
513	28	68.3	274	2	Q9HLY6_THEAC	Q9hly6 thermoplasm
514	28	68.3	277	2	Q7Z5U4_HUMAN	Q7z5u4 homo sapien
515	28	68.3	277	2	Q84N24_VITVI	Q84n24 vitis vinif
516	28	68.3	284	2	Q7NCT5_GLOVI	Q7nct5 gloeobacter
517	28	68.3	285	2	Q5K120_9ROSI	Q5k120 populus tre
518	28	68.3	288	2	Q9ATM6_MAIZE	Q9atm6 zea mays (m
519	28	68.3	291	2	Q5C122_SCHJA	Q5c122 schistosoma
520	28	68.3	291	2	Q69IX3_ORYSA	Q69ix3 oryza sativ
521	28	68.3	292	2	Q51Y08_MAGGR	Q51y08 magnaporthe
522	28	68.3	294	2	Q5CLI7_CRYHO	Q5cli7 cryptospori
523	28	68.3	294	2	Q89QD8_BRAJA	Q89qd8 bradyrhizob
524	28	68.3	295	2	Q6CVY4_KLULA	Q6cvy4 kluyveromyc
525	28	68.3	297	2	Q7SG71_NEUCR	Q7sg71 neurospora
526	28	68.3	303	2	Q5TWH4_ANOGA	Q5twh4 anopheles g
527	28	68.3	303	2	Q4HD00_9DEIO	Q4hd00 deinococcus
528	28	68.3	304	2	Q6D898_ERWCT	Q6d898 erwinia car
529	28	68.3	305	2	Q9PVP2_ORYLA	Q9pvp2 oryzias lat
530	28	68.3	306	1	DIMH_DROME	Q9vaq5 drosophila
531	28	68.3	309	2	Q7N2I6_PHOLL	Q7n2i6 photorhabdu
532	28	68.3	311	2	Q6D4X9_ERWCT	Q6d4x9 erwinia car
533	28	68.3	313	2	Q6DCM4_XENLA	Q6dcm4 xenopus lae
534	28	68.3	314	2	Q6XYD9_HUMAN	Q6xyd9 homo sapien
535	28	68.3	315	2	Q4YSR6_PLABE	Q4ysr6 plasmodium
536	28	68.3	316	2	Q6D0M9_ERWCT	Q6d0m9 erwinia car
537	28	68.3	317	2	Q6G981_STAAS	Q6g981 staphylococ
538	28	68.3	317	2	Q6GGS9_STAAR	Q6ggs9 staphylococ
539	28	68.3	317	2	Q5HFU0_STAAC	Q5hfu0 staphylococ
540	28	68.3	317	2	Q7A0U8_STAAW	Q7a0u8 staphylococ
541	28	68.3	317	2	Q7A5I4_STAAN	Q7a5i4 staphylococ
542	28	68.3	317	2	Q99U07_STAAM	Q99u07 staphylococ

543	28	68.3	319	2	Q6CNZ8_KLULA	Q6cnz8	kluyveromyc	616	28	68.3	434	2	Q64MZ1_BACFR	Q64mz1	bacteroides		
544	28	68.3	319	2	Q8WST3_CIOIN	Q8wst3	ciona intes	617	28	68.3	438	2	Q5J882_PICPA	Q5j882	pichia past		
545	28	68.3	321	2	Q9JVN0_NEIMA	Q9jvn0	neisseria m	618	28	68.3	442	2	Q4Z607_PLABE	Q4z607	plasmodium		
546	28	68.3	323	2	Q67SR4_SYMTH	Q67sr4	symbiobacte	619	28	68.3	444	2	Q8VWR5_ARATH	Q8vwr5	arabidopsis		
547	28	68.3	327	2	Q7MQ61_VIBVY	Q7mq61	vibrio vuln	620	28	68.3	444	2	Q9XGM8_ARATH	Q9xgm8	arabidopsis		
548	28	68.3	328	2	Q9LSD3_ARATH	Q9lsd3	arabidopsis	621	28	68.3	445	2	Q6FX91_CANGA	Q6fx91	candida gla		
549	28	68.3	328	2	Q82W06_NITEU	Q82w06	nitrosomona	622	28	68.3	446	2	Q8VXD3_TOBAC	Q8vxd3	nicotiana t		
550	28	68.3	328	2	Q832A6_ENTFA	Q832a6	enterococcu	623	28	68.3	446	2	Q8VXD4_TOBAC	Q8vxd4	nicotiana t		
551	28	68.3	332	2	Q6N838_RHOPA	Q6n838	rhodopseudo	624	28	68.3	446	2	Q9ST97_TOBAC	Q9st97	nicotiana t		
552	28	68.3	337	2	Q4Y634_PLACH	Q4y634	plasmodium	625	28	68.3	446	2	Q9A887_CAUCR	Q9a887	caulobacter		
553	28	68.3	343	2	P96007_SULSO	P96007	sulfolobus	626	28	68.3	447	2	Q7P1G0_CHRVO	Q7p1g0	chromobacte		
554	28	68.3	343	2	Q884I7_PSESM	Q884i7	pseudomonas	627	28	68.3	454	2	Q9SVG1_ARATH	Q9svg1	arabidopsis		
555	28	68.3	345	2	Q9CST5_MOUSE	Q9cst5	mus musculu	628	28	68.3	454	2	Q9D7X0_MOUSE	Q9d7x0	mus musculu		
556	28	68.3	354	1	DCUP_ECO57	Q8x6x5	escherichia	629	28	68.3	455	2	Q9CNF7_PASMU	Q9cnf7	pasteurella		
557	28	68.3	354	1	DCUP_ECOL6	Q8fb74	escherichia	630	28	68.3	455	2	Q8YMU4_ANASP	Q8ymu4	anabaena sp		
558	28	68.3	354	1	DCUP_ECOLI	P29680	escherichia	631	28	68.3	457	2	Q9SZM4_ARATH	Q9szm4	arabidopsis		
559	28	68.3	354	1	DCUP_SALTI	Q8z329	salmonella	632	28	68.3	458	1	COBB_ARCFU	O28054	archaeoglob		
560	28	68.3	354	1	DCUP_SALTY	Q9l9i4	salmonella	633	28	68.3	459	2	Q60DJ6_ORYSA	Q60dj6	oryza sativ		
561	28	68.3	354	1	DCUP_SHIFL	Q83pb7	shigella fl	634	28	68.3	463	2	Q99P69_MOUSE	Q99p69	mus musculu		
562	28	68.3	354	2	Q59UH5_CANAL	Q59uh5	candida alb	635	28	68.3	463	2	Q8VE05_MOUSE	Q8ve05	mus musculu		
563	28	68.3	354	2	Q57H58_SALCH	Q57h58	salmonella	636	28	68.3	466	2	Q93T90_AZOBR	Q93t90	azospirillu		
564	28	68.3	354	2	Q5PKA3_SALPA	Q5pka3	salmonella	637	28	68.3	469	2	Q9I2K9_PSEAE	Q9i2k9	pseudomonas		
565	28	68.3	355	2	Q4UCG1_THEAN	Q4ucg1	theileria a	638	28	68.3	472	2	Q7XCR5_ORYSA	Q7xcr5	oryza sativ		
566	28	68.3	355	2	Q684P6_9SOLA	Q684p6	nicotiana s	639	28	68.3	472	2	Q94HX4_ORYSA	Q94hx4	oryza sativ		
567	28	68.3	361	2	O72464_9REOV	O72464	nelson bay	640	28	68.3	474	2	Q9G8P5_NAEGR	Q9g8p5	naegleria g		
568	28	68.3	361	2	Q69C22_9REOV	Q69c22	pulau reovi	641	28	68.3	476	2	Q8N9V3_HUMAN	Q8n9v3	homo sapien		
569	28	68.3	362	1	COTH_BACSU	Q45535	bacillus su	642	28	68.3	476	2	Q63LA5_BURPS	Q63la5	burkholderi		
570	28	68.3	362	1	VU8_HHV7J	P52523	human herpe	643	28	68.3	488	1	PTMCB_MYCPN	P75146	m pts syste		
571	28	68.3	362	2	Q77Y90_9BETA	Q77y90	human herpe	644	28	68.3	488	2	Q8CDM5_MOUSE	Q8cdm5	mus musculu		
572	28	68.3	364	2	Q4ML82_BACCE	Q4ml82	bacillus ce	645	28	68.3	489	2	Q65PG3_BACLD	Q65pg3	bacillus li		
573	28	68.3	371	2	Q8A3V9_BACTN	Q8a3v9	bacteroides	646	28	68.3	492	2	Q7N0K9_PHOLL	Q7n0k9	photorhabdu		
574	28	68.3	371	2	Q6G6P7_STAAS	Q6g6p7	staphylococ	647	28	68.3	496	2	Q91TW0_TUHV1	Q91tw0	tupaiid her		
575	28	68.3	371	2	Q6GE09_STAAR	Q6ge09	staphylococ	648	28	68.3	502	2	Q4U950_THEAN	Q4u950	theileria a		
576	28	68.3	371	2	Q5HDD0_STAAC	Q5hdd0	staphylococ	649	28	68.3	509	2	Q4Q9U9_LEIMA	Q4q9u9	leishmania		
577	28	68.3	371	2	Q7A3S0_STAAN	Q7a3s0	staphylococ	650	28	68.3	512	2	Q8SV22_ENCCU	Q8sv22	encephalito		
578	28	68.3	371	2	Q8NV06_STAAW	Q8nv06	staphylococ	651	28	68.3	513	2	Q5JK35_ORYSA	Q5jk35	oryza sativ		
579	28	68.3	371	2	Q99RK8_STAAM	Q99rk8	staphylococ	652	28	68.3	528	2	Q6CL15_KLULA	Q6cl15	kluyveromyc		
580	28	68.3	373	2	Q6FU83_CANGA	Q6fu83	candida gla	653	28	68.3	529	2	Q5N3Q4_SYNP6	Q5n3q4	synechococc		
581	28	68.3	374	2	Q6MZV9_HUMAN	Q6mzv9	homo sapien	654	28	68.3	532	2	Q5K808_CRYNE	Q5k808	cryptococcu		
582	28	68.3	381	1	Y255_RICPR	Q9zds0	rickettsia	655	28	68.3	532	2	Q5TWC7_ANOGA	Q5twc7	anopheles g		
583	28	68.3	381	2	O45459_CAEEL	O45459	caenorhabdi	656	28	68.3	535	2	Q4T144_TETNG	Q4t144	tetraodon n		
584	28	68.3	384	2	Q8N6N8_HUMAN	Q8n6n8	homo sapien	657	28	68.3	536	2	Q5MWV9_BARHE	Q5mwv9	bartonella		
585	28	68.3	384	2	Q503T0_BRARE	Q503t0	brachydanio	658	28	68.3	541	2	Q6FBX5_ACIAD	Q6fbx5	acinetobact		
586	28	68.3	385	2	Q6PEN0_MOUSE	Q6pen0	mus musculu	659	28	68.3	546	2	O31813_BACSU	O31813	bacillus su		
587	28	68.3	385	2	Q8R109_MOUSE	Q8r109	mus musculu	660	28	68.3	547	2	Q9KFB9_BACHD	Q9kfb9	bacillus ha		
588	28	68.3	387	2	Q81ZZ4_NITEU	Q81zz4	nitrosomona	661	28	68.3	548	2	Q7RC45_PLAYO	Q7rc45	plasmodium		
589	28	68.3	392	2	Q9SX93_ARATH	Q9sx93	arabidopsis	662	28	68.3	553	2	O04518_ARATH	O04518	arabidopsis		
590	28	68.3	393	1	SLAP_BACTI	P35826	bacillus th	663	28	68.3	553	2	Q65NJ2_BACLD	Q65nj2	bacillus li		
591	28	68.3	395	2	Q877P5_XYLFT	Q877p5	xylella fas	664	28	68.3	558	2	Q9HPA9_HALSA	Q9hpa9	halobacteri		
592	28	68.3	396	1	S18L1_HUMAN	O75177	homo sapien	665	28	68.3	559	2	Q4PHM7_USTMA	Q4phm7	ustilago ma		
593	28	68.3	396	2	Q80XL7_MOUSE	Q80xl7	mus musculu	666	28	68.3	561	2	Q8K8R4_STRP3	Q8k8r4	streptococc		
594	28	68.3	397	2	Q8BLU5_MOUSE	Q8blu5	mus musculu	667	28	68.3	562	2	Q4WZW9_ASPFU	Q4wzw9	aspergillus		
595	28	68.3	399	2	Q6NTH3_HUMAN	Q6nth3	homo sapien	668	28	68.3	562	2	Q65XU0_ORYSA	Q65xu0	oryza sativ		
596	28	68.3	401	2	Q88QI9_PSEPK	Q88qi9	pseudomonas	669	28	68.3	574	2	Q8TJ01_METAC	Q8tj01	methanosarc		
597	28	68.3	401	2	Q91XJ0_RAT	Q91xj0	rattus norv	670	28	68.3	575	2	Q879N8_STRP3	Q879n8	streptococc		
598	28	68.3	402	2	Q8BW22_MOUSE	Q8bw22	m mus muscu	671	28	68.3	575	2	Q5XE24_STRP6	Q5xe24	streptococc		
599	28	68.3	402	2	Q8BYQ7_MOUSE	Q8byq7	mus musculu	672	28	68.3	575	2	Q8P2S5_STRP8	Q8p2s5	streptococc		
600	28	68.3	402	2	Q7TQF3_MOUSE	Q7tqf3	mus musculu	673	28	68.3	575	2	Q9A1M9_STRPY	Q9a1m9	streptococc		
601	28	68.3	404	2	Q8AAJ3_BACTN	Q8aaj3	bacteroides	674	28	68.3	576	2	Q7F248_ORYSA	Q7f248	oryza sativ		
602	28	68.3	406	2	O17460_SCHMA	O17460	schistosoma	675	28	68.3	578	1	PSP2_YEAST	P50109	saccharomyc		
603	28	68.3	406	2	Q6Z2T4_ORYSA	Q6z2t4	oryza sativ	676	28	68.3	580	2	Q82PR6_STRAW	Q82pr6	streptomyce		
604	28	68.3	407	2	Q6A014_MOUSE	Q6a014	mus musculu	677	28	68.3	594	2	O94569_SCHPO	O94569	schizosacch		
605	28	68.3	410	2	Q96MJ4_HUMAN	Q96mj4	homo sapien	678	28	68.3	602	2	Q7RMH8_PLAYO	Q7rmh8	plasmodium		
606	28	68.3	410	2	Q54XR1_DICDI	Q54xr1	dictyosteli	679	28	68.3	602	2	Q4XN24_PLACH	Q4xn24	plasmodium		
607	28	68.3	411	2	Q39773_GRACH	Q39773	gracilaria	680	28	68.3	602	2	Q4RVH2_TETNG	Q4rvh2	tetraodon n		
608	28	68.3	416	2	Q5TY62_ANOGA	Q5ty62	anopheles g	681	28	68.3	606	2	Q8R1U9_MOUSE	Q8r1u9	mus musculu		
609	28	68.3	418	1	Y4186_STRCO	Q9k4f4	streptomyce	682	28	68.3	607	2	Q680T1_ARATH	Q680t1	arabidopsis		
610	28	68.3	418	2	Q7Q053_ANOGA	Q7q053	anopheles g	683	28	68.3	622	2	Q54YM8_DICDI	Q54ym8	dictyosteli		
611	28	68.3	421	2	Q8GUA5_NICBE	Q8gua5	nicotiana b	684	28	68.3	624	2	Q5A788_CANAL	Q5a788	candida alb		
612	28	68.3	427	2	Q75TZ8_BACHD	Q75tz8	bacillus ha	685	28	68.3	631	2	Q8I1U1_PLAF7	Q8i1u1	plasmodium		
613	28	68.3	429	2	Q7QB77_ANOGA	Q7qb77	anopheles g	686	28	68.3	639	2	Q50Q70_ENTHI	Q50q70	entamoeba h		
614	28	68.3	431	2	Q7XTY1_ORYSA	Q7xty1	oryza sativ	687	28	68.3	642	2	Q55B86_DICDI	Q55b86	dictyosteli		
615	28	68.3	431	2	Q8VX55_SOLTU	Q8vx55	solanum tub	688	28	68.3	648	2	Q7PNZ5_ANOGA	Q7pnz5	anopheles g		

689	28	68.3	650	2	Q8YWV4_ANASP	Q8ywv4 anabaena sp
690	28	68.3	654	2	Q8R133_MOUSE	Q8r133 mus musculu
691	28	68.3	673	2	Q758C0_ASHGO	Q758c0 ashbya goss
692	28	68.3	675	2	Q8C8L6_MOUSE	Q8c816 mus musculu
693	28	68.3	680	2	Q7UXV5_RHOBA	Q7uxv5 rhodopirell
694	28	68.3	680	2	Q882T4_PSESM	Q882t4 pseudomonas
695	28	68.3	682	2	Q6NTA5_MOUSE	Q6nta5 mus musculu
696	28	68.3	686	2	Q5XIQ5_RAT	Q5xiq5 rattus norv
697	28	68.3	687	2	Q80UZ2_MOUSE	Q80uz2 mus musculu
698	28	68.3	687	2	Q8CDL7_MOUSE	Q8cdl7 mus musculu
699	28	68.3	692	2	Q4WFE5_ASPFU	Q4wfe5 aspergillus
700	28	68.3	698	2	Q5WEY2_BACSK	Q5wey2 bacillus cl
701	28	68.3	702	2	Q76XL1_9CAUD	Q76xl1 enterobacte
702	28	68.3	708	2	Q9VK01_DROME	Q9vk01 drosophila
703	28	68.3	724	2	Q750U2_ASHGO	Q750u2 ashbya goss
704	28	68.3	727	2	Q7UYN5_RHOBA	Q7uyn5 rhodopirell
705	28	68.3	737	2	Q641D6_XENLA	Q641d6 xenopus lae
706	28	68.3	748	2	P70092_XENLA	P70092 xenopus lae
707	28	68.3	766	2	Q6CN37_KLULA	Q6cn37 kluyveromyc
708	28	68.3	778	2	Q9UPR8_HUMAN	Q9upr8 homo sapien
709	28	68.3	784	2	Q7SAJ4_NEUCR	Q7saj4 neurospora
710	28	68.3	785	2	Q9GQ82_DROME	Q9gq82 drosophila
711	28	68.3	789	1	RIR1_EHV4	P50642 equine herp
712	28	68.3	789	2	O39263_9ALPH	O39263 equid herpe
713	28	68.3	799	1	GLGB_MAIZE	Q08047 zea mays (m
714	28	68.3	799	2	O81387_MAIZE	O81387 zea mays (m
715	28	68.3	803	2	Q7XZK7_SORBI	Q7xzk7 sorghum bic
716	28	68.3	816	2	Q75BF4_ASHGO	Q75bf4 ashbya goss
717	28	68.3	821	2	Q8CHT5_MOUSE	Q8cht5 mus musculu
718	28	68.3	825	2	Q6H6P8_ORYSA	Q6h6p8 oryza sativ
719	28	68.3	825	2	Q40663_ORYSA	Q40663 oryza sativ
720	28	68.3	829	2	Q9ZTB6_HORVU	Q9ztb6 hordeum vul
721	28	68.3	835	2	Q8R4Y7_MOUSE	Q8r4y7 mus musculu
722	28	68.3	839	2	Q87HB0_VIBPA	Q87hb0 vibrio para
723	28	68.3	841	2	Q6N5Q8_RHOPA	Q6n5q8 rhodopseudo
724	28	68.3	846	2	Q7Q2U1_ANOGA	Q7q2u1 anopheles g
725	28	68.3	849	1	ZN507_HUMAN	Q8tcn5 homo sapien
726	28	68.3	854	2	Q51ND0_MAGGR	Q51nd0 magnaporthe
727	28	68.3	855	2	Q4Q6M4_LEIMA	Q4q6m4 leishmania
728	28	68.3	861	2	O06944_SYNY3	O06944 synechocyst
729	28	68.3	866	2	Q6MC94_PARUW	Q6mc94 parachlamyd
730	28	68.3	874	2	Q65X17_ORYSA	Q65x17 oryza sativ
731	28	68.3	878	1	CAPP_PHOLL	Q7max5 photorhabdu
732	28	68.3	887	2	Q4YST3_PLABE	Q4yst3 plasmodium
733	28	68.3	905	2	Q4RLG1_TETNG	Q4rlg1 tetraodon n
734	28	68.3	906	2	Q7RQF1_PLAYO	Q7rqf1 plasmodium
735	28	68.3	912	2	Q4YCI1_PLABE	Q4yci1 plasmodium
736	28	68.3	913	2	Q54NL5_DICDI	Q54nl5 dictyosteli
737	28	68.3	918	2	Q54F92_DICDI	Q54f92 dictyosteli
738	28	68.3	919	2	Q7PDV9_PLAYO	Q7pdv9 plasmodium
739	28	68.3	941	2	Q80VK1_MOUSE	Q80vk1 mus musculu
740	28	68.3	953	2	Q5RDQ6_PONPY	Q5rdq6 pongo pygma
741	28	68.3	960	2	Q8CIE4_MOUSE	Q8cie4 mus musculu
742	28	68.3	960	2	Q8BSZ1_MOUSE	Q8bsz1 mus musculu
743	28	68.3	962	2	Q65Z14_RAT	Q65z14 rattus norv
744	28	68.3	984	2	Q6FIV9_CANGA	Q6fiv9 candida gla
745	28	68.3	999	2	Q6MZU0_HUMAN	Q6mzu0 homo sapien
746	28	68.3	1009	2	Q4SAF4_TETNG	Q4saf4 tetraodon n
747	28	68.3	1013	2	Q6ZPY5_MOUSE	Q6zpy5 mus musculu
748	28	68.3	1052	2	Q7QX55_GIALA	Q7qx55 giardia lam
749	28	68.3	1063	1	PDR1_YEAST	P12383 saccharomyc
750	28	68.3	1063	1	RBL1_MOUSE	Q64701 mus musculu
751	28	68.3	1063	2	Q6PAR4_MOUSE	Q6par4 mus musculu
752	28	68.3	1066	2	Q92CI2_LISIN	Q92ci2 listeria in
753	28	68.3	1066	2	Q720K3_LISMF	Q720k3 listeria mo
754	28	68.3	1066	2	Q8Y7P7_LISMO	Q8y7p7 listeria mo
755	28	68.3	1080	2	Q8AVN3_XENLA	Q8avn3 xenopus lae
756	28	68.3	1089	2	Q8IS97_9ACAR	Q8is97 varroa dest
757	28	68.3	1093	2	Q88HE7_PSEPK	Q88he7 pseudomonas
758	28	68.3	1099	2	Q98QT2_MYCPU	Q98qt2 mycoplasma
759	28	68.3	1105	2	Q5A7T2_CANAL	Q5a7t2 candida alb
760	28	68.3	1105	2	Q875J0_CANAL	Q875j0 candida alb
761	28	68.3	1114	2	Q96JH8_HUMAN	Q96jh8 homo sapien
762	28	68.3	1133	2	Q6MKG4_BDEBA	Q6mkg4 bdellovibri
763	28	68.3	1148	2	Q9C6N3_ARATH	Q9c6n3 arabidopsis
764	28	68.3	1163	2	Q87M83_VIBPA	Q87m83 vibrio para
765	28	68.3	1166	2	O96219_PLAF7	O96219 plasmodium
766	28	68.3	1228	2	Q61HA0_CAEBR	Q61ha0 caenorhabdi
767	28	68.3	1252	2	Q8GZ77_ARATH	Q8gz77 arabidopsis
768	28	68.3	1252	2	Q8H6F5_ARATH	Q8h6f5 arabidopsis
769	28	68.3	1252	2	Q9LJX0_ARATH	Q91jx0 arabidopsis
770	28	68.3	1253	2	Q90YM8_BRARE	Q90ym8 brachydanio
771	28	68.3	1328	2	Q7RT99_PLAYO	Q7rt99 plasmodium
772	28	68.3	1343	2	Q5A309_CANAL	Q5a309 candida alb
773	28	68.3	1351	2	Q6Y7R2_9VIRU	Q6y7r2 staphylococ
774	28	68.3	1352	2	Q4ZA08_9CAUD	Q4za08 bacteriopha
775	28	68.3	1401	2	Q5A0G3_CANAL	Q5a0g3 candida alb
776	28	68.3	1408	2	Q55X59_CRYNE	Q55x59 cryptococcu
777	28	68.3	1408	2	Q5KMS3_CRYNE	Q5kms3 cryptococcu
778	28	68.3	1444	2	Q4P7L2_USTMA	Q4p712 ustilago ma
779	28	68.3	1655	2	Q24754_DROVI	Q24754 drosophila
780	28	68.3	1700	2	Q94GR9_ORYSA	Q94gr9 oryza sativ
781	28	68.3	1744	2	O17008_CAEEL	O17008 caenorhabdi
782	28	68.3	1807	2	Q55GM7_DICDI	Q55gm7 dictyosteli
783	28	68.3	1988	2	Q4VZK7_CUCSA	Q4vzk7 cucumis sat
784	28	68.3	1990	2	Q4VZM5_CUCSA	Q4vzm5 cucumis sat
785	28	68.3	2215	2	Q86D77_9ACAR	Q86d77 varroa dest
786	28	68.3	2216	2	Q9LV03_ARATH	Q9lv03 arabidopsis
787	28	68.3	2222	2	Q619R0_CAEBR	Q619r0 caenorhabdi
788	28	68.3	2294	1	YCF2_ARATH	P56786 arabidopsis
789	28	68.3	2358	1	MOK13_SCHPO	Q9y719 schizosacch
790	28	68.3	2719	2	Q6LF68_PLAF7	Q6lf68 plasmodium
791	28	68.3	3036	2	Q6G4Z7_BARHE	Q6g4z7 bartonella
792	28	68.3	3071	2	Q4IJN1_GIBZE	Q4ijn1 gibberella
793	28	68.3	3184	2	Q5CSC7_CRYPV	Q5csc7 cryptospori
794	28	68.3	3582	2	Q7RAR5_PLAYO	Q7rar5 plasmodium
795	28	68.3	4337	2	Q54B24_DICDI	Q54b24 dictyosteli
796	28	68.3	4880	2	Q6FIU8_CANGA	Q6fiu8 candida gla
797	28	68.3	5129	2	Q4S817_TETNG	Q4s817 tetraodon n
798	27	65.9	40	2	Q4Z5S8_PLABE	Q4z5s8 plasmodium
799	27	65.9	41	2	Q4XU24_PLACH	Q4xu24 plasmodium
800	27	65.9	44	2	Q54S24_DICDI	Q54s24 dictyosteli
801	27	65.9	56	2	Q91G77_IRV6	Q91g77 chilo iride
802	27	65.9	58	2	Q4ZC79_9VIRU	Q4zc79 bacteriopha
803	27	65.9	63	2	Q9HQM1_HALSA	Q9hqm1 halobacteri
804	27	65.9	65	2	Q9KU17_VIBCH	Q9ku17 vibrio chol
805	27	65.9	65	2	Q9KV44_VIBCH	Q9kv44 vibrio chol
806	27	65.9	66	2	Q69KQ9_ORYSA	Q69kq9 oryza sativ
807	27	65.9	72	2	Q97JQ2_CLOAB	Q97jq2 clostridium
808	27	65.9	73	2	O05282_ECOLI	O05282 escherichia
809	27	65.9	73	2	Q7DB83_ECO57	Q7db83 escherichia
810	27	65.9	75	2	Q5BY02_SCHJA	Q5by02 schistosoma
811	27	65.9	78	2	Q97AD7_THEVO	Q97ad7 thermoplasm
812	27	65.9	79	2	Q69KR2_ORYSA	Q69kr2 oryza sativ
813	27	65.9	79	2	Q702T8_BURTH	Q702t8 burkholderi
814	27	65.9	79	2	Q702U5_BURPS	Q702u5 burkholderi
815	27	65.9	79	2	Q702V0_BURMA	Q702v0 burkholderi
816	27	65.9	79	2	Q8X2T4_ECO57	Q8x2t4 escherichia
817	27	65.9	80	1	PRGI_SALTY	P41784 salmonella
818	27	65.9	80	2	Q58FE7_SALGL	Q58fe7 salmonella
819	27	65.9	80	2	Q57KQ1_SALCH	Q57kq1 salmonella
820	27	65.9	80	2	Q5PEB4_SALPA	Q5peb4 salmonella
821	27	65.9	80	2	Q8Z4A0_SALTI	Q8z4a0 salmonella
822	27	65.9	81	2	Q6KZ37_PICTO	Q6kz37 picrophilus
823	27	65.9	82	1	Y1576_ARCFU	O28696 archaeoglob
824	27	65.9	83	1	MXIH_SHIFL	P0a223 shigella fl
825	27	65.9	83	1	MXIH_SHISO	P0a224 shigella so
826	27	65.9	83	2	Q6XVY0_SHIFL	Q6xvy0 shigella fl
827	27	65.9	84	2	Q7NVC1_CHRVO	Q7nvc1 chromobacte
828	27	65.9	89	2	Q4XHB5_PLACH	Q4xhb5 plasmodium
829	27	65.9	89	2	Q63K18_BURPS	Q63k18 burkholderi
830	27	65.9	89	2	Q62AZ2_BURMA	Q62az2 burkholderi
831	27	65.9	90	2	Q5WXM3_LEGPL	Q5wxm3 legionella
832	27	65.9	90	2	Q5X3X5_LEGPA	Q5x3x5 legionella
833	27	65.9	91	2	Q80LQ8_NPVAH	Q80lq8 adoxophyes
834	27	65.9	96	2	Q84355_MNPV	Q84355 mastomys na

835	27	65.9	100	1	TGB3_NMV	P15098	narcissus m
836	27	65.9	100	2	Q6XLP0_NMV	Q6xlp0	narcissus m
837	27	65.9	101	2	Q4HGL7_CAMCO	Q4hgl7	campylobact
838	27	65.9	104	2	Q5A1P9_CANAL	Q5a1p9	candida alb
839	27	65.9	104	2	Q5A1V6_CANAL	Q5a1v6	candida alb
840	27	65.9	105	2	Q9BKS8_CAEEL	Q9bks8	caenorhabdi
841	27	65.9	106	2	Q9LB72_HELPY	Q91b72	helicobacte
842	27	65.9	107	1	T2AG_SCHPO	O74948	schizosacch
843	27	65.9	109	2	Q02628_YEAST	Q02628	saccharomyc
844	27	65.9	109	2	Q9LB50_HELPY	Q91b50	helicobacte
845	27	65.9	112	2	Q84FS1_HELPY	Q84fs1	helicobacte
846	27	65.9	116	2	O64580_ARATH	O64580	arabidopsis
847	27	65.9	118	2	Q5R047_IDILO	Q5r047	idiomarina
848	27	65.9	121	2	Q4U963_THEAN	Q4u963	theileria a
849	27	65.9	122	2	Q9L8N2_HAEIN	Q9l8n2	haemophilus
850	27	65.9	123	2	Q8F1N3_LEPIN	Q8f1n3	leptospira
851	27	65.9	124	2	Q4RC79_TETNG	Q4rc79	tetraodon n
852	27	65.9	129	2	Q6ZW40_HUMAN	Q6zw40	homo sapien
853	27	65.9	130	2	Q4N1V4_THEPA	Q4n1v4	theileria p
854	27	65.9	132	2	Q97KY4_CLOAB	Q97ky4	clostridium
855	27	65.9	134	2	Q4VZS2_9DIPT	Q4vzs2	culiseta an
856	27	65.9	135	2	Q55IE7_CRYNE	Q55ie7	cryptococcu
857	27	65.9	135	2	Q5K7Y6_CRYNE	Q5k7y6	cryptococcu
858	27	65.9	135	2	Q4L5J8_STAHJ	Q4l5j8	staphylococ
859	27	65.9	144	2	Q4TDM6_TETNG	Q4tdm6	tetraodon n
860	27	65.9	145	2	Q5E7J0_VIBF1	Q5e7j0	vibrio fisc
861	27	65.9	146	2	Q6IWU7_9CAUD	Q6iwu7	burkholderi
862	27	65.9	148	1	VE6_HPV52	P36814	human papil
863	27	65.9	148	2	Q8NAS0_HUMAN	Q8nas0	homo sapien
864	27	65.9	148	2	Q9HAI4_HUMAN	Q9hai4	homo sapien
865	27	65.9	148	2	Q9R445_HELPY	Q9r445	helicobacte
866	27	65.9	148	2	Q9R843_HELPY	Q9r843	helicobacte
867	27	65.9	148	2	Q9R847_HELPY	Q9r847	helicobacte
868	27	65.9	148	2	Q9R849_HELPY	Q9r849	helicobacte
869	27	65.9	148	2	Q9R850_HELPY	Q9r850	helicobacte
870	27	65.9	148	2	Q9R852_HELPY	Q9r852	helicobacte
871	27	65.9	148	2	Q9R853_HELPY	Q9r853	helicobacte
872	27	65.9	148	2	Q9S3H7_HELPY	Q9s3h7	helicobacte
873	27	65.9	148	2	Q9S3H9_HELPY	Q9s3h9	helicobacte
874	27	65.9	148	2	Q9S3I0_HELPY	Q9s3i0	helicobacte
875	27	65.9	148	2	Q9S3I2_HELPY	Q9s3i2	helicobacte
876	27	65.9	148	2	Q9S3I3_HELPY	Q9s3i3	helicobacte
877	27	65.9	148	2	Q8VL78_HELPY	Q8vl78	helicobacte
878	27	65.9	148	2	Q8VNB8_HELPY	Q8vnb8	helicobacte
879	27	65.9	148	2	Q8VNB9_HELPY	Q8vnb9	helicobacte
880	27	65.9	148	2	Q8VNC9_HELPY	Q8vnc9	helicobacte
881	27	65.9	148	2	Q4TUH6_HPV52	Q4tuh6	human papil
882	27	65.9	148	2	Q4TUH7_HPV52	Q4tuh7	human papil
883	27	65.9	148	2	Q4TUH4_HPV52	Q4tuh4	human papil
884	27	65.9	150	2	Q9AZM7_9CAUD	Q9azm7	bacteriopha
885	27	65.9	150	2	Q9CI98_LACLA	Q9ci98	lactococcus
886	27	65.9	151	2	Q8LTL3_9CAUD	Q8ltl3	lactococcus
887	27	65.9	154	2	Q68VP0_RICTY	Q68vp0	rickettsia
888	27	65.9	154	2	Q82U29_NITEU	Q82u29	nitrosomona
889	27	65.9	155	2	Q8CUV0_OCEIH	Q8cuv0	oceanobacil
890	27	65.9	156	2	Q9LSB6_ARATH	Q9lsb6	arabidopsis
891	27	65.9	157	2	Q94MB4_9CAUD	Q94mb4	lactococcus
892	27	65.9	157	2	Q9AZT2_9CAUD	Q9azt2	bacteriopha
893	27	65.9	157	2	Q9CFR5_LACLA	Q9cfr5	lactococcus
894	27	65.9	159	1	M1050_ARATH	P92539	arabidopsis
895	27	65.9	159	2	Q6MAD7_PARUW	Q6mad7	parachlamyd
896	27	65.9	160	2	O32656_HELPY	O32656	helicobacte
897	27	65.9	160	2	O32658_HELPY	O32658	helicobacte
898	27	65.9	160	2	O32663_HELPY	O32663	helicobacte
899	27	65.9	160	2	O32664_HELPY	O32664	helicobacte
900	27	65.9	160	2	O32666_HELPY	O32666	helicobacte
901	27	65.9	160	2	O32667_HELPY	O32667	helicobacte
902	27	65.9	160	2	O32668_HELPY	O32668	helicobacte
903	27	65.9	160	2	O32669_HELPY	O32669	helicobacte
904	27	65.9	160	2	O32670_HELPY	O32670	helicobacte
905	27	65.9	160	2	O32671_HELPY	O32671	helicobacte
906	27	65.9	160	2	O32672_HELPY	O32672	helicobacte
907	27	65.9	160	2	O32674_HELPY	O32674	helicobacte
908	27	65.9	160	2	O32676_HELPY	O32676	helicobacte
909	27	65.9	160	2	O32678_HELPY	O32678	helicobacte
910	27	65.9	160	2	O32680_HELPY	O32680	helicobacte
911	27	65.9	160	2	O32683_HELPY	O32683	helicobacte
912	27	65.9	160	2	O32685_HELPY	O32685	helicobacte
913	27	65.9	160	2	O32686_HELPY	O32686	helicobacte
914	27	65.9	160	2	O32687_HELPY	O32687	helicobacte
915	27	65.9	161	2	Q6CHJ4_YARLI	Q6chj4	yarrowia li
916	27	65.9	162	1	RECX_ERWCT	Q6d1s9	erwinia car
917	27	65.9	163	2	Q8GX53_ARATH	Q8gx53	arabidopsis
918	27	65.9	164	2	Q5L1F0_GEOKA	Q5l1f0	geobacillus
919	27	65.9	164	2	Q8D682_VIBVU	Q8d682	vibrio vuln
920	27	65.9	165	1	Y872_RICPR	Q9zc94	rickettsia
921	27	65.9	165	2	Q985D5_RHILO	Q985d5	rhizobium l
922	27	65.9	166	2	O23694_ARATH	O23694	arabidopsis
923	27	65.9	167	2	Q67LT0_SYMTH	Q67lt0	symbiobacte
924	27	65.9	169	2	Q9K8I6_BACHD	Q9k8i6	bacillus ha
925	27	65.9	170	2	Q9XJW2_9CAUD	Q9xjw2	streptococc
926	27	65.9	170	2	Q5SJC1_THET8	Q5sjc1	thermus the
927	27	65.9	170	2	Q72JP0_THET2	Q72jp0	thermus the
928	27	65.9	171	2	Q8S3G0_9FABA	Q8s3g0	medicago ed
929	27	65.9	171	2	Q8S3H5_9FABA	Q8s3h5	medicago ed
930	27	65.9	172	2	Q9MCL0_9CAUD	Q9mcl0	streptococc
931	27	65.9	173	2	Q7VP23_HAEDU	Q7vp23	haemophilus
932	27	65.9	173	2	Q7U8G8_SYNPX	Q7u8g8	synechococc
933	27	65.9	174	2	Q5UEJ2_9VIBR	Q5uej2	vibrio cras
934	27	65.9	175	2	Q9XJW4_9CAUD	Q9xjw4	streptococc
935	27	65.9	177	2	Q7MA96_WOLSU	Q7ma96	wolinella s
936	27	65.9	178	2	Q619E7_CAEBR	Q619e7	caenorhabdi
937	27	65.9	178	2	Q4TCS2_TETNG	Q4tcs2	tetraodon n
938	27	65.9	181	2	Q8E9Q6_SHEON	Q8e9q6	shewanella
939	27	65.9	182	1	RECX_YERPS	Q66e69	yersinia ps
940	27	65.9	185	2	Q9XJD9_9CAUD	Q9xjd9	streptococc
941	27	65.9	185	2	Q6Y7I0_ANAPH	Q6y7i0	anaplasma p
942	27	65.9	186	2	Q5X932_LEGPA	Q5x932	legionella
943	27	65.9	187	1	RECX_YERPE	P37867	yersinia pe
944	27	65.9	187	2	Q6M3R3_CORGL	Q6m3r3	corynebacte
945	27	65.9	187	2	Q4JN24_9BACT	Q4jn24	uncultured
946	27	65.9	188	2	Q5V2R3_HALMA	Q5v2r3	haloarcula
947	27	65.9	191	2	Q938Q1_HELPY	Q938q1	helicobacte
948	27	65.9	191	2	Q8NNM3_CORGL	Q8nnm3	corynebacte
949	27	65.9	192	2	O52306_SYNP2	O52306	synechococc
950	27	65.9	193	2	Q8TRY6_METAC	Q8try6	methanosarc
951	27	65.9	197	1	SN309_ASHGO	Q758s6	ashbya goss
952	27	65.9	201	2	P95889_SULSO	P95889	sulfolobus
953	27	65.9	201	2	Q57M58_SALCH	Q57m58	salmonella
954	27	65.9	201	2	Q5PC78_SALPA	Q5pc78	salmonella
955	27	65.9	201	2	Q8Z543_SALTI	Q8z543	salmonella
956	27	65.9	201	2	Q8ZNF4_SALTY	Q8znf4	salmonella
957	27	65.9	202	2	Q6J9M0_9PRIM	Q6j9m0	gorilla gor
958	27	65.9	202	2	Q6J9M1_PANTR	Q6j9m1	pan troglod
959	27	65.9	202	2	Q8EPF9_OCEIH	Q8epf9	oceanobacil
960	27	65.9	203	2	P73083_SYNY3	P73083	synechocyst
961	27	65.9	206	2	Q7QRS2_GIALA	Q7qrs2	giardia lam
962	27	65.9	207	2	Q6YT98_ORYSA	Q6yt98	oryza sativ
963	27	65.9	208	2	Q6LM97_PHOPR	Q6lm97	photobacter
964	27	65.9	209	2	Q8VR94_ECOLI	Q8vr94	escherichia
965	27	65.9	210	2	Q9R2X1_HELPY	Q9r2x1	helicobacte
966	27	65.9	210	2	Q9R355_HELPY	Q9r355	helicobacte
967	27	65.9	210	2	Q9R356_HELPY	Q9r356	helicobacte
968	27	65.9	210	2	Q9S653_HELPY	Q9s653	helicobacte
969	27	65.9	210	2	Q9S654_HELPY	Q9s654	helicobacte
970	27	65.9	210	2	Q9S655_HELPY	Q9s655	helicobacte
971	27	65.9	211	2	Q7Q524_ANOGA	Q7q524	anopheles g
972	27	65.9	212	2	Q8FKV9_ECOL6	Q8fkv9	escherichia
973	27	65.9	214	2	Q96IA3_HUMAN	Q96ia3	homo sapien
974	27	65.9	214	2	Q5M8N1_MOUSE	Q5m8n1	mus musculu
975	27	65.9	215	2	Q65U36_MANSM	Q65u36	mannheimia
976	27	65.9	215	2	Q8YTN3_ANASP	Q8ytn3	anabaena sp
977	27	65.9	217	2	Q9HK66_THEAC	Q9hk66	thermoplasm
978	27	65.9	218	2	Q813T3_BACCR	Q813t3	bacillus ce
979	27	65.9	219	2	Q9DA97_MOUSE	Q9da97	mus musculu
980	27	65.9	220	2	Q8N949_HUMAN	Q8n949	homo sapien

981	27	65.9	220	2	Q5UEJ3_9VIBR	Q5uej3 vibrio giga
982	27	65.9	221	2	Q88K43_PSEPK	Q88k43 pseudomonas
983	27	65.9	223	2	Q8WYI3_HUMAN	Q8wyi3 homo sapien
984	27	65.9	224	1	RNFE_PASMU	Q9cnp5 pasteurella
985	27	65.9	224	2	Q5B664_EMENI	Q5b664 aspergillus
986	27	65.9	224	2	Q55W40_CRYNE	Q55w40 cryptococcu
987	27	65.9	224	2	Q9LTS9_ARATH	Q9lts9 arabidopsis
988	27	65.9	224	2	Q5UEJ4_9VIBR	Q5uej4 vibrio giga
989	27	65.9	225	2	Q4PMI6_IXOSC	Q4pmi6 ixodes scap
990	27	65.9	227	2	Q9YA97_AERPE	Q9ya97 aeropyrum p
991	27	65.9	227	2	Q5UEJ0_9VIBR	Q5uej0 vibrio pome
992	27	65.9	228	1	SAMP_RAT	P23680 rattus norv
993	27	65.9	228	2	Q5UEI7_9VIBR	Q5uei7 vibrio chag
994	27	65.9	228	2	Q6HL29_BACHK	Q6hl29 bacillus th
995	27	65.9	228	2	Q81SU6_BACAN	Q81su6 bacillus an
996	27	65.9	228	2	Q63DK6_BACCZ	Q63dk6 bacillus ce
997	27	65.9	229	2	Q5UEI9_9VIBR	Q5uei9 vibrio tasm
998	27	65.9	229	2	Q5UEJ5_9VIBR	Q5uej5 vibrio giga
999	27	65.9	229	2	Q6AN87_DESPS	Q6an87 desulfotale
1000	27	65.9	230	2	Q8RJL2_VIBCH	Q8rjl2 vibrio chol

ALIGNMENTS

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RESULT 1
Q4NNX7_9DELT
ID   Q4NNX7_9DELT PRELIMINARY;      PRT;   310 AA.
AC   Q4NNX7;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   ABC transporter.
GN   ORFNames=AdehDRAFT_0441;
OS   Anaeromyxobacter dehalogenans 2CP-C.
OC   Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
OC   Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
OX   NCBI_TaxID=290397;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=2CP-C;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome assembly of Anaeromyxobacter
RT   dehalogenans 2CP-C.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=2CP-C;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Anaeromyxobacter
RT   dehalogenans 2CP-C.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
CC   -!- SIMILARITY: Belongs to the ABC transporter family.
DR   EMBL; AAHD01000051; EAL77302.1; -; Genomic_DNA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transp_like.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW   ATP-binding; Inner membrane; Membrane; Nucleotide-binding; Transport.
SQ   SEQUENCE   310 AA;  33514 MW;  66EB6A3959AF0E37 CRC64;

  Query Match             90.2%;  Score 37;  DB 2;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 14;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |||||||
Db         92 QQYSLYR 98


RESULT 2
Q4S5J9_TETNG
ID   Q4S5J9_TETNG PRELIMINARY;      PRT;   452 AA.
AC   Q4S5J9;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 9 SCAF14729, whole genome shotgun sequence.
GN   ORFNames=GSTENG00023706001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01014729; CAG04083.1; -; Genomic_DNA.
SQ   SEQUENCE   452 AA;  48860 MW;  759C6F32A6ED6E92 CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 452;
  Best Local Similarity   87.5%;  Pred. No. 60;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| |||
Db        411 QQYSSYRS 418


RESULT 3
Q8STS4_ENCCU
ID   Q8STS4_ENCCU PRELIMINARY;      PRT;   655 AA.
AC   Q8STS4;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein ECU09_0880.
GN   OrderedLocusNames=ECU09_0880;
OS   Encephalitozoon cuniculi.
OC   Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
OX   NCBI_TaxID=6035;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
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RC   STRAIN=GB-M1;
RX   MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
RA   Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA   Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P.,
RA   Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA   Weissenbach J., Vivares C.P.;
RT   "Genome sequence and gene compaction of the eukaryote parasite
RT   Encephalitozoon cuniculi.";
RL   Nature 414:450-453(2001).
DR   EMBL; AL590451; CAD27061.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   655 AA;  75753 MW;  150AC93F4A9EE6FE CRC64;

  Query Match             85.4%;  Score 35;  DB 2;  Length 655;
  Best Local Similarity   87.5%;  Pred. No. 91;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              | ||||||
Db        127 QTYSLYRS 134


RESULT 4
ATE_RHILO
ID   ATE_RHILO      STANDARD;      PRT;   254 AA.
AC   Q983E4;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Putative arginyl-tRNA--protein transferase (EC 2.3.2.8) (R-
DE   transferase) (Arginyltransferase).
GN   Name=ate; OrderedLocusNames=mll8364;
OS   Rhizobium loti (Mesorhizobium loti).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Phyllobacteriaceae; Mesorhizobium.
OX   NCBI_TaxID=381;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=MAFF303099;
RX   MEDLINE=21082930; PubMed=11214968;
RA   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA   Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA   Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT   Mesorhizobium loti.";
RL   DNA Res. 7:331-338(2000).
CC   -!- FUNCTION: May conjugate Arg from its aminoacyl-tRNA to the N-
CC       termini of proteins containing an N-terminal aspartate or
CC       glutamate (Potential).
CC   -!- CATALYTIC ACTIVITY: L-arginyl-tRNA + protein = tRNA + L-arginyl-
CC       protein.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC   -!- SIMILARITY: Belongs to the R-transferase family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; BA000012; BAB53937.1; -; Genomic_DNA.
DR   HAMAP; MF_00689; -; 1.
DR   InterPro; IPR007472; ATE_C.
DR   InterPro; IPR007471; ATE_N.
DR   Pfam; PF04377; ATE_C; 1.
DR   Pfam; PF04376; ATE_N; 1.
KW   Acyltransferase; Complete proteome; Transferase.
SQ   SEQUENCE   254 AA;  29100 MW;  A94E2AADC905F876 CRC64;

  Query Match             82.9%;  Score 34;  DB 1;  Length 254;
  Best Local Similarity   75.0%;  Pred. No. 51;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              :||||:||
Db        107 EQYSLFRS 114


RESULT 5
Q88NF4_PSEPK
ID   Q88NF4_PSEPK PRELIMINARY;      PRT;   315 AA.
AC   Q88NF4;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Dihydrodipicolinate synthase family protein.
GN   OrderedLocusNames=PP1257;
OS   Pseudomonas putida (strain KT2440).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=160488;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22423060; PubMed=12534463;
RX   DOI=10.1046/j.1462-2920.2002.00366.x;
RA   Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA   Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA   Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA   Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA   Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA   Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA   Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA   Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA   Fraser C.M.;
RT   "Complete genome sequence and comparative analysis of the
RT   metabolically versatile Pseudomonas putida KT2440.";
RL   Environ. Microbiol. 4:799-808(2002).
DR   EMBL; AE016778; AAN66881.1; -; Genomic_DNA.
DR   TIGR; PP1257; -.
DR   InterPro; IPR002220; DHDPS.
DR   Pfam; PF00701; DHDPS; 1.
DR   PRINTS; PR00146; DHPICSNTHASE.
DR   ProDom; PD001859; DHDPS; 1.
KW   Complete proteome.
SQ   SEQUENCE   315 AA;  34074 MW;  93E1E004D84C2AC5 CRC64;

  Query Match             82.9%;  Score 34;  DB 2;  Length 315;
  Best Local Similarity   75.0%;  Pred. No. 65;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||:|:||
Db        296 QQYALFRS 303


RESULT 6
ALG11_YEAST
ID   ALG11_YEAST    STANDARD;      PRT;   548 AA.
AC   P53954;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Glycosyltransferase ALG11 (EC 2.4.1.-).
GN   Name=ALG11; OrderedLocusNames=YNL048W; ORFNames=N2510, YNL2510W;
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Dean N., Yan Q., Chi J.H.;
RT   "The S. cerevisiae ALG11 gene encodes a protein required for
RT   asparagine-linked glycosylation.";
RL   Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
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RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=S288c / FY1676;
RX   MEDLINE=96021608; PubMed=8533472;
RA   Bergez P., Doignon F., Crouzet M.;
RT   "The sequence of a 44 420 bp fragment located on the left arm of
RT   chromosome XIV from Saccharomyces cerevisiae.";
RL   Yeast 11:967-974(1995).
RN   [3]
RP   ERRATUM.
RX   MEDLINE=97060022; PubMed=8904343;
RX   DOI=10.1002/(SICI)1097-0061(19960315)12:3<297::AID-YEA940>3.0.CO;2-D;
RA   Bergez P., Doignon F., Crouzet M.;
RL   Yeast 12:297-297(1996).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=S288c / FY1679;
RX   MEDLINE=96310629; PubMed=8740423;
RX   DOI=10.1002/(SICI)1097-0061(199604)12:5<493::AID-YEA929>3.3.CO;2-N;
RA   Nasr F., Becam A.-M., Herbert C.J.;
RT   "The sequence of 12.8 kb from the left arm of chromosome XIV reveals a
RT   sigma element, a pro-tRNA and six complete open reading frames, one of
RT   which encodes a protein similar to the human leukotriene A4
RT   hydrolase.";
RL   Yeast 12:493-499(1996).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=S288c / FY1679;
RX   MEDLINE=97313269; PubMed=9169873;
RA   Philippsen P., Kleine K., Poehlmann R., Duesterhoeft A., Hamberg K.,
RA   Hegemann J.H., Obermaier B., Urrestarazu L.A., Aert R., Albermann K.,
RA   Altmann R., Andre B., Baladron V., Ballesta J.P.G., Becam A.-M.,
RA   Beinhauer J.D., Boskovic J., Buitrago M.J., Bussereau F., Coster F.,
RA   Crouzet M., D'Angelo M., Dal Pero F., De Antoni A., del Rey F.,
RA   Doignon F., Domdey H., Dubois E., Fiedler T.A., Fleig U., Floeth M.,
RA   Fritz C., Gaillardin C., Garcia-Cantalejo J.M., Glansdorff N.,
RA   Goffeau A., Gueldener U., Herbert C.J., Heumann K., Heuss-Neitzel D.,
RA   Hilbert H., Hinni K., Iraqui Houssaini I., Jacquet M., Jimenez A.,
RA   Jonniaux J.-L., Karpfinger-Hartl L., Lanfranchi G., Lepingle A.,
RA   Levesque H., Lyck R., Maftahi M., Mallet L., Maurer C.T.C.,
RA   Messenguy F., Mewes H.-W., Moestl D., Nasr F., Nicaud J.-M.,
RA   Niedenthal R.K., Pandolfo D., Pierard A., Piravandi E., Planta R.J.,
RA   Pohl T.M., Purnelle B., Rebischung C., Remacha M.A., Revuelta J.L.,
RA   Rinke M., Saiz J.E., Sartorello F., Scherens B., Sen-Gupta M.,
RA   Soler-Mira A., Urbanus J.H.M., Valle G., Van Dyck L., Verhasselt P.,
RA   Vierendeels F., Vissers S., Voet M., Volckaert G., Wach A.,
RA   Wambutt R., Wedler H., Zollner A., Hani J.;
RT   "The nucleotide sequence of Saccharomyces cerevisiae chromosome XIV
RT   and its evolutionary implications.";
RL   Nature 387:93-98(1997).
RN   [6]
RP   INTERACTION WITH ALG1.
RX   PubMed=15044395; DOI=10.1093/glycob/cwh072;
RA   Gao X.-D., Nishikawa A., Dean N.;
RT   "Physical interactions between the Alg1, Alg2, and Alg11
RT   mannosyltransferases of the endoplasmic reticulum.";
RL   Glycobiology 14:559-570(2004).
CC   -!- FUNCTION: Required for N-linked oligosaccharide assembly.
CC   -!- SUBUNIT: Interacts with ALG1.
CC   -!- SIMILARITY: Belongs to the glycosyltransferase 1 family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; U62941; AAB49937.1; -; Genomic_DNA.
DR   EMBL; U12141; AAA99664.1; -; Genomic_DNA.
DR   EMBL; X94547; CAA64234.1; -; Genomic_DNA.
DR   EMBL; Z71324; CAA95916.1; -; Genomic_DNA.
DR   PIR; S61096; S61096.
DR   GermOnline; 143055; -.
DR   Ensembl; YNL048W; Saccharomyces cerevisiae.
DR   SGD; S000004993; ALG11.
DR   GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR   GO; GO:0000026; F:alpha-1,2-mannosyltransferase activity; IGI.
DR   GO; GO:0006486; P:protein amino acid glycosylation; IGI.
DR   InterPro; IPR001296; Glyco_trans_1.
DR   Pfam; PF00534; Glycos_transf_1; 1.
KW   Complete proteome; Glycoprotein; Glycosyltransferase; Transferase;
KW   Transmembrane.
FT   TRANSMEM     21     41       Potential.
FT   COMPBIAS     84     87       Poly-Gly.
FT   COMPBIAS    543    546       Poly-Glu.
FT   CARBOHYD    262    262       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    393    393       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    480    480       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    490    490       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   548 AA;  63143 MW;  2A3AD59924C762CC CRC64;

  Query Match             82.9%;  Score 34;  DB 1;  Length 548;
  Best Local Similarity   85.7%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |||||:
Db        514 QQYSLYK 520


RESULT 7
Q4YP95_PLABE
ID   Q4YP95_PLABE PRELIMINARY;      PRT;   132 AA.
AC   Q4YP95;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   BIR protein (Fragment).
GN   ORFNames=PB000762.03.0;
OS   Plasmodium berghei.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5821;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA   Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA   James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA   Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA   Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C.,
RA   Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT   "A comprehensive survey of the Plasmodium life cycle by genomic,
RT   transcriptomic, and proteomic analyses.";
RL   Science 307:82-86(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAI01003191; CAI00164.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   132 AA;  15826 MW;  A545F8B38856D6B8 CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 132;
  Best Local Similarity   75.0%;  Pred. No. 40;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||| ||:|
Db        122 QQYPLYKS 129


RESULT 8
Q91ER5_GVCP
ID   Q91ER5_GVCP PRELIMINARY;      PRT;   347 AA.
AC   Q91ER5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
```

```
DE   ORF140 similar to XcGV ORF178.
GN   Name=orf140;
OS   Cydia pomonella granulosis virus (CpGV) (Cydia pomonella
OS   granulovirus).
OC   Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX   NCBI_TaxID=28289;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Mexican 1;
RX   MEDLINE=96207404; PubMed=8615018; DOI=10.1006/viro.1996.0175;
RA   Theilmann D.A., Chantler J.K., Stewart S., Flipsen H.T.M., Vlak J.M.,
RA   Crook N.E.;
RT   "Characterization of a highly conserved baculovirus structural protein
RT   that is specific for occlusion-derived virions.";
RL   Virology 218:148-158(1996).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Mexican 1;
RX   MEDLINE=97380577; PubMed=9237352; DOI=10.1023/A:1007917317770;
RA   Kang W., Crook N.E., Winstanley D., O'Reilly D.R.;
RT   "Complete sequence and transposon mutagenesis of the BamHI J fragment
RT   of Cydia pomonella granulosis virus.";
RL   Virus Genes 14:131-136(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Mexican 1;
RX   MEDLINE=93188168; PubMed=8445726;
RA   Crook N.E., Clem R.J., Miller L.K.;
RT   "An apoptosis-inhibiting baculovirus gene with a zinc finger-like
RT   motif.";
RL   J. Virol. 67:2168-2174(1993).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Mexican 1;
RX   MEDLINE=98418511; PubMed=9747739;
RA   Kang W., Tristem M., Maeda S., Crook N.E., O'Reilly D.R.;
RT   "Identification and characterization of the Cydia pomonella
RT   granulovirus cathepsin and chitinase genes.";
RL   J. Gen. Virol. 79:2283-2292(1998).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Mexican 1;
RX   MEDLINE=21446686; PubMed=11562546;
RA   Luque T., Finch R., Crook N., O'Reilly D.R., Winstanley D.;
RT   "The complete sequence of the Cydia pomonella granulovirus genome.";
RL   J. Gen. Virol. 82:2531-2547(2001).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Mexican 1;
RA   Kang W.;
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Mexican 1;
RA   Luque T., Finch R., Crook N., O'Reilly D.R., Winstanley D.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U53466; AAK70800.1; -; Genomic_DNA.
DR   GO; GO:0008083; F:growth factor activity; IEA.
DR   InterPro; IPR002348; IL1_HBGF.
DR   ProDom; PD000831; IL1_HBGF; 1.
SQ   SEQUENCE   347 AA;  39392 MW;  0AE2D670EA18A10A CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 347;
  Best Local Similarity   85.7%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              ||||||:
Db        163 QYSLYRN 169


RESULT 9
Q802V1_BRARE
ID   Q802V1_BRARE PRELIMINARY;      PRT;   368 AA.
AC   Q802V1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Synovial sarcoma translocation, chromosome 18.
GN   Name=ss18;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AB; TISSUE=Whole body;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AB; TISSUE=Whole body;
RG   NIH MGC Project;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC047188; AAH47188.1; -; mRNA.
DR   Ensembl; ENSDARG00000002970; Danio rerio.
DR   ZFIN; ZDB-GENE-030131-4867; ss18.
DR   InterPro; IPR007726; SSXT.
DR   Pfam; PF05030; SSXT; 1.
SQ   SEQUENCE   368 AA;  40170 MW;  897464610D5225C7 CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 368;
  Best Local Similarity   75.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| ||:
Db        335 QQYSAYRA 342


RESULT 10
Q96CH7_HUMAN
ID   Q96CH7_HUMAN PRELIMINARY;      PRT;   390 AA.
AC   Q96CH7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   PARP10 protein (Fragment).
GN   Name=PARP10;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
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RC   TISSUE=Skin;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Skin;
RA   Director MGC Project;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC014229; AAH14229.2; -; mRNA.
DR   InterPro; IPR001290; PARP.
DR   InterPro; IPR003903; UIM.
DR   Pfam; PF00644; PARP; 1.
DR   Pfam; PF02809; UIM; 2.
FT   NON_TER       1       1
SQ   SEQUENCE   390 AA;  42915 MW;  E0C264F76B702F88 CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 390;
  Best Local Similarity   85.7%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              ||| |||
Db        228 QQYELYR 234


RESULT 11
Q4IDE6_GIBZE
ID   Q4IDE6_GIBZE PRELIMINARY;      PRT;   405 AA.
AC   Q4IDE6;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=FG04762.1;
OS   Gibberella zeae PH-1.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX   NCBI_TaxID=229533;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PH-1;
RA   Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA   Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA   Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA   Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA   Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA   Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA   Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA   Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA   Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA   Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA   Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA   Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA   Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA   Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA   Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA   Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA   Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA   Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA   Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA   Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA   Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA   Lander E.;
RT   "Fusarium graminearum genome sequence.";
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AACM01000196; EAA75721.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   405 AA;  46007 MW;  B2B84ABCDE626ED1 CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 405;
  Best Local Similarity   75.0%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||: |||
Db         53 QQYTTYRS 60


RESULT 12
Q8N2I0_HUMAN
ID   Q8N2I0_HUMAN PRELIMINARY;      PRT;   640 AA.
AC   Q8N2I0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein FLJ90769.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thyroid gland;
RA   Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA   Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA   Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA   Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK075250; BAC11498.1; -; mRNA.
DR   Ensembl; ENSG00000178685; Homo sapiens.
DR   InterPro; IPR001290; PARP.
DR   InterPro; IPR003903; UIM.
DR   Pfam; PF00644; PARP; 1.
DR   Pfam; PF02809; UIM; 2.
DR   SMART; SM00726; UIM; 3.
SQ   SEQUENCE   640 AA;  69000 MW;  FF2EB05ED11D217E CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 640;
  Best Local Similarity   85.7%;  Pred. No. 2.5e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              ||| |||
Db        459 QQYELYR 465


RESULT 13
Q7RL96_PLAYO
ID   Q7RL96_PLAYO PRELIMINARY;      PRT;   659 AA.
AC   Q7RL96;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
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DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   Name=PY02650;
OS   Plasmodium yoelii yoelii.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=73239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=17XNL;
RX   MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA   Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA   Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA   Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA   Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA   Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA   Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA   Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA   van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA   Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA   Carucci D.J.;
RT   "Genome sequence and comparative analysis of the model rodent malaria
RT   parasite Plasmodium yoelii yoelii.";
RL   Nature 419:512-519(2002).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABL01000729; EAA22127.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   659 AA;  78636 MW;  4892223D36F2ED66 CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 659;
  Best Local Similarity   75.0%;  Pred. No. 2.5e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||| ||:|
Db        649 QQYPLYKS 656


RESULT 14
Q8WV05_HUMAN
ID   Q8WV05_HUMAN PRELIMINARY;      PRT;   669 AA.
AC   Q8WV05;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   PARP10 protein (Fragment).
GN   Name=PARP10;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Uterus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Uterus;
RA   Director MGC Project;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC019030; AAH19030.2; -; mRNA.
DR   InterPro; IPR001290; PARP.
DR   InterPro; IPR003903; UIM.
DR   Pfam; PF00644; PARP; 1.
DR   Pfam; PF02809; UIM; 2.
FT   NON_TER       1       1
SQ   SEQUENCE   669 AA;  72542 MW;  0BBA544FC23060A0 CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 669;
  Best Local Similarity   85.7%;  Pred. No. 2.6e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              ||| |||
Db        507 QQYELYR 513


RESULT 15
Q53GL7_HUMAN
ID   Q53GL7_HUMAN PRELIMINARY;      PRT;  1025 AA.
AC   Q53GL7;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Poly (ADP-ribose) polymerase family, member 10 variant
DE   (Fragment).
GN   Name=PARP10;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Maruyama K., Sugano S.;
RT   "Oligo-capping : a simple method to replace the cap structure of
RT   eucaryotic mRNAs with oligoribonucleotides.";
RL   Gene 138:171-174(1994).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT   "Construction and characterization of a full length-enriched and a 5'-
RT   end-enriched cDNA library.";
RL   Gene 200:149-156(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Kidney;
RA   Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA   Tanaka A., Yokoyama S.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK222914; BAD96634.1; -; mRNA.
DR   HGNC; HGNC:25895; PARP10.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
DR   GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
FT   NON_TER       1       1
SQ   SEQUENCE   1025 AA;  109939 MW;  AC9CCFCF984CA989 CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 1025;
  Best Local Similarity   85.7%;  Pred. No. 4.2e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 QQYSLYR 7
              ||| |||
Db        863 QQYELYR 869
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RESULT 16
Q96K72_HUMAN
ID   Q96K72_HUMAN PRELIMINARY;      PRT;  1025 AA.
AC   Q96K72;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein FLJ14464.
GN   Name=PARP10;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mammary gland;
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA   Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA   Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA   Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA   Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA   Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA   Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA   Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA   Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA   Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA   Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
DR   EMBL; AK027370; BAB55067.1; -; mRNA.
DR   Ensembl; ENSG00000178685; Homo sapiens.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003950; F:NAD+ ADP-ribosyltransferase activity; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0006471; P:protein amino acid ADP-ribosylation; IEA.
DR   InterPro; IPR012677; a_b_plait_nuc_bd.
DR   InterPro; IPR001290; PARP.
DR   InterPro; IPR012317; PARP_catalytic.
DR   InterPro; IPR003903; UIM.
DR   Pfam; PF00644; PARP; 1.
DR   Pfam; PF02809; UIM; 2.
DR   SMART; SM00726; UIM; 3.
DR   PROSITE; PS51059; PARP_CATALYTIC; 1.
SQ   SEQUENCE   1025 AA;  109884 MW;  87C4DBB8F42DB84C CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 1025;
  Best Local Similarity   85.7%;  Pred. No. 4.2e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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Qy          1 QQYSLYR 7
              ||| |||
Db        863 QQYELYR 869
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RESULT 17
Q70KN5_9NIDO
ID   Q70KN5_9NIDO PRELIMINARY;      PRT;  1576 AA.
AC   Q70KN5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Spike protein.
OS   Porcine torovirus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC   Coronaviridae; Torovirus.
OX   NCBI_TaxID=237020;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Markelo;
RX   MEDLINE=22797164; PubMed=12915570;
RX   DOI=10.1128/JVI.77.17.9567-9577.2003;
RA   Smits S.L., Lavazza A., Matiz K., Horzinek M.C., Koopmans M.P.,
RA   de Groot R.J.;
RT   "Phylogenetic and evolutionary relationships among torovirus field
RT   variants: evidence for multiple intertypic recombination events.";
RL   J. Virol. 77:9567-9577(2003).
DR   EMBL; AJ575372; CAE01338.1; -; Genomic_RNA.
SQ   SEQUENCE   1576 AA;  178056 MW;  A2D878C27015D381 CRC64;

  Query Match             80.5%;  Score 33;  DB 2;  Length 1576;
  Best Local Similarity   75.0%;  Pred. No. 6.9e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;
```

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Qy          1 QQYSLYRS 8
              ||||:| |
Db       1204 QQYSIYMS 1211
```

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RESULT 18
Q8U5G9_AGRT5
ID   Q8U5G9_AGRT5 PRELIMINARY;      PRT;   198 AA.
AC   Q8U5G9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   AGR_C_1733p.
GN   OrderedLocusNames=AGR_C_1733;
OS   Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX   NCBI_TaxID=176299;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Cereon;
RX   MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA   Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA   Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA   Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA   Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA   Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA   Cielo C., Slater S.;
RT   "Genome sequence of the plant pathogen and biotechnology agent
RT   Agrobacterium tumefaciens C58.";
RL   Science 294:2323-2328(2001).
DR   EMBL; AE008025; AAK86756.1; -; Genomic_DNA.
DR   PIR; C97475; C97475.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003661; His_kinA_N.
DR   SMART; SM00388; HisKA; 1.
```

```
SQ   SEQUENCE   198 AA;  21866 MW;  02E09660D9B3CDCC CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 198;
  Best Local Similarity   62.5%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||:|:||:
Db         88 QQFSMYRN 95


RESULT 19
Q7PYZ5_ANOGA
ID   Q7PYZ5_ANOGA PRELIMINARY;      PRT;   201 AA.
AC   Q7PYZ5;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ENSANGP00000018022 (Fragment).
GN   ORFNames=ENSANGG00000015533;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RT   "Anopheles gambiae re-annotation.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Contains 1 RING-type zinc finger.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008986; EAA00484.2; -; Genomic_DNA.
DR   GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0016567; P:protein ubiquitination; IEA.
DR   InterPro; IPR000571; Znf_CCCH.
DR   InterPro; IPR001841; Znf_ring.
DR   Pfam; PF00097; zf-C3HC4; 1.
DR   Pfam; PF00642; zf-CCCH; 1.
DR   SMART; SM00184; RING; 1.
DR   PROSITE; PS00518; ZF_RING_1; 1.
DR   PROSITE; PS50089; ZF_RING_2; 1.
KW   Metal-binding; Zinc; Zinc-finger.
FT   NON_TER       1      1
SQ   SEQUENCE   201 AA;  23406 MW;  9DB7CD07E613F502 CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 201;
  Best Local Similarity   62.5%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              :||::|||
Db        157 RQYAIYRS 164


RESULT 20
Q7V3C7_PROMP
ID   Q7V3C7_PROMP PRELIMINARY;      PRT;   237 AA.
AC   Q7V3C7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=PMM0151;
OS   Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
OC   Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC   Prochlorococcus.
OX   NCBI_TaxID=59919;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA   Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA   Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA   Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA   Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA   Webb E.A., Zinser E.R., Chisholm S.W.;
RT   "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT   niche differentiation.";
RL   Nature 424:1042-1047(2003).
DR   EMBL; BX572090; CAE18610.1; -; Genomic_DNA.
DR   InterPro; IPR003768; ScpA.
DR   Pfam; PF02616; DUF173; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   237 AA;  27367 MW;  A3A25130FB048E7D CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 237;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              ||||||
Db        200 QQYSLY 205


RESULT 21
Q83AP7_COXBU
ID   Q83AP7_COXBU PRELIMINARY;      PRT;   304 AA.
AC   Q83AP7;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Glucose-1-phosphate thymidylyltransferase.
GN   Name=rmlA; OrderedLocusNames=CBU1834;
OS   Coxiella burnetii.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC   Coxiellaceae; Coxiella.
OX   NCBI_TaxID=777;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Nine Mile phase I / RSA 493;
RX   MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
RA   Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
RA   Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J.,
RA   DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
RA   Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
RA   Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
RT   "Complete genome sequence of the Q-fever pathogen, Coxiella
RT   burnetii.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
DR   EMBL; AE016965; AAO91327.1; -; Genomic_DNA.
DR   HSSP; P37744; 1H5R.
DR   TIGR; CBU1834; -.
DR   GO; GO:0008879; F:glucose-1-phosphate thymidylyltransferase a. . .; IEA.
DR   GO; GO:0016301; F:kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0009058; P:biosynthesis; IEA.
DR   GO; GO:0045226; P:extracellular polysaccharide biosynthesis; IEA.
DR   InterPro; IPR005907; G1P_thy_trans_l.
DR   InterPro; IPR005835; NTP_transferase.
DR   Pfam; PF00483; NTP_transferase; 1.
DR   TIGRFAMs; TIGR01207; rmlA; 1.
KW   Complete proteome; Kinase; Nucleotidyltransferase; Transferase.
SQ   SEQUENCE   304 AA;  34288 MW;  60924BD5F5D4BFD0 CRC64;
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  Query Match             78.0%;  Score 32;  DB 2;  Length 304;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYR 7
              ||||||
Db        290 QYSLYR 295


RESULT 22
Q8MSM4_DROME
ID   Q8MSM4_DROME PRELIMINARY;      PRT;   328 AA.
AC   Q8MSM4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   AT21810p.
GN   ORFNames=CG14861;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY118704; AAM50564.1; -; mRNA.
DR   Ensembl; CG14861; Drosophila melanogaster.
DR   FlyBase; FBgn0038280; CG14861.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR002048; EF_hand_Ca_bd.
DR   Pfam; PF00036; efhand; 1.
KW   Repeat.
SQ   SEQUENCE   328 AA;  37176 MW;  AA0FC779F754F5EB CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 328;
  Best Local Similarity   62.5%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |:||:|:|
Db        115 QEYSIYQS 122


RESULT 23
Q6W1N7_RHISN
ID   Q6W1N7_RHISN PRELIMINARY;      PRT;   335 AA.
AC   Q6W1N7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   ABC Transporter ATP-binding protein.
GN   ORFNames=RNGR00559;
OS   Rhizobium sp. (strain NGR234).
OG   Plasmid megaplasmid 2.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX   NCBI_TaxID=394;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NGR234;
RA   Broughton W.J., Perret X., Staehelin C., Schmitz R.A., Raasch C.,
RA   Liesegang H., Gottschalk G., Streit W.R.;
RT   "Comparative DNA analysis of two large contigs of the Rhizobium sp.
RT   NGR234 megaplasmid 2.";
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY316747; AAQ87331.1; -; Genomic_DNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016887; F:ATPase activity; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transp_like.
DR   InterPro; IPR002110; ANK.
DR   Pfam; PF00005; ABC_tran; 1.
DR   PRINTS; PR01415; ANKYRIN.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   ATP-binding; Plasmid.
SQ   SEQUENCE   335 AA;  36900 MW;  652679B3E8D90D2D CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 335;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              ||||||
Db         82 QQYSLY 87


RESULT 24
Q98C49_RHILO
ID   Q98C49_RHILO PRELIMINARY;      PRT;   337 AA.
AC   Q98C49;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ABC transporter ATP-binding protein.
GN   OrderedLocusNames=mll5297;
OS   Rhizobium loti (Mesorhizobium loti).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Phyllobacteriaceae; Mesorhizobium.
OX   NCBI_TaxID=381;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=MAFF303099;
RX   MEDLINE=21082930; PubMed=11214968;
RA   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA   Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA   Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT   Mesorhizobium loti.";
RL   DNA Res. 7:331-338(2000).
DR   EMBL; BA000012; BAB51772.1; -; Genomic_DNA.
DR   HSSP; Q9YGA6; 1G29.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016887; F:ATPase activity; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transp_like.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   ATP-binding; Complete proteome.
SQ   SEQUENCE   337 AA;  36690 MW;  7094FB4B989086F4 CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 337;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              ||||||
Db         82 QQYSLY 87
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RESULT 25
Q89PB1_BRAJA
ID   Q89PB1_BRAJA PRELIMINARY;      PRT;   342 AA.
AC   Q89PB1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ABC transporter ATP-binding protein.
GN   OrderedLocusNames=blr3571;
OS   Bradyrhizobium japonicum.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Bradyrhizobiaceae; Bradyrhizobium.
OX   NCBI_TaxID=375;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=USDA 110;
RX   MEDLINE=22484998; PubMed=12597275;
RA   Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA   Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA   Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA   Tabata S.;
RT   "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT   Bradyrhizobium japonicum USDA110.";
RL   DNA Res. 9:189-197(2002).
CC   -!- FUNCTION: Part of the ABC transporter complex fbpABC involved in
CC       Fe(3+) ions import. Responsible for energy coupling to the
CC       transport system (By similarity).
CC   -!- CATALYTIC ACTIVITY: ATP + H(2)O + Fe(3+)(Out) = ADP + phosphate +
CC       Fe(3+)(In).
CC   -!- SUBUNIT: The complex is composed of two ATP-binding proteins
CC       (fbpC), two transmembrane proteins (fbpB) and a solute-binding
CC       protein (fbpA) (By similarity).
CC   -!- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
CC   -!- SIMILARITY: Belongs to the ABC transporter family.
DR   EMBL; BA000040; BAC48836.1; -; Genomic_DNA.
DR   HSSP; Q9YGA6; 1G29.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016887; F:ATPase activity; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transp_like.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   ATP-binding; Complete proteome; Hydrolase; Inner membrane; Iron;
KW   Iron transport; Membrane; Nucleotide-binding; Transport.
SQ   SEQUENCE   342 AA;  37917 MW;  5F2F6CEBD0088008 CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 342;
  Best Local Similarity   100.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              ||||||
Db         82 QQYSLY 87


RESULT 26
Q7Q6R9_ANOGA
ID   Q7Q6R9_ANOGA PRELIMINARY;      PRT;   348 AA.
AC   Q7Q6R9;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ENSANGP00000004354 (Fragment).
GN   ORFNames=ENSANGG00000003429;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RT   "Anopheles gambiae re-annotation.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008960; EAA10743.2; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   InterPro; IPR008795; Prominin.
DR   Pfam; PF05478; Prominin; 1.
FT   NON_TER     348    348
SQ   SEQUENCE   348 AA;  38693 MW;  DC9C70BF5C5EAE21 CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 348;
  Best Local Similarity   71.4%;  Pred. No. 2e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              :|||:||
Db        152 EQYSIYR 158


RESULT 27
Q63NB3_BURPS
ID   Q63NB3_BURPS PRELIMINARY;      PRT;   348 AA.
AC   Q63NB3;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=BPSS0384;
OS   Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia; pseudomallei group.
OX   NCBI_TaxID=28450;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=K96243;
RX   PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA   Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA   Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA   Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
RA   Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA   Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
RA   Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA   Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA   Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA   Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA   Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT   "Genomic plasticity of the causative agent of melioidosis,
RT   Burkholderia pseudomallei.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR   EMBL; BX571966; CAH37834.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   348 AA;  40069 MW;  ABF74CE93FE300CA CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 348;
  Best Local Similarity   85.7%;  Pred. No. 2e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              || ||||
Db          2 QYGLYRS 8
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RESULT 28
Q58AE7_9BURK
ID   Q58AE7_9BURK PRELIMINARY;      PRT;   355 AA.
AC   Q58AE7;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Putative porin signal peptide protein.
GN   Name=RMe0358;
OS   Ralstonia metallidurans CH34.
OG   Plasmid pMOL30.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Cupriavidus.
OX   NCBI_TaxID=266264;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CH34;
RX   MEDLINE=95260447; PubMed=7766206;
RA   Diels L., Dong Q., van der Lelie D., Baeyens W., Mergeay M.;
RT   "The czc operon of Alcaligenes eutrophus CH34: from resistance
RT   mechanism to the removal of heavy metals.";
RL   J. Ind. Microbiol. 14:142-153(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CH34;
RX   MEDLINE=21429239; PubMed=11544228;
RX   DOI=10.1128/JB.183.19.5651-5658.2001;
RA   Borremans B., Hobman J.L., Provoost A., Brown N.L., van der Lelie D.;
RT   "Cloning and functional analysis of the pbr lead resistance
RT   determinant of Ralstonia metallidurans CH34.";
RL   J. Bacteriol. 183:5651-5658(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CH34;
RA   Monchy S., Van der Lelie D., Vallaeys T., Taghavi S., Benotmane M.,
RA   McCorkle S., Dunn J., Lapidus A., Mergeay M.;
RT   "Sequence and features of the Ralstonia metallidurans CH34 heavy
RT   metals plasmids pMOL28 and pMOL30.";
RL   Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CH34;
RA   Van der Lelie D.;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X71400; CAI11320.1; -; Genomic_DNA.
KW   Plasmid; Porin.
SQ   SEQUENCE   355 AA;  37333 MW;  DE1BCD2695DD834B CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 355;
  Best Local Similarity   85.7%;  Pred. No. 2.1e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              :||||||
Db        138 RYSLYRS 144


RESULT 29
Q92YX7_RHIME
ID   Q92YX7_RHIME PRELIMINARY;      PRT;   358 AA.
AC   Q92YX7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Probable ABC transporter ATP-binding protein.
GN   OrderedLocusNames=RA0735; ORFNames=SMa1345;
OS   Rhizobium meliloti (Sinorhizobium meliloti).
OG   Plasmid pSymA.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX   NCBI_TaxID=382;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=1021;
RX   MEDLINE=21396509; PubMed=11481432; DOI=10.1073/pnas.161294798;
RA   Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
RA   Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
RA   Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
RA   Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
RA   Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
RT   "Nucleotide sequence and predicted functions of the entire
RT   Sinorhizobium meliloti pSymA megaplasmid.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
CC   -!- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
CC   -!- SIMILARITY: Belongs to the ABC transporter family.
DR   EMBL; AE007260; AAK65393.1; -; Genomic_DNA.
DR   PIR; G95353; G95353.
DR   HSSP; Q9YGA6; 1G29.
DR   GO; GO:0019866; C:inner membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016887; F:ATPase activity; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transp_like.
DR   InterPro; IPR005116; TOBE.
DR   Pfam; PF00005; ABC_tran; 1.
DR   Pfam; PF03459; TOBE; 1.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   ATP-binding; Complete proteome; Inner membrane; Membrane;
KW   Nucleotide-binding; Plasmid; Transport.
SQ   SEQUENCE   358 AA;  39531 MW;  46C23A364E9443DC CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 358;
  Best Local Similarity   100.0%;  Pred. No. 2.1e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              ||||||
Db         82 QQYSLY 87


RESULT 30
Q9VFE1_DROME
ID   Q9VFE1_DROME PRELIMINARY;      PRT;   364 AA.
AC   Q9VFE1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CG14861-PA.
GN   Name=CG14861; ORFNames=CG14861;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
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RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RG   Berkeley Drosophila Genome Project;
RA   Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA   Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA   Yu C., Rubin G.;
RT   "Drosophila melanogaster release 4 sequence.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RG   FlyBase;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003707; AAF55119.1; -; Genomic_DNA.
DR   Ensembl; CG14861; Drosophila melanogaster.
DR   FlyBase; FBgn0038280; CG14861.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR002048; EF_hand_Ca_bd.
DR   Pfam; PF00036; efhand; 1.
KW   Repeat.
SQ   SEQUENCE   364 AA;  41222 MW;  098D11FC82B1571B CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 364;
  Best Local Similarity   62.5%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |:||:|:|
Db        151 QEYSIYQS 158


RESULT 31
Q22899_CAEEL
ID   Q22899_CAEEL PRELIMINARY;      PRT;   392 AA.
AC   Q22899;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=C16D9.5;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; U64858; AAB18283.2; -; Genomic_DNA.
DR   PIR; T29554; T29554.
DR   Ensembl; C16D9.5; Caenorhabditis elegans.
DR   InterPro; IPR012444; DUF1647.
DR   Pfam; PF07801; DUF1647; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   392 AA;  44947 MW;  B98DD1ABB35D1680 CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 392;
  Best Local Similarity   75.0%;  Pred. No. 2.3e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              | | ||||
Db        379 QDYKLYRS 386


RESULT 32
Q5WYA9_LEGPL
ID   Q5WYA9_LEGPL PRELIMINARY;      PRT;   415 AA.
AC   Q5WYA9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=lpl0830;
OS   Legionella pneumophila (strain Lens).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC   Legionellaceae; Legionella.
OX   NCBI_TaxID=297245;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15467720; DOI=10.1038/ng1447;
RA   Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA   Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
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RA   Etienne J., Glaser P., Buchrieser C.;
RT   "Evidence in the Legionella pneumophila genome for exploitation of
RT   host cell functions and high genome plasticity.";
RL   Nat. Genet. 36:1165-1173(2004).
DR   EMBL; CR628337; CAH15064.1; -; Genomic_DNA.
DR   LegioList; lpl0830; -.
DR   GO; GO:0019866; C:inner membrane; IEA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR007114; MFS.
DR   InterPro; IPR011701; MFS_1.
DR   Pfam; PF07690; MFS_1; 1.
DR   PROSITE; PS50850; MFS; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   415 AA;  45653 MW;  8EA64600178EAD93 CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 415;
  Best Local Similarity   85.7%;  Pred. No. 2.5e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              :||||||
Db        278 RYSLYRS 284


RESULT 33
Q8ECU0_SHEON
ID   Q8ECU0_SHEON PRELIMINARY;      PRT;   700 AA.
AC   Q8ECU0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Ferric alcaligin siderophore receptor.
GN   OrderedLocusNames=SO3033;
OS   Shewanella oneidensis.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC   Shewanellaceae; Shewanella.
OX   NCBI_TaxID=70863;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=MR-1;
RX   MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA   Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA   Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA   Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA   Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA   Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA   White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA   Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA   Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA   Venter J.C., Nealson K.H., Fraser C.M.;
RT   "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT   Shewanella oneidensis.";
RL   Nat. Biotechnol. 20:1118-1123(2002).
DR   EMBL; AE015739; AAN56045.1; -; Genomic_DNA.
DR   TIGR; SO3033; -.
DR   GO; GO:0019867; C:outer membrane; IEA.
DR   GO; GO:0005506; F:iron ion binding; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0015343; F:siderophore-iron transporter activity; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006826; P:iron ion transport; IEA.
DR   GO; GO:0015891; P:siderophore transport; IEA.
DR   InterPro; IPR000531; TonB_receptor.
DR   InterPro; IPR010917; TonB_recept_C.
DR   InterPro; IPR010105; TonB_sdpr_recept.
DR   Pfam; PF00593; TonB_dep_Rec; 1.
DR   TIGRFAMs; TIGR01783; TonB-siderophor; 1.
DR   PROSITE; PS01156; TONB_DEPENDENT_REC_2; UNKNOWN_1.
KW   Complete proteome.
SQ   SEQUENCE   700 AA;  77995 MW;  AF1BA7B267382B62 CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 700;
  Best Local Similarity   75.0%;  Pred. No. 4.5e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              :|||||  |
Db        473 EQYSLYAS 480


RESULT 34
DYRK2_DROME
ID   DYRK2_DROME    STANDARD;      PRT;   722 AA.
AC   Q9V3D5; Q8T0L9;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Dual-specificity tyrosine-phosphorylation regulated kinase 2
DE   (EC 2.7.1.112) (EC 2.7.1.37) (dDyrk2) (Smell impaired protein at 35A).
GN   Name=smi35A; Synonyms=Dyrk2; ORFNames=CG4551;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE, FUNCTION, COFACTOR, ENZYME REGULATION,
RP   SUBCELLULAR LOCATION, DEVELOPMENTAL STAGE, PHOSPHORYLATION SITES
RP   TYR-356 AND TYR-358, AND MUTAGENESIS OF TYR-356 AND TYR-358.
RC   STRAIN=Oregon-R; TISSUE=Embryo;
RX   PubMed=12786602; DOI=10.1042/BJ20030500;
RA   Lochhead P.A., Sibbet G., Kinstrie R., Cleghon T., Rylatt M.,
RA   Morrison D.K., Cleghon V.;
RT   "dDYRK2: a novel dual-specificity tyrosine-phosphorylation-regulated
RT   kinase in Drosophila.";
RL   Biochem. J. 374:381-391(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Berkeley;
RX   MEDLINE=99403001; PubMed=10471707;
RA   Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R.G., Davis T.,
RA   Doyle C., Galle R.F., George R.A., Harris N.L., Hartzell G.,
RA   Harvey D.A., Hong L., Houston K.A., Hoskins R.A., Johnson G.,
RA   Martin C., Moshrefi A.R., Palazzolo M., Reese M.G., Spradling A.C.,
RA   Tsang G., Wan K.H., Whitelaw K., Celniker S.E., Rubin G.M.;
RT   "An exploration of the sequence of a 2.9-Mb region of the genome of
RT   Drosophila melanogaster: the Adh region.";
RL   Genetics 153:179-219(1999).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
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RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [4]
RP   GENOME REANNOTATION.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Berkeley; TISSUE=Embryo;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D.E., Frise E.,
RA   George R.A., Gonzalez M., Guarin H., Kronmiller B., Li P.W., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J.M., Paragas V., Park S.,
RA   Patel S., Phouanenavong S., Wan K.H., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.E.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 381-722.
RC   STRAIN=Berkeley; TISSUE=Head;
RX   MEDLINE=22426066; PubMed=12537569;
RA   Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA   George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA   Rubin G.M., Celniker S.E.;
RT   "A Drosophila full-length cDNA resource.";
RL   Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC   -!- FUNCTION: In vitro; can phosphorylate exogenous substrates on Ser
CC       and Thr residues. May have a physiological role in development
CC       being involved in cellular growth and differentiation.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + a protein
CC       tyrosine phosphate.
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- COFACTOR: Magnesium.
CC   -!- ENZYME REGULATION: Autophosphorylates on Tyr-356 and Tyr-358.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- DEVELOPMENTAL STAGE: Highly expressed and active during
CC       embryogenesis and pupation and at lower levels in larva and adult.
CC   -!- PTM: Phosphorylated on serine/threonine residues.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. MNB/DYRK
CC       subfamily.
CC   -!- CAUTION: Ref.6 sequence differs from that shown due to a deletion
CC       within an exon that does not correspond to an intron.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF168467; AAD47290.1; -; mRNA.
DR   EMBL; AE003409; AAF44860.1; -; Genomic_DNA.
DR   EMBL; AE003642; AAF53380.1; -; Genomic_DNA.
DR   EMBL; BT010088; AAQ22557.1; -; mRNA.
DR   EMBL; AY069183; AAL39328.1; ALT_SEQ; mRNA.
DR   HSSP; Q03656; 1HOW.
DR   Ensembl; CG4551; Drosophila melanogaster.
DR   FlyBase; FBgn0016930; smi35A.
DR   GO; GO:0005829; C:cytosol; IDA.
DR   GO; GO:0005524; F:ATP binding; IDA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.
DR   GO; GO:0016740; F:transferase activity; IDA.
DR   GO; GO:0042048; P:olfactory behavior; IMP.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
DR   GO; GO:0042221; P:response to chemical substance; IMP.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Magnesium; Nucleotide-binding; Phosphorylation;
KW   Serine/threonine-protein kinase; Transferase; Tyrosine-protein kinase.
FT   DOMAIN      198    494       Protein kinase.
FT   NP_BIND     204    212       ATP (By similarity).
FT   ACT_SITE    324    324       Proton acceptor (By similarity).
FT   BINDING     227    227       ATP (By similarity).
FT   MOD_RES     356    356       Phosphotyrosine (by autocatalysis).
FT   MOD_RES     358    358       Phosphotyrosine (by autocatalysis).
FT   MUTAGEN     356    356       Y->D,F: Blocks tyrosine phosphorylation.
FT   MUTAGEN     358    358       Y->D,F: Blocks tyrosine phosphorylation.
SQ   SEQUENCE   722 AA;  79609 MW;  E431C03DDFE81F4E CRC64;

  Query Match             78.0%;  Score 32;  DB 1;  Length 722;
  Best Local Similarity   85.7%;  Pred. No. 4.7e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |||||:|
Db        612 QQYSLHR 618


RESULT 35
Q7Q3B4_ANOGA
ID   Q7Q3B4_ANOGA PRELIMINARY;      PRT;   785 AA.
AC   Q7Q3B4;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ENSANGP00000010035.
GN   ORFNames=ENSANGG00000007546;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RT   "Anopheles gambiae re-annotation.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008964; EAA12912.1; -; Genomic_DNA.
DR   HSSP; P08473; 1DMT.
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DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0008237; F:metallopeptidase activity; IEA.
DR   GO; GO:0004245; F:neprilysin activity; IEA.
DR   GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR   InterPro; IPR000718; Peptidase_M13.
DR   InterPro; IPR008753; Peptidase_M13_N.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   Pfam; PF01431; Peptidase_M13; 1.
DR   Pfam; PF05649; Peptidase_M13_N; 1.
DR   PRINTS; PR00786; NEPRILYSIN.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW   Hydrolase; Metalloprotease; Protease; Zinc.
SQ   SEQUENCE   785 AA;  90018 MW;  45A1255B99F873F9 CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 785;
  Best Local Similarity   85.7%;  Pred. No. 5.2e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |||| ||
Db        659 QQYSAYR 665


RESULT 36
Q4I1F1_GIBZE
ID   Q4I1F1_GIBZE PRELIMINARY;      PRT;  1749 AA.
AC   Q4I1F1;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=FG08957.1;
OS   Gibberella zeae PH-1.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX   NCBI_TaxID=229533;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PH-1;
RA   Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA   Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA   Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA   Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA   Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA   Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA   Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA   Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA   Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA   Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA   Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA   Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA   Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA   Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA   Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA   Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA   Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA   Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA   Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA   Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA   Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA   Lander E.;
RT   "Fusarium graminearum genome sequence.";
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AACM01000367; EAA77315.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   1749 AA;  196934 MW;  05C3071DAC7CD728 CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 1749;
  Best Local Similarity   75.0%;  Pred. No. 1.3e+03;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||:||| |
Db       1660 QQFSLYNS 1667


RESULT 37
Q4WZM5_ASPFU
ID   Q4WZM5_ASPFU PRELIMINARY;      PRT;  2913 AA.
AC   Q4WZM5;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=Afu2g16420;
OS   Aspergillus fumigatus Af293.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=330879;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Af293;
RA   Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA   Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA   Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
RA   Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA   Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA   Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
RA   Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA   Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA   Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA   Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA   Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
RA   Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
RA   Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
RA   Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA   Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA   Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA   Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA   White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA   Machida M., Hall N., Barrell B., Denning D.W.;
RT   "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT   Aspergillus fumigatus.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAHF01000001; EAL93940.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   2913 AA;  330598 MW;  8E1DE0BC87185E66 CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 2913;
  Best Local Similarity   100.0%;  Pred. No. 2.3e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYR 7
              ||||||
Db        802 QYSLYR 807


RESULT 38
Q520T8_MAGGR
ID   Q520T8_MAGGR PRELIMINARY;      PRT;  2941 AA.
AC   Q520T8;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=MG05262.4;
OS   Magnaporthe grisea 70-15.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
OX   NCBI_TaxID=242507;
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RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=70-15;
RA   Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA   Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA   Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA   Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA   Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA   Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA   Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA   David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA   Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA   Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA   Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA   Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA   Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA   Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA   Jaffe D., Jones C., Kamal M., Kamat A., Kamvysselis M., Karlsson E.,
RA   Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
RA   Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA   Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
RA   Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA   Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA   Mccarthy M., Mcdonough S., Mcghee T., Meldrim J., Meneus L.,
RA   Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA   Mozes J., Mulrain L., Munson G., Naylor J., Newes C., Nguyen C.,
RA   Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA   Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA   O'neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piqani B.,
RA   Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA   Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA   Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA   Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA   Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA   Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA   Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA   Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA   Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA   Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA   Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA   Zimmer A., Zody M., Lander E.;
RT   "The genome sequence of Magnaporthe grisea.";
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=70-15;
RA   Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=70-15;
RA   Zhu H., Blackmon B.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AACU01000806; EAA52570.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   2941 AA;  330467 MW;  C8F1F26BC0F2957D CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 2941;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYR 7
              ||||||
Db        814 QYSLYR 819


RESULT 39
Q5AWI2_EMENI
ID   Q5AWI2_EMENI PRELIMINARY;      PRT;  3043 AA.
AC   Q5AWI2;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=AN7348.2;
OS   Aspergillus nidulans FGSC A4.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; Emericella.
OX   NCBI_TaxID=227321;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FGSC A4;
RA   Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA   Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavkiy L.,
RA   Boukhgalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
RA   Choepel Y., Collymore A., Cook A., Cooke P., Corum B., DeArellano K.,
RA   Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA   Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
RA   Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
RA   Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA   Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA   Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA   Ma L.-J., Mabbitt R., MacLean C., Macdonald P., Major J., Manning J.,
RA   Matthews C., Mauceli E., McCarthy M., Meldrim J., Meneus L.,
RA   Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA   Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
RA   Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
RA   Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA   Roman J., Schauer S., Schupback R., Seaman S., Severy P., Smirnov S.,
RA   Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA   Talamas J., Tesfaye S., Theodore J., Topham K., Travers M.,
RA   Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA   Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA   Lander E.;
RT   "Genome Sequence of Aspergillus nidulans.";
RL   Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AACD01000128; EAA61719.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   3043 AA;  344661 MW;  E8B73D781D6616A5 CRC64;

  Query Match             78.0%;  Score 32;  DB 2;  Length 3043;
  Best Local Similarity   100.0%;  Pred. No. 2.5e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYR 7
              ||||||
Db        801 QYSLYR 806


RESULT 40
Q7RXY5_NEUCR
ID   Q7RXY5_NEUCR PRELIMINARY;      PRT;  3054 AA.
AC   Q7RXY5;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   Name=NCU00459.1;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=OR74A;
RA   Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA   Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA   Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA   Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA   Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
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RA   Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA   Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA   Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA   Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA   Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA   DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA   Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA   Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA   Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT   "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL   Nature 0:0-0(2003).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABX01000735; EAA27542.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   3054 AA;  340678 MW;  E80A580CE094E113 CRC64;

  Query Match            78.0%;  Score 32;  DB 2;  Length 3054;
  Best Local Similarity  100.0%;  Pred. No. 2.5e+03;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYR 7
              ||||||
Db        812 QYSLYR 817


RESULT 41
Q6H8C9_ORYSA
ID   Q6H8C9_ORYSA PRELIMINARY;      PRT;    66 AA.
AC   Q6H8C9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein OJ1006_A02.32.
GN   Name=OJ1006_A02.32;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP003977; BAD25020.1; -; Genomic_DNA.
DR   Gramene; Q6H8C9; -.
KW   Hypothetical protein.
SQ   SEQUENCE   66 AA;  7266 MW;  0287B1938B53AE92 CRC64;

  Query Match            75.6%;  Score 31;  DB 2;  Length 66;
  Best Local Similarity  71.4%;  Pred. No. 50;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              :||:|||
Db         58 EYSIYRS 64


RESULT 42
Q8XS41_RALSO
ID   Q8XS41_RALSO PRELIMINARY;      PRT;    68 AA.
AC   Q8XS41;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein RSp0640.
GN   OrderedLocusNames=RSp0640; ORFNames=RS03727;
OS   Ralstonia solanacearum (Pseudomonas solanacearum).
OG   Plasmid megaplasmid.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Ralstonia.
OX   NCBI_TaxID=305;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=GMI1000;
RX   MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA   Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA   Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA   Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
RA   Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA   Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA   Weissenbach J., Boucher C.A.;
RT   "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL   Nature 415:497-502(2002).
DR   EMBL; AL646079; CAD17791.1; -; Genomic_DNA.
DR   InterPro; IPR005153; MbtH.
DR   Pfam; PF03621; MbtH; 1.
KW   Complete proteome; Hypothetical protein; Plasmid.
SQ   SEQUENCE   68 AA;  7721 MW;  683DDA987D9BAF19 CRC64;

  Query Match            75.6%;  Score 31;  DB 2;  Length 68;
  Best Local Similarity  85.7%;  Pred. No. 52;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              ||||:||
Db         22 QYSLWRS 28


RESULT 43
Q8GGS3_STRAZ
ID   Q8GGS3_STRAZ PRELIMINARY;      PRT;    72 AA.
AC   Q8GGS3;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   MbtH-like protein.
OS   Streptomyces atroolivaceus.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=66869;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22336326; PubMed=12446651;
RX   DOI=10.1128/JB.184.24.7013-7024.2002;
RA   Cheng Y.-Q., Tang G.-L., Shen B.;
RT   "Identification and localization of the gene cluster encoding
RT   biosynthesis of the antitumor macrolactam leinamycin in Streptomyces
RT   atroolivaceus S-140.";
RL   J. Bacteriol. 184:7013-7024(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22531819; PubMed=12598647; DOI=10.1073/pnas.0537286100;
RA   Cheng Y.-Q., Tang G.-L., Shen B.;
RT   "Type I polyketide synthase requiring a discrete acyltransferase for
RT   polyketide biosynthesis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:3149-3154(2003).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15112993; DOI=10.1016/S1074-5521(03)00286-2;
RA   Tang G.-L., Cheng Y.-Q., Shen B.;
RT   "Leinamycin biosynthesis revealing unprecedented architectural
RT   complexity for a hybrid polyketide synthase and nonribosomal peptide
RT   synthetase.";
RL   Chem. Biol. 11:33-45(2004).
DR   EMBL; AF484556; AAN85492.1; -; Genomic_DNA.
DR   InterPro; IPR005153; MbtH.
DR   Pfam; PF03621; MbtH; 1.
SQ   SEQUENCE   72 AA;  8044 MW;  B5C91EA4B18DA031 CRC64;

  Query Match            75.6%;  Score 31;  DB 2;  Length 72;
  Best Local Similarity  62.5%;  Pred. No. 55;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
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```
              ||||::|:
Db         19 QQYSIWRA 26


RESULT 44
CH10_SCHPO
ID   CH10_SCHPO     STANDARD;      PRT;   104 AA.
AC   O59804;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   10 kDa heat shock protein, mitochondrial (HSP10) (10 kDa chaperonin).
GN   Name=hsp10; ORFNames=SPCC550.06c;
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=972;
RX   MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M.H., Lyne R., Stewart A.,
RA   Sgouros J.G., Peat N., Hayles J., Baker S.G., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D.E., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K.D., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K.L., Murphy L.D., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K.M., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M.N., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J.R., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Duesterhoeft A., Fritzc C., Holzer E., Moestl D.,
RA   Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R.,
RA   Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).
CC   -!- FUNCTION: Eukaryotic CPN10 homolog which is essential for
CC       mitochondrial protein biogenesis, together with CPN60. Binds to
CC       CPN60 in the presence of Mg-ATP and suppresses the ATPase activity
CC       of the latter (By similarity).
CC   -!- SUBUNIT: Homohexamer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC   -!- SIMILARITY: Belongs to the groES chaperonin family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AL023592; CAA19110.1; -; Genomic_DNA.
DR   PIR; T41381; T41381.
DR   HSSP; P09621; 1P3H.
DR   GeneDB_Spombe; SPCC550.06c; -.
DR   InterPro; IPR001476; Chaprnin_Cpn10.
DR   PANTHER; PTHR10772; Chaprnin_Cpn10; 1.
DR   Pfam; PF00166; Cpn10; 1.
DR   PRINTS; PR00297; CHAPERONIN10.
DR   ProDom; PD000566; Chaprnin_Cpn10; 1.
DR   PROSITE; PS00681; CHAPERONINS_CPN10; 1.
KW   Chaperone; Complete proteome; Mitochondrion.
SQ   SEQUENCE   104 AA;  11282 MW;  16BF6870BCB10222 CRC64;

  Query Match             75.6%;  Score 31;  DB 1;  Length 104;
  Best Local Similarity   71.4%;  Pred. No. 84;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              ::|||||
Db         88 EEYSLYR 94


RESULT 45
Q55D69_DICDI
ID   Q55D69_DICDI PRELIMINARY;      PRT;   120 AA.
AC   Q55D69;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=DDB0216698;
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AX4;
RA   Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA   Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA   Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA   Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA   Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA   Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA   Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA   Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA   Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA   Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA   Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA   Loulseged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA   Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
RA   Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA   Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA   Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA   Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA   Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT   "The genome of the social amoeba Dictyostelium discoideum.";
RL   Nature 0:0-0(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAFI01000011; EAL72821.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   120 AA;  13320 MW;  F4BCBB2980C64C7B CRC64;

  Query Match             75.6%;  Score 31;  DB 2;  Length 120;
  Best Local Similarity   75.0%;  Pred. No. 99;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||| || | |
Db         44 QQYHLYHS 51


RESULT 46
Q55D70_DICDI
ID   Q55D70_DICDI PRELIMINARY;      PRT;   120 AA.
AC   Q55D70;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=DDB0190538;
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
```

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OX   NCBI_TaxID=44689;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AX4;
RA   Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA   Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA   Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA   Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA   Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA   Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA   Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA   Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA   Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA   Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA   Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA   Loulseged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA   Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
RA   Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA   Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA   Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA   Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA   Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT   "The genome of the social amoeba Dictyostelium discoideum.";
RL   Nature 0:0-0(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAFI01000011; EAL72233.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   120 AA;  13286 MW;  D8A264F6457F1E7D CRC64;

  Query Match             75.6%;  Score 31;  DB 2;  Length 120;
  Best Local Similarity   75.0%;  Pred. No. 99;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||| || |
Db         44 QQYHLYHS 51


RESULT 47
Q7RQK6_PLAYO
ID   Q7RQK6_PLAYO PRELIMINARY;      PRT;   134 AA.
AC   Q7RQK6;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   Name=PY01090;
OS   Plasmodium yoelii yoelii.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=73239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=17XNL;
RX   MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA   Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA   Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA   Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA   Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA   Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA   Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA   Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA   van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA   Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA   Carucci D.J.;
RT   "Genome sequence and comparative analysis of the model rodent malaria
RT   parasite Plasmodium yoelii yoelii.";
RL   Nature 419:512-519(2002).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABL01000288; EAA20213.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   134 AA;  16043 MW;  A0444E3F76A2F623 CRC64;

  Query Match             75.6%;  Score 31;  DB 2;  Length 134;
  Best Local Similarity   62.5%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              | ||:||:
Db         23 QNYSIYRN 30


RESULT 48
Q6E6C8_ANTLO
ID   Q6E6C8_ANTLO PRELIMINARY;      PRT;   157 AA.
AC   Q6E6C8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   CDC20-like protein (Fragment).
OS   Antonospora locustae (Nosema locustae).
OC   Eukaryota; Fungi; Microsporidia; Antonospora.
OX   NCBI_TaxID=278021;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15186746; DOI=10.1016/j.cub.2004.04.041;
RA   Slamovits C.H., Fast N.M., Law J.S., Keeling P.J.;
RT   "Genome compaction and stability in microsporidian intracellular
RT   parasites.";
RL   Curr. Biol. 14:891-896(2004).
DR   EMBL; AY548901; AAT12359.1; -; Genomic_DNA.
DR   InterPro; IPR000002; Fizzy.
FT   NON_TER     157    157
SQ   SEQUENCE   157 AA;  17667 MW;  884030BC501CCAED CRC64;

  Query Match             75.6%;  Score 31;  DB 2;  Length 157;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| :||
Db        131 QQYSAHRS 138


RESULT 49
Q6RKG9_GIBZE
ID   Q6RKG9_GIBZE PRELIMINARY;      PRT;   161 AA.
AC   Q6RKG9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Polyketide synthase (Fragment).
GN   Name=PKS11;
OS   Gibberella zeae (Fusarium graminearum).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX   NCBI_TaxID=5518;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=GZ-3639;
RX   PubMed=14676319; DOI=10.1073/pnas.2532165100;
RA   Kroken S., Glass N.L., Taylor J.W., Yoder O.C., Turgeon B.G.;
RT   "Phylogenomic analysis of type I polyketide synthase genes in
RT   pathogenic and saprobic ascomycetes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:15670-15675(2003).
DR   EMBL; AY495636; AAS57295.1; -; mRNA.
DR   GO; GO:0003824; F:catalytic activity; IEA.
DR   GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR   InterPro; IPR000794; Ketoacyl_synth.
DR   Pfam; PF00109; ketoacyl-synt; 1.
FT   NON_TER       1      1
FT   NON_TER     161    161
SQ   SEQUENCE   161 AA;  18247 MW;  6A6DE6D274478533 CRC64;
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  Query Match             75.6%;  Score 31;  DB 2;  Length 161;
  Best Local Similarity   71.4%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              ||| :||
Db        133 QQYGIYR 139


RESULT 50
Q5IXM2_MONPV
ID   Q5IXM2_MONPV PRELIMINARY;      PRT;   196 AA.
AC   Q5IXM2;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   MPXV-WRAIR147.
GN   ORFNames=MPXV-WRAIR147;
OS   Monkeypox virus.
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10244;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=MPXV-WRAIR7-61;
RA   Chen N., Li G., Jarhling P., Feng Z., Buller R.M.L., Buck C., Wang C.,
RA   Lefkowitz E.J., Damon I.K., Esposito J.J., Roper R.L., Upton C.;
RT   "Comparison of the genomic sequences of West and Central African
RT   isolates of monkeypox virus, a case for differences in virulence.";
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY603973; AAU01357.1; -; Genomic_DNA.
DR   InterPro; IPR009487; Orthopox_A43R.
DR   Pfam; PF06517; Orthopox_A43R; 1.
SQ   SEQUENCE   196 AA;  22959 MW;  408DEDA4B94C41DC CRC64;

  Query Match             75.6%;  Score 31;  DB 2;  Length 196;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YSLYRS 8
              ||||||
Db        139 YSLYRS 144


Search completed: March 23, 2006, 02:03:28
Job time : 101.965 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:05:22 ; Search time 17.3151 Seconds
(without alignments)
38.198 Million cell updates/sec

Title: US-10-755-382-22
Perfect score: 41
Sequence: 1 QQYSLYRS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	41	100.0	8	2	US-09-253-794-22	Sequence 22, Appl
3	41	100.0	106	1	US-08-318-157B-4	Sequence 4, Appli
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269	26	63.4	145	2	US-09-003-574-7	Sequence 7, Appli
270	26	63.4	145	2	US-09-003-570-7	Sequence 7, Appli
271	26	63.4	145	2	US-09-864-541A-7	Sequence 7, Appli
272	26	63.4	145	2	US-10-226-795-17	Sequence 17, Appl
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275	26	63.4	193	2	US-09-902-540-10797	Sequence 10797, A
276	26	63.4	200	2	US-09-562-737-110	Sequence 110, App
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282	26	63.4	229	2	US-09-371-710-34	Sequence 34, Appl
283	26	63.4	229	2	US-09-648-386-32	Sequence 32, Appl
284	26	63.4	229	2	US-09-648-386-33	Sequence 33, Appl
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288	26	63.4	232	2	US-09-314-235-23	Sequence 23, Appl
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293	26	63.4	233	2	US-08-695-692B-7	Sequence 7, Appli
294	26	63.4	233	2	US-08-882-431B-4	Sequence 4, Appli
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367	26	63.4	631	1	US-08-478-373-111	Sequence 111, App
368	26	63.4	631	2	US-08-474-671-111	Sequence 111, App
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370	26	63.4	631	2	US-08-897-438-111	Sequence 111, App
371	26	63.4	631	2	US-08-637-654-111	Sequence 111, App
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540	25	61.0	227	2	US-09-303-518D-728	Sequence 728, App
541	25	61.0	229	2	US-09-248-796A-23816	Sequence 23816, A
542	25	61.0	231	1	US-08-622-354-5	Sequence 5, Appli
543	25	61.0	232	2	US-09-134-001C-5367	Sequence 5367, Ap
544	25	61.0	236	2	US-09-902-540-9715	Sequence 9715, Ap
545	25	61.0	237	2	US-09-216-295-19	Sequence 19, Appl
546	25	61.0	237	2	US-09-632-570-19	Sequence 19, Appl
547	25	61.0	237	2	US-09-632-575-49	Sequence 49, Appl
548	25	61.0	244	2	US-08-918-148-77	Sequence 77, Appl
549	25	61.0	244	2	US-09-138-091A-75	Sequence 75, Appl
550	25	61.0	245	2	US-08-918-148-75	Sequence 75, Appl
551	25	61.0	245	2	US-08-918-148-76	Sequence 76, Appl
552	25	61.0	245	2	US-08-918-148-78	Sequence 78, Appl
553	25	61.0	245	2	US-09-138-091A-73	Sequence 73, Appl
554	25	61.0	245	2	US-09-138-091A-74	Sequence 74, Appl
555	25	61.0	245	2	US-09-138-091A-76	Sequence 76, Appl
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558	25	61.0	250	2	US-09-538-092-355	Sequence 355, App
559	25	61.0	254	2	US-10-104-047-2701	Sequence 2701, Ap
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561	25	61.0	267	1	US-07-706-872-3	Sequence 3, Appli
562	25	61.0	272	2	US-09-605-703B-774	Sequence 774, App
563	25	61.0	276	2	US-09-489-039A-13021	Sequence 13021, A
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567	25	61.0	280	2	US-09-328-775-2	Sequence 2, Appli
568	25	61.0	280	2	US-09-994-177-2	Sequence 2, Appli
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575	25	61.0	312	2	US-09-312-283C-142	Sequence 142, App
576	25	61.0	314	2	US-09-328-352-6781	Sequence 6781, Ap
577	25	61.0	314	2	US-09-964-956-31	Sequence 31, Appl
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586	25	61.0	354	2	US-09-835-811-4	Sequence 4, Appli
587	25	61.0	357	2	US-09-107-433-3022	Sequence 3022, Ap
588	25	61.0	359	2	US-09-328-352-6329	Sequence 6329, Ap
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595	25	61.0	370	2	US-09-710-279-1328	Sequence 1328, Ap
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634	25	61.0	469	2	US-09-990-444-289	Sequence 289, App
635	25	61.0	469	2	US-09-997-333-289	Sequence 289, App
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694	25	61.0	649	2	US-09-605-703B-70	Sequence 70, Appl
695	25	61.0	656	1	US-08-444-005-15	Sequence 15, Appl
696	25	61.0	656	2	US-09-069-023-28	Sequence 28, Appl
697	25	61.0	656	2	US-09-345-473E-30	Sequence 30, Appl
698	25	61.0	656	2	US-09-862-027-30	Sequence 30, Appl
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713	25	61.0	797	2	US-09-134-000C-4997	Sequence 4997, Ap
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715	25	61.0	798	2	US-09-964-956-28	Sequence 28, Appl
716	25	61.0	806	2	US-09-949-016-8753	Sequence 8753, Ap
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721	25	61.0	841	2	US-09-964-956-2	Sequence 2, Appli
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741	25	61.0	883	2	US-08-242-344-2	Sequence 2, Appli
742	25	61.0	894	2	US-09-489-039A-12248	Sequence 12248, A
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745	25	61.0	912	1	US-08-005-002C-8	Sequence 8, Appli
746	25	61.0	912	1	US-08-487-203A-8	Sequence 8, Appli
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753	25	61.0	1069	2	US-09-270-767-45497	Sequence 45497, A
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755	25	61.0	1090	2	US-09-252-991A-23149	Sequence 23149, A
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757	25	61.0	1113	2	US-09-332-522E-2	Sequence 2, Appli
758	25	61.0	1233	2	US-09-328-352-7874	Sequence 7874, Ap
759	25	61.0	1241	2	US-08-714-741-34	Sequence 34, Appl
760	25	61.0	1258	2	US-09-538-092-886	Sequence 886, App
761	25	61.0	1273	2	US-09-170-496D-289	Sequence 289, App
762	25	61.0	1273	2	US-09-364-425B-54	Sequence 54, Appl
763	25	61.0	1488	2	US-09-605-703B-772	Sequence 772, App
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768	25	61.0	1541	2	US-10-645-655-3	Sequence 3, Appli
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770	25	61.0	1589	2	US-08-755-587-189	Sequence 189, App
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773	25	61.0	2441	2	US-09-514-247A-8	Sequence 8, Appli
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775	25	61.0	2938	4	PCT-US94-00198-3	Sequence 3, Appli
776	25	61.0	3092	2	US-09-487-558B-172	Sequence 172, App
777	25	61.0	3852	2	US-10-025-225-4	Sequence 4, Appli
778	25	61.0	4536	2	US-09-180-422B-27	Sequence 27, Appl
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780	25	61.0	4563	2	US-09-108-006C-1	Sequence 1, Appli
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783	25	61.0	4588	2	US-10-025-225-8	Sequence 8, Appli
784	25	61.0	4589	2	US-10-025-225-2	Sequence 2, Appli
785	25	61.0	5032	2	US-09-538-092-979	Sequence 979, App
786	25	61.0	5037	2	US-09-424-783-4	Sequence 4, Appli
787	24.5	59.8	434	2	US-09-513-151A-6	Sequence 6, Appli
788	24.5	59.8	583	2	US-09-489-039A-13918	Sequence 13918, A
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792	24	58.5	12	2	US-08-747-599A-21	Sequence 21, Appl
793	24	58.5	19	2	US-09-732-357B-9	Sequence 9, Appli
794	24	58.5	20	6	5196333-11	Patent No. 5196333
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796	24	58.5	24	1	US-08-484-631-113	Sequence 113, App
797	24	58.5	24	1	US-08-827-570-113	Sequence 113, App
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805	24	58.5	29	2	US-09-932-161-3	Sequence 3, Appli
806	24	58.5	45	2	US-09-270-767-57330	Sequence 57330, A
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ALIGNMENTS

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RESULT 1
US-08-318-157B-22
; Sequence 22, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-22

  Query Match           100.0%;  Score 41;  DB 1;  Length 8;
  Best Local Similarity  100.0%;  Pred. No. 4.6e+05;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
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; Sequence 22, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 22:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 8 amino acids
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;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
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US-09-253-794-22

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RESULT 3
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; Sequence 4, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
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;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-4

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RESULT 4
US-08-318-157B-19
; Sequence 19, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
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;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-19

  Query Match           100.0%;  Score 41;  DB 1;  Length 106;
  Best Local Similarity  100.0%;  Pred. No. 0.68;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db         89 QQYSLYRS 96


RESULT 5
US-09-253-794-4
; Sequence 4, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 106 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-253-794-4

  Query Match           100.0%;  Score 41;  DB 2;  Length 106;
  Best Local Similarity  100.0%;  Pred. No. 0.68;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db         89 QQYSLYRS 96
```

```
RESULT 6
US-09-253-794-19
; Sequence 19, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 106 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-253-794-19

  Query Match             100.0%;  Score 41;  DB 2;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 0.68;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db         89 QQYSLYRS 96


RESULT 7
US-09-270-767-49147
; Sequence 49147, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49147
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-49147

  Query Match             82.9%;  Score 34;  DB 2;  Length 251;
  Best Local Similarity   85.7%;  Pred. No. 40;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              |||:|||
Db        226 QYSIYRS 232


RESULT 8
US-09-270-767-47089
; Sequence 47089, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47089
;   LENGTH: 265
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-47089

  Query Match             82.9%;  Score 34;  DB 2;  Length 265;
  Best Local Similarity   85.7%;  Pred. No. 42;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              |||:|||
Db        240 QYSIYRS 246


RESULT 9
US-09-902-540-11105
; Sequence 11105, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11105
;   LENGTH: 1040
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-11105

  Query Match             80.5%;  Score 33;  DB 2;  Length 1040;
  Best Local Similarity   75.0%;  Pred. No. 2.8e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              | |:||||
Db        813 QHYNLYRS 820


RESULT 10
US-09-543-681A-7437
; Sequence 7437, Application US/09543681A
; Patent No. 6605709
```

```
; GENERAL INFORMATION:
;  APPLICANT: GARY BRETON
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
;  TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.1002-001
;  CURRENT APPLICATION NUMBER: US/09/543,681A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/128,706
;  PRIOR FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7437
;   LENGTH: 414
;   TYPE: PRT
;   ORGANISM: Proteus mirabilis
US-09-543-681A-7437

  Query Match             78.0%;  Score 32;  DB 2;  Length 414;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              ||||||
Db         56 QQYSLY 61


RESULT 11
US-09-328-352-5892
; Sequence 5892, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
;  APPLICANT: Gary L. Breton et al.
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
;  TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC99-03PA
;  CURRENT APPLICATION NUMBER: US/09/328,352
;  CURRENT FILING DATE: 1999-06-04
;  NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5892
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Acinetobacter baumannii
US-09-328-352-5892

  Query Match             75.6%;  Score 31;  DB 2;  Length 110;
  Best Local Similarity   62.5%;  Pred. No. 64;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||| ||::
Db         91 QQYQLYKA 98


RESULT 12
US-09-270-767-46847
; Sequence 46847, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46847
;   LENGTH: 135
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-46847

  Query Match             75.6%;  Score 31;  DB 2;  Length 135;
  Best Local Similarity   62.5%;  Pred. No. 80;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||| :|:|
Db        118 QQYQIYQS 125


RESULT 13
US-09-270-767-62478
; Sequence 62478, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62478
;   LENGTH: 135
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-62478

  Query Match             75.6%;  Score 31;  DB 2;  Length 135;
  Best Local Similarity   62.5%;  Pred. No. 80;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||| :|:|
Db        118 QQYQIYQS 125


RESULT 14
US-09-543-681A-8237
; Sequence 8237, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
;  APPLICANT: GARY BRETON
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
;  TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.1002-001
;  CURRENT APPLICATION NUMBER: US/09/543,681A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/128,706
;  PRIOR FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 8237
;   LENGTH: 277
;   TYPE: PRT
;   ORGANISM: Proteus mirabilis
US-09-543-681A-8237

  Query Match             75.6%;  Score 31;  DB 2;  Length 277;
  Best Local Similarity   75.0%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||: ||
Db        185 QQYSILRS 192


RESULT 15
US-08-672-814D-11
; Sequence 11, Application US/08672814D
; Patent No. 5952480
;  GENERAL INFORMATION:
;    APPLICANT:  Leung, David W.
;    APPLICANT:  Weeks, Reitha
;    TITLE OF INVENTION:  MAMMALIAN
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cell Therapeutics, Inc.
```

```
;      STREET:  201 Elliott Avenue West
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  U.S.A.
;      ZIP:  98119
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" disk, 1.44Mb, double side, high density
;      COMPUTER:  PC Clone (486 microprocessor)
;      OPERATING SYSTEM:  MS-DOS Version 6.1, Windows NT
;      SOFTWARE:  WORD 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/672,814D
;      FILING DATE:  28-Jun-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faciszewski, Stephen
;      REGISTRATION NUMBER:  36,131
;      REFERENCE/DOCKET NUMBER:  1803
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)282-7100
;      TELEFAX:  (206)284-6206
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  446
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:  Drosophila
;      STRAIN:
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
;      CELL TYPE:
;      CELL LINE:
;      ORGANELLE:
;    FEATURE:
;      NAME/KEY:  CDP-diacylglycerol synthase (CDS)
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
US-08-672-814D-11

  Query Match             75.6%;  Score 31;  DB 1;  Length 446;
  Best Local Similarity   62.5%;  Pred. No. 2.8e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||| :|:|
Db        429 QQYQIYQS 436


RESULT 16
US-09-333-696-11
; Sequence 11, Application US/09333696
; Patent No. 6200769
;  GENERAL INFORMATION:
;    APPLICANT:  Leung, David W.
;    APPLICANT:  Weeks, Reitha
;    TITLE OF INVENTION:  MAMMALIAN
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cell Therapeutics, Inc.
;      STREET:  201 Elliott Avenue West
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  U.S.A.
;      ZIP:  98119
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" disk, 1.44Mb, double side, high density
;      COMPUTER:  PC Clone (486 microprocessor)
;      OPERATING SYSTEM:  MS-DOS Version 6.1, Windows NT
;      SOFTWARE:  WORD 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/333,696
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/672,814
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Faciszewski, Stephen
;      REGISTRATION NUMBER:  36,131
;      REFERENCE/DOCKET NUMBER:  1803
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206)282-7100
;      TELEFAX:  (206)284-6206
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  446
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:  Drosophila
;      STRAIN:
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
;      CELL TYPE:
;      CELL LINE:
;      ORGANELLE:
;    FEATURE:
;      NAME/KEY:  CDP-diacylglycerol synthase (CDS)
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
US-09-333-696-11

  Query Match             75.6%;  Score 31;  DB 2;  Length 446;
  Best Local Similarity   62.5%;  Pred. No. 2.8e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||| :|:|
Db        429 QQYQIYQS 436


RESULT 17
US-09-282-218A-19
; Sequence 19, Application US/09282218A
; Patent No. 6503700
; GENERAL INFORMATION:
;  APPLICANT:  LEUNG, David W.
;  TITLE OF INVENTION:  MAMMALIAN CDP-DIACYLGLYCEROL SYNTHASE
;  FILE REFERENCE:  077319/0153
;  CURRENT APPLICATION NUMBER: US/09/282,218A
;  CURRENT FILING DATE:  1999-03-31
;  NUMBER OF SEQ ID NOS:  19
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 446
;   TYPE: PRT
;   ORGANISM: Drosophila
US-09-282-218A-19

  Query Match             75.6%;  Score 31;  DB 2;  Length 446;
  Best Local Similarity   62.5%;  Pred. No. 2.8e+02;
```

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 QQYSLYRS 8
              ||| :|:|
Db        429 QQYQIYQS 436
```

RESULT 18
US-08-895-601-5
; Sequence 5, Application US/08895601
; Patent No. 6060262
; GENERAL INFORMATION:
; APPLICANT: Beer-Romero, Peggy
; APPLICANT: Strack, Peter J.
; APPLICANT: Glass, Susan J.
; APPLICANT: Rolfe, Mark
; TITLE OF INVENTION: REGULATION OF KAPPA B (IkB) DEGRADATION,
; TITLE OF INVENTION: AND METHODS AND REAGENTS RELATED THERETO
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/895,601
; FILING DATE: 16-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-096.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1083 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-895-601-5

Query Match 75.6%; Score 31; DB 2; Length 1083;
Best Local Similarity 75.0%; Pred. No. 7.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 QQYSLYRS 8
              |||| :||
Db         64 QQYSIQRS 71
```

RESULT 19
US-09-653-755A-5
; Sequence 5, Application US/09653755A
; Patent No. 6824989
; GENERAL INFORMATION:
; APPLICANT: Eisinger, Dominic P.
; APPLICANT: Stiles, Lynn
; APPLICANT: LaMarche, Arthur
; APPLICANT: Jelinek, Thomas
; TITLE OF INVENTION: Recombinant Monoclonal Antibody Specific for
; TITLE OF INVENTION: Phosphotyrosine-Containing Proteins
; FILE REFERENCE: 724650-3
; CURRENT APPLICATION NUMBER: US/09/653,755A
; CURRENT FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Amino acid
; OTHER INFORMATION: sequence for light chain of recombinant antibody
US-09-653-755A-5

Query Match 73.2%; Score 30; DB 2; Length 214;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 QQYSLYRS 8
              |||| ||:
Db         90 QQYSGYRT 97
```

RESULT 20
US-09-902-540-11463
; Sequence 11463, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11463
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11463

Query Match 73.2%; Score 30; DB 2; Length 316;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 QQYSLYRS 8
              |||:|| :
Db         64 QQYTLYET 71
```

RESULT 21
US-09-270-767-57763
; Sequence 57763, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57763
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57763

Query Match 73.2%; Score 30; DB 2; Length 575;
Best Local Similarity 71.4%; Pred. No. 5.7e+02;

```
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              | ||:||
Db          6 QMYSMYR 12


RESULT 22
US-09-543-681A-7900
; Sequence 7900, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
;  APPLICANT: GARY BRETON
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
;  TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.1002-001
;  CURRENT APPLICATION NUMBER: US/09/543,681A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/128,706
;  PRIOR FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7900
;   LENGTH: 805
;   TYPE: PRT
;   ORGANISM: Proteus mirabilis
US-09-543-681A-7900

  Query Match             73.2%;  Score 30;  DB 2;  Length 805;
  Best Local Similarity   62.5%;  Pred. No. 8.1e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              :|| |||:
Db        423 EQYRLYRN 430


RESULT 23
US-08-470-260-3
; Sequence 3, Application US/08470260
; Patent No. 6077706
;  GENERAL INFORMATION:
;    APPLICANT:  Covacci, Antonello
;    APPLICANT:  Bugnoli, Massimo
;    APPLICANT:  Telford, John
;    APPLICANT:  Macchia, Giovanni
;    APPLICANT:  Rappuoli, Rino
;    TITLE OF INVENTION:  Helicobacter Pylori Proteins Useful
;    TITLE OF INVENTION:  for Vaccines and Diagnostics
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Chiron Corporation
;      STREET:  4560 Horton Street
;      CITY:  Emeryville
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94608-2916
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,260
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/256,848
;      FILING DATE:  21-OCT-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McClung, Barbara G.
;      REGISTRATION NUMBER:  33,113
;      REFERENCE/DOCKET NUMBER:  0316.001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2708
;      TELEFAX:  (510) 655-3542
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1296 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-470-260-3

  Query Match             73.2%;  Score 30;  DB 2;  Length 1296;
  Best Local Similarity   62.5%;  Pred. No. 1.3e+03;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ::| ||||
Db         96 KEYDLYRS 103


RESULT 24
US-08-471-491-3
; Sequence 3, Application US/08471491B
; Patent No. 6090611
; GENERAL INFORMATION:
;  APPLICANT: Covacci, Antonello
;  APPLICANT: Bugnoli, Massimo
;  APPLICANT: Telford, John
;  APPLICANT: Macchia, Giovanni
;  APPLICANT: Rappuoli, Rino
;  TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
;  TITLE OF INVENTION: Diagnostics
;  FILE REFERENCE: CHIR0044
;  CURRENT APPLICATION NUMBER: US/08/471,491B
;  CURRENT FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1296
;   TYPE: PRT
;   ORGANISM: Helicobacter pylori
US-08-471-491-3

  Query Match             73.2%;  Score 30;  DB 2;  Length 1296;
  Best Local Similarity   62.5%;  Pred. No. 1.3e+03;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ::| ||||
Db         96 KEYDLYRS 103


RESULT 25
US-08-466-662-3
; Sequence 3, Application US/08466662B
; Patent No. 6130059
; GENERAL INFORMATION:
;  APPLICANT: Covacci, Antonello
;  APPLICANT: Bugnoli, Massimo
;  APPLICANT: Telford, John
;  APPLICANT: Macchia, Giovanni
;  APPLICANT: Rappuoli, Rino
;  TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
;  TITLE OF INVENTION: Diagnostics
;  FILE REFERENCE: CHIR0057
;  CURRENT APPLICATION NUMBER: US/08/466,662B
;  CURRENT FILING DATE: 1995-06-06
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1296
;   TYPE: PRT
;   ORGANISM: Helicobacter pylori
```

US-08-466-662-3

Query Match 73.2%; Score 30; DB 2; Length 1296;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
::| ||||
Db 96 KEYDLYRS 103

RESULT 26
US-09-248-796A-23186
; Sequence 23186, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23186
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-23186

Query Match 70.7%; Score 29; DB 2; Length 72;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYSLYRS 8
|| |||:
Db 65 QYKLYRN 71

RESULT 27
US-09-270-767-38717
; Sequence 38717, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38717
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-38717

Query Match 70.7%; Score 29; DB 2; Length 135;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QYSLYRS 8
:|||||:
Db 98 RYSLYRN 104

RESULT 28
US-09-270-767-53934
; Sequence 53934, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53934
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-53934

Query Match 70.7%; Score 29; DB 2; Length 135;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QYSLYRS 8
:|||||:
Db 98 RYSLYRN 104

RESULT 29
US-08-631-607-3
; Sequence 3, Application US/08631607
; Patent No. 5767252
; GENERAL INFORMATION:
; APPLICANT: Worley et al, Paul
; TITLE OF INVENTION: NOVEL NEURONAL CELL GROWTH FACTOR
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/631,607
; FILING DATE: 08-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07265/086001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 208 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-631-607-3

Query Match 70.7%; Score 29; DB 1; Length 208;
Best Local Similarity 83.3%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLY 6
:|||||

```
Db         69 EQYSLY 74


RESULT 30
US-09-098-358B-3
; Sequence 3, Application US/09098358B
; Patent No. 6436673
; GENERAL INFORMATION:
;  APPLICANT: THE JOHN HOPKINS SCHOOL OF MEDICINE
;  APPLICANT:  WORLEY, PAUL
;  APPLICANT:  TSUI, CYNTHIA
;  TITLE OF INVENTION: NOVEL NEURONAL CELL GROWTH FACTOR
;  FILE REFERENCE: JHU 1340-1 (07265/086002)
;  CURRENT APPLICATION NUMBER: US/09/098,358B
;  CURRENT FILING DATE:  1998-06-16
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 208
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL
;   FEATURE:
;   OTHER INFORMATION: RAT SAP
US-09-098-358B-3

  Query Match             70.7%;  Score 29;  DB 2;  Length 208;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              :|||||
Db         69 EQYSLY 74


RESULT 31
US-09-248-796A-19483
; Sequence 19483, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19483
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-09-248-796A-19483

  Query Match             70.7%;  Score 29;  DB 2;  Length 241;
  Best Local Similarity   50.0%;  Pred. No. 3.6e+02;
  Matches    4;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||::|::
Db        105 QQYAIYQN 112


RESULT 32
US-09-270-767-57322
; Sequence 57322, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57322
;   LENGTH: 286
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
;   FEATURE:
;   OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57322

  Query Match             70.7%;  Score 29;  DB 2;  Length 286;
  Best Local Similarity   62.5%;  Pred. No. 4.3e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ::| ||||
Db        150 RRYKLYRS 157


RESULT 33
US-09-134-000C-3579
; Sequence 3579, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION:  ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 032796-032
;  CURRENT APPLICATION NUMBER: US/09/134,000C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3579
;   LENGTH: 288
;   TYPE: PRT
;   ORGANISM: Enterococcus faecalis
US-09-134-000C-3579

  Query Match             70.7%;  Score 29;  DB 2;  Length 288;
  Best Local Similarity   62.5%;  Pred. No. 4.3e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              :||||| :
Db          9 RQYSLYHT 16


RESULT 34
US-09-310-463-12
; Sequence 12, Application US/09310463A
; Patent No. 6384203
; GENERAL INFORMATION:
;  APPLICANT: Cosman, David J.
;  APPLICANT: Anderson, Dirk M.
;  APPLICANT: Borges, Luis
;  TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
;  TITLE OF INVENTION: Like Receptors (LIR)
;  FILE REFERENCE: 2624-A
;  CURRENT APPLICATION NUMBER: US/09/310,463A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: 08/842,248
;  EARLIER FILING DATE: 1997-04-24
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 289
;   TYPE: PRT
;   ORGANISM: human
US-09-310-463-12
```

```
  Query Match             70.7%;  Score 29;  DB 2;  Length 289;
  Best Local Similarity   71.4%;  Pred. No. 4.4e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         56 QEYRLYR 62


RESULT 35
US-08-842-248A-12
; Sequence 12, Application US/08842248A
; Patent No. 6448035
;  GENERAL INFORMATION:
;    APPLICANT:  Cosman, David J.
;    TITLE OF INVENTION:  Family of Immunoregulators Designated
;    TITLE OF INVENTION:  Leukocyte Immunoglobulin-Like Receptors (LIR)
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janis C. Henry, Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  US
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM/PC Compatible
;      OPERATING SYSTEM:  Microsoft Word 7.0
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/842,248A
;      FILING DATE:  April 24, 1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Henry, Janis C.
;      REGISTRATION NUMBER:  34,347
;      REFERENCE/DOCKET NUMBER:  2624
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  289 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-842-248A-12

  Query Match             70.7%;  Score 29;  DB 2;  Length 289;
  Best Local Similarity   71.4%;  Pred. No. 4.4e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         56 QEYRLYR 62


RESULT 36
US-09-976-594-807
; Sequence 807, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
;  APPLICANT: Furness, Michael
;  APPLICANT:  Buchbinder, Jenny
;  TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
;  FILE REFERENCE: PA-0041 US
;  CURRENT APPLICATION NUMBER: US/09/976,594
;  CURRENT FILING DATE:  2001-10-12
;  PRIOR APPLICATION NUMBER: 60/240,409
;  PRIOR FILING DATE: 2000-10-12
;  NUMBER OF SEQ ID NOS: 1143
;  SOFTWARE: PERL Program
; SEQ ID NO 807
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6673549 2770104CD1
US-09-976-594-807

  Query Match             70.7%;  Score 29;  DB 2;  Length 310;
  Best Local Similarity   71.4%;  Pred. No. 4.7e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db        100 QEYRLYR 106


RESULT 37
US-09-134-000C-5220
; Sequence 5220, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION:  ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 032796-032
;  CURRENT APPLICATION NUMBER: US/09/134,000C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5220
;   LENGTH: 395
;   TYPE: PRT
;   ORGANISM: Enterococcus faecalis
US-09-134-000C-5220

  Query Match             70.7%;  Score 29;  DB 2;  Length 395;
  Best Local Similarity   71.4%;  Pred. No. 6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              :||| ||
Db        145 KQYSFYR 151


RESULT 38
US-08-985-950-14
; Sequence 14, Application US/08985950
; Patent No. 6140076
;  GENERAL INFORMATION:
;    APPLICANT:  Adema, Gosse Jan
;    TITLE OF INVENTION:  Isolated Mammalian Monocyte Cell Genes;
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,950
;      FILING DATE:  05-DEC-1997
```

```
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/041,279
;      FILING DATE:  21-MARCH-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,181
;      FILING DATE:  16-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/032,252
;      FILING DATE:  06-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0670K
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1204
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  431 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-985-950-14

  Query Match             70.7%;  Score 29;  DB 2;  Length 431;
  Best Local Similarity   71.4%;  Pred. No. 6.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         73 QEYRLYR 79


RESULT 39
US-08-985-950-20
; Sequence 20, Application US/08985950
; Patent No. 6140076
;  GENERAL INFORMATION:
;    APPLICANT:  Adema, Gosse Jan
;    TITLE OF INVENTION:  Isolated Mammalian Monocyte Cell Genes;
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,950
;      FILING DATE:  05-DEC-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/041,279
;      FILING DATE:  21-MARCH-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,181
;      FILING DATE:  16-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/032,252
;      FILING DATE:  06-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0670K
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1204
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  431 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-985-950-20

  Query Match             70.7%;  Score 29;  DB 2;  Length 431;
  Best Local Similarity   71.4%;  Pred. No. 6.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         73 QEYRLYR 79


RESULT 40
US-09-546-049-14
; Sequence 14, Application US/09546049
; Patent No. 6479638
;  GENERAL INFORMATION:
;       APPLICANT: Adema, Gosse Jan
;                  Meyaard, Linde
;                  Gorman, Daniel M.
;                  McClanahan, Terrill K.
;                  Zurawski, Sandra M.
;                  Zurawski, Gerard
;                  Lanier, Lewis L.
;                  Phillips Jr., Joseph H.
;       TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
;                           Related Reagents
;       NUMBER OF SEQUENCES: 22
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: DNAX Research Institute
;            STREET: 901 California Avenue
;            CITY: Palo Alto
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94304-1104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/546,049
;            FILING DATE: 10-Apr-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/985,950
;            FILING DATE: 05-DEC-1997
;            APPLICATION NUMBER: US 60/041,279
;            FILING DATE: 21-MARCH-1997
;            APPLICATION NUMBER: US 60/033,181
;            FILING DATE: 16-DEC-1996
;            APPLICATION NUMBER: US 60/032,252
;            FILING DATE: 06-DEC-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ching, Edwin P.
;            REGISTRATION NUMBER: 34,090
;            REFERENCE/DOCKET NUMBER: DX0670K
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (650)852-9196
;            TELEFAX: (650)496-1204
;  INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 431 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-546-049-14
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  Query Match             70.7%;  Score 29;  DB 2;  Length 431;
  Best Local Similarity   71.4%;  Pred. No. 6.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         73 QEYRLYR 79


RESULT 41
US-09-546-049-20
; Sequence 20, Application US/09546049
; Patent No. 6479638
;  GENERAL INFORMATION:
;       APPLICANT: Adema, Gosse Jan
;                  Meyaard, Linde
;                  Gorman, Daniel M.
;                  McClanahan, Terrill K.
;                  Zurawski, Sandra M.
;                  Zurawski, Gerard
;                  Lanier, Lewis L.
;                  Phillips Jr., Joseph H.
;       TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
;                           Related Reagents
;       NUMBER OF SEQUENCES: 22
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: DNAX Research Institute
;            STREET: 901 California Avenue
;            CITY: Palo Alto
;            STATE: California
;            COUNTRY: USA
;            ZIP: 94304-1104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/546,049
;            FILING DATE: 10-Apr-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/985,950
;            FILING DATE: 05-DEC-1997
;            APPLICATION NUMBER: US 60/041,279
;            FILING DATE: 21-MARCH-1997
;            APPLICATION NUMBER: US 60/033,181
;            FILING DATE: 16-DEC-1996
;            APPLICATION NUMBER: US 60/032,252
;            FILING DATE: 06-DEC-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Ching, Edwin P.
;            REGISTRATION NUMBER: 34,090
;            REFERENCE/DOCKET NUMBER: DX0670K
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (650)852-9196
;            TELEFAX: (650)496-1204
;   INFORMATION FOR SEQ ID NO: 20:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 431 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-546-049-20

  Query Match             70.7%;  Score 29;  DB 2;  Length 431;
  Best Local Similarity   71.4%;  Pred. No. 6.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         73 QEYRLYR 79


RESULT 42
US-09-248-796A-18684
; Sequence 18684, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18684
;   LENGTH: 437
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-09-248-796A-18684

  Query Match             70.7%;  Score 29;  DB 2;  Length 437;
  Best Local Similarity   62.5%;  Pred. No. 6.7e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||: |:||
Db         53 QQFQLFRS 60


RESULT 43
US-08-985-950-12
; Sequence 12, Application US/08985950
; Patent No. 6140076
;  GENERAL INFORMATION:
;    APPLICANT:  Adema, Gosse Jan
;    TITLE OF INVENTION:  Isolated Mammalian Monocyte Cell Genes;
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,950
;      FILING DATE:  05-DEC-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/041,279
;      FILING DATE:  21-MARCH-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,181
;      FILING DATE:  16-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/032,252
;      FILING DATE:  06-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0670K
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1204
```

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;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  439 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-985-950-12

  Query Match             70.7%;  Score 29;  DB 2;  Length 439;
  Best Local Similarity   71.4%;  Pred. No. 6.7e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         56 QEYHLYR 62


RESULT 44
US-09-310-463-8
; Sequence 8, Application US/09310463A
; Patent No. 6384203
; GENERAL INFORMATION:
;  APPLICANT: Cosman, David J.
;  APPLICANT: Anderson, Dirk M.
;  APPLICANT: Borges, Luis
;  TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
;  TITLE OF INVENTION: Like Receptors (LIR)
;  FILE REFERENCE: 2624-A
;  CURRENT APPLICATION NUMBER: US/09/310,463A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: 08/842,248
;  EARLIER FILING DATE: 1997-04-24
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 439
;   TYPE: PRT
;   ORGANISM: human
US-09-310-463-8

  Query Match             70.7%;  Score 29;  DB 2;  Length 439;
  Best Local Similarity   71.4%;  Pred. No. 6.7e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         56 QEYHLYR 62


RESULT 45
US-08-842-248A-8
; Sequence 8, Application US/08842248A
; Patent No. 6448035
;  GENERAL INFORMATION:
;    APPLICANT:  Cosman, David J.
;    TITLE OF INVENTION:  Family of Immunoregulators Designated
;    TITLE OF INVENTION:  Leukocyte Immunoglobulin-Like Receptors (LIR)
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janis C. Henry, Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  US
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM/PC Compatible
;      OPERATING SYSTEM:  Microsoft Word 7.0
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/842,248A
;      FILING DATE:  April 24, 1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Henry, Janis C.
;      REGISTRATION NUMBER:  34,347
;      REFERENCE/DOCKET NUMBER:  2624
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  439 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-842-248A-8

  Query Match             70.7%;  Score 29;  DB 2;  Length 439;
  Best Local Similarity   71.4%;  Pred. No. 6.7e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         56 QEYHLYR 62


RESULT 46
US-09-546-049-12
; Sequence 12, Application US/09546049
; Patent No. 6479638
;   GENERAL INFORMATION:
;        APPLICANT: Adema, Gosse Jan
;                   Meyaard, Linde
;                   Gorman, Daniel M.
;                   McClanahan, Terrill K.
;                   Zurawski, Sandra M.
;                   Zurawski, Gerard
;                   Lanier, Lewis L.
;                   Phillips Jr., Joseph H.
;        TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
;                            Related Reagents
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: DNAX Research Institute
;             STREET: 901 California Avenue
;             CITY: Palo Alto
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94304-1104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/546,049
;             FILING DATE: 10-Apr-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/985,950
;             FILING DATE: 05-DEC-1997
;             APPLICATION NUMBER: US 60/041,279
;             FILING DATE: 21-MARCH-1997
;             APPLICATION NUMBER: US 60/033,181
;             FILING DATE: 16-DEC-1996
;             APPLICATION NUMBER: US 60/032,252
;             FILING DATE: 06-DEC-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ching, Edwin P.
;             REGISTRATION NUMBER: 34,090
;             REFERENCE/DOCKET NUMBER: DX0670K
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (650)852-9196
;             TELEFAX: (650)496-1204
;
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;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 439 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-546-049-12

  Query Match             70.7%;  Score 29;  DB 2;  Length 439;
  Best Local Similarity   71.4%;  Pred. No. 6.7e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         56 QEYHLYR 62


RESULT 47
US-09-310-463-14
; Sequence 14, Application US/09310463A
; Patent No. 6384203
; GENERAL INFORMATION:
;  APPLICANT: Cosman, David J.
;  APPLICANT: Anderson, Dirk M.
;  APPLICANT: Borges, Luis
;  TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
;  TITLE OF INVENTION: Like Receptors (LIR)
;  FILE REFERENCE: 2624-A
;  CURRENT APPLICATION NUMBER: US/09/310,463A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: 08/842,248
;  EARLIER FILING DATE: 1997-04-24
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 489
;   TYPE: PRT
;   ORGANISM: human
US-09-310-463-14

  Query Match             70.7%;  Score 29;  DB 2;  Length 489;
  Best Local Similarity   71.4%;  Pred. No. 7.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         56 QEYRLYR 62


RESULT 48
US-08-842-248A-14
; Sequence 14, Application US/08842248A
; Patent No. 6448035
;  GENERAL INFORMATION:
;    APPLICANT:  Cosman, David J.
;    TITLE OF INVENTION:  Family of Immunoregulators Designated
;    TITLE OF INVENTION:  Leukocyte Immunoglobulin-Like Receptors (LIR)
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janis C. Henry, Immunex Corporation
;      STREET:  51 University Street
;      CITY:  Seattle
;      STATE:  WA
;      COUNTRY:  US
;      ZIP:  98101
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM/PC Compatible
;      OPERATING SYSTEM:  Microsoft Word 7.0
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/842,248A
;      FILING DATE:  April 24, 1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Henry, Janis C.
;      REGISTRATION NUMBER:  34,347
;      REFERENCE/DOCKET NUMBER:  2624
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 587-0430
;      TELEFAX:  (206) 233-0644
;      TELEX:  756822
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  489 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-842-248A-14

  Query Match             70.7%;  Score 29;  DB 2;  Length 489;
  Best Local Similarity   71.4%;  Pred. No. 7.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         56 QEYRLYR 62


RESULT 49
US-09-949-016-6765
; Sequence 6765, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6765
;   LENGTH: 489
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-6765

  Query Match             70.7%;  Score 29;  DB 2;  Length 489;
  Best Local Similarity   71.4%;  Pred. No. 7.6e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         56 QEYRLYR 62


RESULT 50
US-09-252-991A-23182
; Sequence 23182, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23182
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23182

Query Match 70.7%; Score 29; DB 2; Length 509;
Best Local Similarity 71.4%; Pred. No. 7.9e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 QYSLYRS 8
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Db        138 RYSLYRN 144
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Search completed: March 23, 2006, 02:08:33
Job time : 26.3151 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:42:16 ; Search time 56.1096 Seconds
(without alignments)
59.573 Million cell updates/sec

Title: US-10-755-382-22
Perfect score: 41
Sequence: 1 QQYSLYRS 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	41	100.0	8	3	US-09-253-794-22	Sequence 22, Appl
2	41	100.0	8	4	US-10-680-734-22	Sequence 22, Appl
3	41	100.0	8	5	US-10-755-382-22	Sequence 22, Appl
4	41	100.0	106	3	US-09-253-794-4	Sequence 4, Appli
5	41	100.0	106	3	US-09-253-794-19	Sequence 19, Appl
6	41	100.0	106	4	US-10-680-734-4	Sequence 4, Appli
7	41	100.0	106	4	US-10-680-734-19	Sequence 19, Appl
8	41	100.0	106	5	US-10-755-382-4	Sequence 4, Appli
9	41	100.0	106	5	US-10-755-382-19	Sequence 19, Appl
10	41	100.0	115	4	US-10-270-073-4	Sequence 4, Appli
11	41	100.0	232	4	US-10-006-771A-6	Sequence 6, Appli
12	41	100.0	232	4	US-10-377-109-4	Sequence 4, Appli
13	41	100.0	256	4	US-10-270-073-6	Sequence 6, Appli
14	41	100.0	257	4	US-10-270-073-8	Sequence 8, Appli
15	41	100.0	261	4	US-10-270-071-18	Sequence 18, Appl
16	41	100.0	261	4	US-10-270-073-2	Sequence 2, Appli
17	41	100.0	261	4	US-10-328-190-6	Sequence 6, Appli
18	41	100.0	262	4	US-10-270-071-20	Sequence 20, Appl
19	41	100.0	262	4	US-10-270-071-24	Sequence 24, Appl
20	41	100.0	262	4	US-10-270-071-28	Sequence 28, Appl
21	41	100.0	262	4	US-10-270-071-34	Sequence 34, Appl
22	41	100.0	358	5	US-10-829-388-12	Sequence 12, Appl
23	41	100.0	363	5	US-10-829-388-2	Sequence 2, Appli
24	41	100.0	364	5	US-10-829-388-11	Sequence 11, Appl
25	41	100.0	370	5	US-10-829-388-1	Sequence 1, Appli
26	41	100.0	391	4	US-10-328-190-14	Sequence 14, Appl
27	41	100.0	443	4	US-10-006-773-2	Sequence 2, Appli
28	41	100.0	443	4	US-10-006-771A-2	Sequence 2, Appli
29	41	100.0	669	5	US-10-900-928-3	Sequence 3, Appli
30	34	82.9	73	4	US-10-424-599-233811	Sequence 233811,
31	33	80.5	393	4	US-10-408-765A-2379	Sequence 2379, Ap
32	32	78.0	8	4	US-10-281-479A-30	Sequence 30, Appl
33	32	78.0	8	4	US-10-275-180A-30	Sequence 30, Appl
34	32	78.0	8	4	US-10-286-132A-30	Sequence 30, Appl
35	32	78.0	91	4	US-10-425-115-259994	Sequence 259994,
36	32	78.0	107	4	US-10-184-300A-4	Sequence 4, Appli
37	32	78.0	107	4	US-10-184-300A-5	Sequence 5, Appli
38	32	78.0	107	4	US-10-184-300A-6	Sequence 6, Appli
39	32	78.0	138	4	US-10-424-599-277659	Sequence 277659,
40	32	78.0	160	4	US-10-424-599-235054	Sequence 235054,
41	32	78.0	212	4	US-10-281-479A-72	Sequence 72, Appl
42	32	78.0	212	4	US-10-275-180A-72	Sequence 72, Appl
43	32	78.0	212	4	US-10-286-132A-72	Sequence 72, Appl
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46	32	78.0	213	4	US-10-281-479A-74	Sequence 74, Appl
47	32	78.0	213	4	US-10-281-479A-75	Sequence 75, Appl
48	32	78.0	213	4	US-10-281-479A-76	Sequence 76, Appl
49	32	78.0	213	4	US-10-275-180A-46	Sequence 46, Appl
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51	32	78.0	213	4	US-10-275-180A-74	Sequence 74, Appl
52	32	78.0	213	4	US-10-275-180A-75	Sequence 75, Appl
53	32	78.0	213	4	US-10-275-180A-76	Sequence 76, Appl
54	32	78.0	213	4	US-10-286-132A-46	Sequence 46, Appl
55	32	78.0	213	4	US-10-286-132A-73	Sequence 73, Appl
56	32	78.0	213	4	US-10-286-132A-74	Sequence 74, Appl
57	32	78.0	213	4	US-10-286-132A-75	Sequence 75, Appl
58	32	78.0	213	4	US-10-286-132A-76	Sequence 76, Appl
59	32	78.0	234	4	US-10-281-479A-24	Sequence 24, Appl
60	32	78.0	234	4	US-10-275-180A-24	Sequence 24, Appl
61	32	78.0	234	4	US-10-286-132A-24	Sequence 24, Appl
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72	31	75.6	446	6	US-11-009-008-19	Sequence 19, Appl
73	31	75.6	446	6	US-11-033-663-19	Sequence 19, Appl
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108	29	70.7	171	4	US-10-477-205-5	Sequence 5, Appli
109	29	70.7	171	4	US-10-477-205-6	Sequence 6, Appli
110	29	70.7	171	4	US-10-477-205-7	Sequence 7, Appli
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126	29	70.7	289	5	US-10-745-447-12	Sequence 12, Appl
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138	29	70.7	431	4	US-10-777-524-20	Sequence 20, Appl
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142	29	70.7	439	4	US-10-139-683-8	Sequence 8, Appli
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178	29	70.7	615	4	US-10-777-524-18	Sequence 18, Appl
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318	28	68.3	747	5	US-10-818-770-14	Sequence 14, Appl
319	28	68.3	760	5	US-10-818-770-17	Sequence 17, Appl
320	28	68.3	762	4	US-10-322-281-438	Sequence 438, App
321	28	68.3	763	5	US-10-501-282-6536	Sequence 6536, Ap
322	28	68.3	764	4	US-10-087-192-1542	Sequence 1542, Ap
323	28	68.3	764	4	US-10-408-765A-876	Sequence 876, App
324	28	68.3	765	5	US-10-501-282-6538	Sequence 6538, Ap
325	28	68.3	798	4	US-10-336-753-70	Sequence 70, Appl
326	28	68.3	799	4	US-10-628-525-15	Sequence 15, Appl
327	28	68.3	799	4	US-10-425-115-317969	Sequence 317969,
328	28	68.3	825	4	US-10-437-963-114379	Sequence 114379,
329	28	68.3	825	5	US-10-204-347A-31	Sequence 31, Appl
330	28	68.3	829	3	US-09-792-127-5	Sequence 5, Appli
331	28	68.3	829	5	US-10-674-309-5	Sequence 5, Appli
332	28	68.3	829	5	US-10-204-347A-28	Sequence 28, Appl
333	28	68.3	836	5	US-10-204-347A-29	Sequence 29, Appl
334	28	68.3	844	5	US-10-818-770-18	Sequence 18, Appl
335	28	68.3	855	3	US-09-792-127-4	Sequence 4, Appli
336	28	68.3	855	5	US-10-674-309-4	Sequence 4, Appli
337	28	68.3	870	4	US-10-336-753-54	Sequence 54, Appl
338	28	68.3	878	4	US-10-369-493-474	Sequence 474, App
339	28	68.3	878	4	US-10-369-493-21180	Sequence 21180, A
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341	28	68.3	979	4	US-10-087-192-1539	Sequence 1539, Ap
342	28	68.3	1063	4	US-10-149-310-294	Sequence 294, App
343	28	68.3	1066	4	US-10-282-122A-60726	Sequence 60726, A
344	28	68.3	1068	3	US-09-801-368-242	Sequence 242, App
345	28	68.3	1068	4	US-10-149-310-292	Sequence 292, App
346	28	68.3	1142	4	US-10-425-115-258785	Sequence 258785,
347	28	68.3	1616	4	US-10-425-115-258794	Sequence 258794,
348	28	68.3	1717	4	US-10-437-963-113088	Sequence 113088,
349	28	68.3	2570	5	US-10-450-763-36734	Sequence 36734, A
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353	27	65.9	9	3	US-09-920-262A-6	Sequence 6, Appli
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355	27	65.9	9	5	US-10-728-420B-6	Sequence 6, Appli
356	27	65.9	9	5	US-10-914-015-6	Sequence 6, Appli
357	27	65.9	9	5	US-10-975-883-6	Sequence 6, Appli
358	27	65.9	9	5	US-10-975-740A-6	Sequence 6, Appli
359	27	65.9	9	5	US-10-975-708-6	Sequence 6, Appli
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363	27	65.9	48	5	US-10-958-862-247	Sequence 247, App
364	27	65.9	53	3	US-09-864-761-34078	Sequence 34078, A
365	27	65.9	53	3	US-09-864-761-38885	Sequence 38885, A
366	27	65.9	54	4	US-10-106-698-6927	Sequence 6927, Ap
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372	27	65.9	64	3	US-09-864-761-42523	Sequence 42523, A
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380	27	65.9	76	4	US-10-044-564-300	Sequence 300, App
381	27	65.9	80	4	US-10-622-220-5	Sequence 5, Appli
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384	27	65.9	82	4	US-10-425-115-249651	Sequence 249651,
385	27	65.9	83	4	US-10-425-114-54699	Sequence 54699, A
386	27	65.9	83	4	US-10-622-220-7	Sequence 7, Appli
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389	27	65.9	85	4	US-10-035-568-8	Sequence 8, Appli
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396	27	65.9	103	4	US-10-437-963-171538	Sequence 171538,
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399	27	65.9	107	3	US-09-949-559-11	Sequence 11, Appl
400	27	65.9	107	3	US-09-875-221A-9	Sequence 9, Appli
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403	27	65.9	108	3	US-09-875-221A-104	Sequence 104, App
404	27	65.9	108	3	US-09-920-262A-8	Sequence 8, Appli
405	27	65.9	108	4	US-10-363-829-486	Sequence 486, App
406	27	65.9	108	5	US-10-912-994-8	Sequence 8, Appli
407	27	65.9	108	5	US-10-975-883-8	Sequence 8, Appli
408	27	65.9	108	5	US-10-975-740A-8	Sequence 8, Appli
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413	27	65.9	130	4	US-10-425-115-188423	Sequence 188423,
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416	27	65.9	137	5	US-10-450-763-33293	Sequence 33293, A
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422	27	65.9	152	4	US-10-767-701-42960	Sequence 42960, A
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426	27	65.9	162	4	US-10-437-963-131049	Sequence 131049,
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434	27	65.9	182	4	US-10-292-798-1374	Sequence 1374, Ap
435	27	65.9	182	4	US-10-292-798-1536	Sequence 1536, Ap
436	27	65.9	182	4	US-10-292-798-1632	Sequence 1632, Ap
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438	27	65.9	184	4	US-10-345-072-77	Sequence 77, Appl
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441	27	65.9	187	3	US-09-882-171-417	Sequence 417, App
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444	27	65.9	187	5	US-10-721-922A-224	Sequence 224, App
445	27	65.9	191	3	US-09-738-626-5878	Sequence 5878, Ap
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447	27	65.9	201	4	US-10-282-122A-75436	Sequence 75436, A
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453	27	65.9	209	6	US-11-057-447-120	Sequence 120, App
454	27	65.9	212	4	US-10-335-977-5104	Sequence 5104, Ap
455	27	65.9	214	3	US-09-949-559-128	Sequence 128, App
456	27	65.9	214	3	US-09-875-221A-128	Sequence 128, App
457	27	65.9	214	4	US-10-310-454-4	Sequence 4, Appli
458	27	65.9	214	5	US-10-728-420B-113	Sequence 113, App
459	27	65.9	214	5	US-10-914-015-113	Sequence 113, App
460	27	65.9	219	4	US-10-424-599-275215	Sequence 275215,
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467	27	65.9	237	3	US-09-726-258-25	Sequence 25, Appl
468	27	65.9	237	3	US-09-796-753-36	Sequence 36, Appl
469	27	65.9	243	4	US-10-094-749-1674	Sequence 1674, Ap
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473	27	65.9	260	4	US-10-294-443-179	Sequence 179, App
474	27	65.9	266	4	US-10-424-599-214605	Sequence 214605,
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476	27	65.9	268	3	US-09-853-079-126	Sequence 126, App
477	27	65.9	268	4	US-10-294-443-126	Sequence 126, App
478	27	65.9	272	4	US-10-424-599-235920	Sequence 235920,
479	27	65.9	272	4	US-10-437-963-144082	Sequence 144082,
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496	27	65.9	339	4	US-10-775-965-112	Sequence 112, App
497	27	65.9	339	5	US-10-844-736-2	Sequence 2, Appli
498	27	65.9	339	5	US-10-648-694-2	Sequence 2, Appli
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508	27	65.9	362	4	US-10-425-114-67948	Sequence 232, App
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513	27	65.9	384	5	US-10-732-923-2861	Sequence 2474, Ap
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515	27	65.9	387	3	US-09-837-751-33	Sequence 13, Appl
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524	27	65.9	387	5	US-10-732-923-4907	Sequence 4908, Ap
525	27	65.9	387	5	US-10-732-923-4908	Sequence 2472, Ap
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536	27	65.9	398	4	US-10-252-408-8	Sequence 4, Appli
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543	27	65.9	398	4	US-10-648-136-8	Sequence 8, Appli
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557	27	65.9	450	4	US-10-451-207-9	Sequence 9, Appli
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568	27	65.9	481	4	US-10-335-977-8870	Sequence 8870, Ap
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572	27	65.9	483	4	US-10-389-647-496	Sequence 496, App
573	27	65.9	486	4	US-10-335-977-8871	Sequence 8871, Ap
574	27	65.9	489	4	US-10-408-765A-1998	Sequence 1998, Ap
575	27	65.9	493	5	US-10-732-923-9652	Sequence 9652, Ap
576	27	65.9	493	5	US-10-732-923-9660	Sequence 9660, Ap
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583	27	65.9	527	5	US-10-872-155-588	Sequence 588, App
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586	27	65.9	550	4	US-10-424-599-284384	Sequence 284384,
587	27	65.9	555	4	US-10-437-963-164983	Sequence 164983,
588	27	65.9	564	4	US-10-437-963-177423	Sequence 177423,
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592	27	65.9	584	4	US-10-369-493-1184	Sequence 1184, Ap
593	27	65.9	584	4	US-10-389-566-1968	Sequence 1968, Ap
594	27	65.9	587	4	US-10-389-566-1097	Sequence 1097, Ap
595	27	65.9	588	6	US-11-097-143-36633	Sequence 36633, A
596	27	65.9	589	4	US-10-389-566-1753	Sequence 1753, Ap
597	27	65.9	592	4	US-10-389-566-1504	Sequence 1504, Ap
598	27	65.9	593	4	US-10-389-566-2405	Sequence 2405, Ap
599	27	65.9	594	4	US-10-369-493-21447	Sequence 21447, A
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613	27	65.9	697	4	US-10-335-977-5110	Sequence 5110, Ap
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635	27	65.9	915	6	US-11-056-730-22	Sequence 22, Appl
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677	27	65.9	1250	4	US-10-641-633-15	Sequence 15, Appl
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692	27	65.9	1497	5	US-10-932-819-7	Sequence 7, Appli
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696	27	65.9	1533	4	US-10-281-644-9	Sequence 9, Appli
697	27	65.9	1533	4	US-10-153-244-260	Sequence 260, App
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725	27	65.9	2458	4	US-10-221-278-257	Sequence 257, App
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737	26	63.4	9	3	US-09-977-797A-66	Sequence 66, Appl
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792	26	63.4	107	4	US-10-389-417-10	Sequence 10, Appl
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794	26	63.4	107	4	US-10-452-357-53	Sequence 53, Appl
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797	26	63.4	107	4	US-10-737-252-130	Sequence 130, App
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802	26	63.4	107	5	US-10-842-011-49	Sequence 49, Appl
803	26	63.4	107	5	US-10-506-997-37	Sequence 37, Appl
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852	26	63.4	188	4	US-10-767-701-49136	Sequence 49136, A
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857	26	63.4	200	5	US-10-490-928-23	Sequence 23, Appl
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861	26	63.4	211	4	US-10-189-346-51	Sequence 51, Appl
862	26	63.4	218	4	US-10-424-599-173346	Sequence 173346,
863	26	63.4	219	4	US-10-424-599-177677	Sequence 177677,
864	26	63.4	222	4	US-10-425-114-68985	Sequence 68985, A
865	26	63.4	224	4	US-10-425-114-41304	Sequence 41304, A
866	26	63.4	224	4	US-10-767-701-38798	Sequence 38798, A
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868	26	63.4	230	4	US-10-425-114-60344	Sequence 60344, A
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870	26	63.4	231	4	US-10-428-817A-182	Sequence 182, App
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872	26	63.4	233	3	US-09-900-766-4	Sequence 4, Appli
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875	26	63.4	233	4	US-10-354-948-4	Sequence 4, Appli
876	26	63.4	233	5	US-10-767-687-4	Sequence 4, Appli
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920	26	63.4	320	3	US-09-769-736-80	Sequence 80, Appl
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923	26	63.4	335	4	US-10-264-049-2721	Sequence 2721, Ap
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958	26	63.4	359	4	US-10-292-798-302	Sequence 302, App
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964	26	63.4	360	4	US-10-781-014-510	Sequence 510, App
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967	26	63.4	369	4	US-10-210-172-78	Sequence 78, Appl
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972	26	63.4	382	3	US-09-978-360A-425	Sequence 425, App
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979	26	63.4	387	3	US-09-895-913A-216	Sequence 216, App
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981	26	63.4	387	5	US-10-662-126-35	Sequence 35, Appl
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983	26	63.4	390	5	US-10-884-695-6	Sequence 6, Appli
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986	26	63.4	395	3	US-09-911-927-17	Sequence 17, Appl
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990	26	63.4	417	5	US-10-349-528-16	Sequence 16, Appl
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992	26	63.4	425	3	US-09-881-752A-58	Sequence 58, Appl
993	26	63.4	425	4	US-10-282-122A-58641	Sequence 58641, A
994	26	63.4	428	5	US-10-450-763-59087	Sequence 59087, A
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997	26	63.4	437	4	US-10-270-875-40	Sequence 40, Appl
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ALIGNMENTS

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RESULT 1
US-09-253-794-22
; Sequence 22, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 22:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 8 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-253-794-22

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Db          1 QQYSLYRS 8


RESULT 2
US-10-680-734-22
; Sequence 22, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 22
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-680-734-22

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Db          1 QQYSLYRS 8


RESULT 3
US-10-755-382-22
; Sequence 22, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
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;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 22:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 8 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-755-382-22

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Db          1 QQYSLYRS 8


RESULT 4
US-09-253-794-4
; Sequence 4, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 106 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-253-794-4

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Db         89 QQYSLYRS 96


RESULT 5
US-09-253-794-19
; Sequence 19, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 106 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-253-794-19

  Query Match             100.0%;  Score 41;  DB 3;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
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Db         89 QQYSLYRS 96


RESULT 6
US-10-680-734-4
; Sequence 4, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
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;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
;   LENGTH: 106
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-680-734-4

  Query Match           100.0%;  Score 41;  DB 4;  Length 106;
  Best Local Similarity  100.0%;  Pred. No. 2.6;
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Qy          1 QQYSLYRS 8
              ||||||||
Db         89 QQYSLYRS 96


RESULT 7
US-10-680-734-19
; Sequence 19, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
;   LENGTH: 106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-19

  Query Match           100.0%;  Score 41;  DB 4;  Length 106;
  Best Local Similarity  100.0%;  Pred. No. 2.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db         89 QQYSLYRS 96


RESULT 8
US-10-755-382-4
; Sequence 4, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 106 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-755-382-4

  Query Match           100.0%;  Score 41;  DB 5;  Length 106;
  Best Local Similarity  100.0%;  Pred. No. 2.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db         89 QQYSLYRS 96


RESULT 9
US-10-755-382-19
; Sequence 19, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;
```

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;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 106 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-755-382-19

  Query Match             100.0%;  Score 41;  DB 5;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 2.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db         89 QQYSLYRS 96


RESULT 10
US-10-270-073-4
; Sequence 4, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 115
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14VK deduced amino acid sequence
US-10-270-073-4

  Query Match             100.0%;  Score 41;  DB 4;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 2.9;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db         89 QQYSLYRS 96


RESULT 11
US-10-006-771A-6
; Sequence 6, Application US/10006771A
; Publication No. US20020165360A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen
;  FILE REFERENCE: 002
;  CURRENT APPLICATION NUMBER: US/10/006,771A
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: 60/250,090
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
;   LENGTH: 232
;   TYPE: PRT
;   ORGANISM: Homo sapiens and Mus sp.
US-10-006-771A-6

  Query Match             100.0%;  Score 41;  DB 4;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        108 QQYSLYRS 115


RESULT 12
US-10-377-109-4
; Sequence 4, Application US/10377109
; Publication No. US20040018557A1
; GENERAL INFORMATION:
;  APPLICANT: QU, ZHENGXING
;  APPLICANT:  HANSEN, HANS
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: BISPECIFIC ANTIBODY POINT MUTATIONS FOR ENHANCING RATE
;  TITLE OF INVENTION:  OF CLEARANCE
;  FILE REFERENCE: 018733/1159
;  CURRENT APPLICATION NUMBER: US/10/377,109
;  CURRENT FILING DATE:  2003-03-03
;  PRIOR APPLICATION NUMBER: 60/361,037
;  PRIOR FILING DATE: 2002-03-01
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 232
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-377-109-4

  Query Match             100.0%;  Score 41;  DB 4;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 5.9;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        108 QQYSLYRS 115


RESULT 13
US-10-270-073-6
; Sequence 6, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
```

; PRIOR APPLICATION NUMBER: 60/341,881
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/345,641
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: 60/404,919
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hMN-14-0 amino acid sequence
US-10-270-073-6

Query Match 100.0%; Score 41; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 230 QQYSLYRS 237

RESULT 14
US-10-270-073-8
; Sequence 8, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
; APPLICANT: ROSSI, EDMUND
; APPLICANT: CHANG, CHIEN-HSING KEN
; APPLICANT: GOLDENBERG, DAVID
; TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
; FILE REFERENCE: 042418/0112
; CURRENT APPLICATION NUMBER: US/10/270,073
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/328,835
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/341,881
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/345,641
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: 60/404,919
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hMN-14-1G amino acid sequence
US-10-270-073-8

Query Match 100.0%; Score 41; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 231 QQYSLYRS 238

RESULT 15
US-10-270-071-18
; Sequence 18, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
; APPLICANT: ROSSI, EDMUND
; APPLICANT: CHANG, CHIEN-HSING KEN
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
; FILE REFERENCE: 042418/0110
; CURRENT APPLICATION NUMBER: US/10/270,071
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/328,835
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/341,881
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; OTHER INFORMATION: sequence of hMN14VK
US-10-270-071-18

Query Match 100.0%; Score 41; DB 4; Length 261;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 235 QQYSLYRS 242

RESULT 16
US-10-270-073-2
; Sequence 2, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
; APPLICANT: ROSSI, EDMUND
; APPLICANT: CHANG, CHIEN-HSING KEN
; APPLICANT: GOLDENBERG, DAVID
; TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
; FILE REFERENCE: 042418/0112
; CURRENT APPLICATION NUMBER: US/10/270,073
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/328,835
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/341,881
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/345,641
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: 60/404,919
; PRIOR FILING DATE: 2002-08-22
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hMN-14scFv-L5 amino acid sequence
US-10-270-073-2

Query Match 100.0%; Score 41; DB 4; Length 261;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYSLYRS 8
||||||||
Db 235 QQYSLYRS 242

RESULT 17
US-10-328-190-6
; Sequence 6, Application US/10328190
; Publication No. US20030162709A1
; GENERAL INFORMATION:

```
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID M.
;  TITLE OF INVENTION: METHODS OF GENERATING MULTISPECIFIC, MULTIVALENT AGENTS
;  TITLE OF INVENTION:  FROM VH AND VL DOMAINS
;  FILE REFERENCE: 042418/0115
;  CURRENT APPLICATION NUMBER: US/10/328,190
;  CURRENT FILING DATE:  2003-04-03
;  PRIOR APPLICATION NUMBER: 60/342,103
;  PRIOR FILING DATE: 2001-12-26
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: hMN14-scFv-L5
;   OTHER INFORMATION: protein sequence
US-10-328-190-6

  Query Match            100.0%;  Score 41;  DB 4;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        235 QQYSLYRS 242


RESULT 18
US-10-270-071-20
; Sequence 20, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 262
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of polypeptide 1 of BS1
US-10-270-071-20

  Query Match            100.0%;  Score 41;  DB 4;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        236 QQYSLYRS 243


RESULT 19
US-10-270-071-24
; Sequence 24, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 262
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of polypeptide 1 of BS1.5
US-10-270-071-24

  Query Match            100.0%;  Score 41;  DB 4;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        236 QQYSLYRS 243


RESULT 20
US-10-270-071-28
; Sequence 28, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 262
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of polypeptide 1 of BS2
US-10-270-071-28

  Query Match            100.0%;  Score 41;  DB 4;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        236 QQYSLYRS 243


RESULT 21
US-10-270-071-34
; Sequence 34, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
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;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
;   LENGTH: 262
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence for polypetide 1 of BS1.5H (h679XhMN14 bispecific
;   OTHER INFORMATION: diabody)
US-10-270-071-34

  Query Match             100.0%;  Score 41;  DB 4;  Length 262;
  Best Local Similarity   100.0%;  Pred. No. 6.6;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        236 QQYSLYRS 243


RESULT 22
US-10-829-388-12
; Sequence 12, Application US/10829388
; Publication No. US20050003403A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN HSING
;  APPLICANT:  MCBRIDE, WILLIAM J.
;  TITLE OF INVENTION: POLYVALENT PROTEIN COMPLEX
;  FILE REFERENCE: 41133-0006US1
;  CURRENT APPLICATION NUMBER: US/10/829,388
;  CURRENT FILING DATE:  2004-04-22
;  PRIOR APPLICATION NUMBER: 60/464,532
;  PRIOR FILING DATE: 2003-04-22
;  PRIOR APPLICATION NUMBER: 60/525,391
;  PRIOR FILING DATE: 2003-11-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
;   LENGTH: 358
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chimeric sequence from multiple species
US-10-829-388-12

  Query Match             100.0%;  Score 41;  DB 5;  Length 358;
  Best Local Similarity   100.0%;  Pred. No. 9.1;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db         90 QQYSLYRS 97


RESULT 23
US-10-829-388-2
; Sequence 2, Application US/10829388
; Publication No. US20050003403A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN HSING
;  APPLICANT:  MCBRIDE, WILLIAM J.
;  TITLE OF INVENTION: POLYVALENT PROTEIN COMPLEX
;  FILE REFERENCE: 41133-0006US1
;  CURRENT APPLICATION NUMBER: US/10/829,388
;  CURRENT FILING DATE:  2004-04-22
;  PRIOR APPLICATION NUMBER: 60/464,532
;  PRIOR FILING DATE: 2003-04-22
;  PRIOR APPLICATION NUMBER: 60/525,391
;  PRIOR FILING DATE: 2003-11-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 363
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chimeric sequence from multiple species
US-10-829-388-2

  Query Match             100.0%;  Score 41;  DB 5;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 9.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db         95 QQYSLYRS 102


RESULT 24
US-10-829-388-11
; Sequence 11, Application US/10829388
; Publication No. US20050003403A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN HSING
;  APPLICANT:  MCBRIDE, WILLIAM J.
;  TITLE OF INVENTION: POLYVALENT PROTEIN COMPLEX
;  FILE REFERENCE: 41133-0006US1
;  CURRENT APPLICATION NUMBER: US/10/829,388
;  CURRENT FILING DATE:  2004-04-22
;  PRIOR APPLICATION NUMBER: 60/464,532
;  PRIOR FILING DATE: 2003-04-22
;  PRIOR APPLICATION NUMBER: 60/525,391
;  PRIOR FILING DATE: 2003-11-24
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
;   LENGTH: 364
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chimeric sequence from multiple species
US-10-829-388-11

  Query Match             100.0%;  Score 41;  DB 5;  Length 364;
  Best Local Similarity   100.0%;  Pred. No. 9.3;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        214 QQYSLYRS 221


RESULT 25
US-10-829-388-1
; Sequence 1, Application US/10829388
; Publication No. US20050003403A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN HSING
;  APPLICANT:  MCBRIDE, WILLIAM J.
;  TITLE OF INVENTION: POLYVALENT PROTEIN COMPLEX
;  FILE REFERENCE: 41133-0006US1
;  CURRENT APPLICATION NUMBER: US/10/829,388
;  CURRENT FILING DATE:  2004-04-22
;  PRIOR APPLICATION NUMBER: 60/464,532
;  PRIOR FILING DATE: 2003-04-22
;  PRIOR APPLICATION NUMBER: 60/525,391
;  PRIOR FILING DATE: 2003-11-24
```

```
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 370
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Chimeric sequence from multiple species
US-10-829-388-1

  Query Match            100.0%;  Score 41;  DB 5;  Length 370;
  Best Local Similarity  100.0%;  Pred. No. 9.4;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        220 QQYSLYRS 227


RESULT 26
US-10-328-190-14
; Sequence 14, Application US/10328190
; Publication No. US20030162709A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID M.
;  TITLE OF INVENTION: METHODS OF GENERATING MULTISPECIFIC, MULTIVALENT AGENTS
;  TITLE OF INVENTION:  FROM VH AND VL DOMAINS
;  FILE REFERENCE: 042418/0115
;  CURRENT APPLICATION NUMBER: US/10/328,190
;  CURRENT FILING DATE:  2003-04-03
;  PRIOR APPLICATION NUMBER: 60/342,103
;  PRIOR FILING DATE: 2001-12-26
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 391
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Protein
;   OTHER INFORMATION: sequence for VL-chain of TS1
US-10-328-190-14

  Query Match            100.0%;  Score 41;  DB 4;  Length 391;
  Best Local Similarity  100.0%;  Pred. No. 10;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        365 QQYSLYRS 372


RESULT 27
US-10-006-773-2
; Sequence 2, Application US/10006773
; Publication No. US20020132983A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor Anti
;  FILE REFERENCE: 003
;  CURRENT APPLICATION NUMBER: US/10/006,773
;  CURRENT FILING DATE:  2001-12-10
;  PRIOR APPLICATION NUMBER: 60/250,089
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 443
;   TYPE: PRT
;   ORGANISM: Homo sapiens and Mus sp.
US-10-006-773-2

  Query Match            100.0%;  Score 41;  DB 4;  Length 443;
  Best Local Similarity  100.0%;  Pred. No. 11;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        108 QQYSLYRS 115


RESULT 28
US-10-006-771A-2
; Sequence 2, Application US/10006771A
; Publication No. US20020165360A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen
;  FILE REFERENCE: 002
;  CURRENT APPLICATION NUMBER: US/10/006,771A
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: 60/250,090
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 443
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-006-771A-2

  Query Match            100.0%;  Score 41;  DB 4;  Length 443;
  Best Local Similarity  100.0%;  Pred. No. 11;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        108 QQYSLYRS 115


RESULT 29
US-10-900-928-3
; Sequence 3, Application US/10900928
; Publication No. US20050069552A1
; GENERAL INFORMATION:
;  APPLICANT: Bleck, Gregory T.
;  APPLICANT:  York, Donna
;  APPLICANT:  Collins, Ian
;  TITLE OF INVENTION: Fusion Antibodies
;  FILE REFERENCE: GALA-09135
;  CURRENT APPLICATION NUMBER: US/10/900,928
;  CURRENT FILING DATE:  2004-07-28
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 669
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-900-928-3

  Query Match            100.0%;  Score 41;  DB 5;  Length 669;
  Best Local Similarity  100.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||||||||
Db        545 QQYSLYRS 552


RESULT 30
US-10-424-599-233811
; Sequence 233811, Application US/10424599
```

```
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 233811
;   LENGTH: 73
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_53156C.1.pep
US-10-424-599-233811

  Query Match             82.9%;  Score 34;  DB 4;  Length 73;
  Best Local Similarity   75.0%;  Pred. No. 41;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |:|:||||
Db          8 QRYNLYRS 15


RESULT 31
US-10-408-765A-2379
; Sequence 2379, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
;  APPLICANT: Ghosh, Soumitra S.
;  APPLICANT:  Fahy, Eoin D.
;  APPLICANT:  Zhang, Bing
;  APPLICANT:  Gibson, Bradford W.
;  APPLICANT:  Taylor, Steven W.
;  APPLICANT:  Glenn, Gary M.
;  APPLICANT:  Warnock, Dale E.
;  TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
;  TITLE OF INVENTION:  IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
;  FILE REFERENCE: 660088.465
;  CURRENT APPLICATION NUMBER: US/10/408,765A
;  CURRENT FILING DATE:  2003-04-04
;  NUMBER OF SEQ ID NOS: 3077
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2379
;   LENGTH: 393
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-765A-2379

  Query Match             80.5%;  Score 33;  DB 4;  Length 393;
  Best Local Similarity   85.7%;  Pred. No. 3.6e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              ||| |||
Db        231 QQYELYR 237


RESULT 32
US-10-281-479A-30
; Sequence 30, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  Oshumi, Jun
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERA
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 21085.0029U6
;  CURRENT APPLICATION NUMBER: US/10/281,479A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 60/391,478
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthet
US-10-281-479A-30

  Query Match             78.0%;  Score 32;  DB 4;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 1.7e+06;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| ||:
Db          1 QQYSSYRT 8


RESULT 33
US-10-275-180A-30
; Sequence 30, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSI
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-275-180A-30

  Query Match             78.0%;  Score 32;  DB 4;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 1.7e+06;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| ||:
Db          1 QQYSSYRT 8


RESULT 34
US-10-286-132A-30
```

```
; Sequence 30, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
;  APPLICANT: Zhou, Tong
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
;  TITLE OF INVENTION:  APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U7
;  CURRENT APPLICATION NUMBER: US/10/286,132A
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: US 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 30
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-30

  Query Match             78.0%;  Score 32;  DB 4;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 1.7e+06;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| ||:
Db          1 QQYSSYRT 8


RESULT 35
US-10-425-115-259994
; Sequence 259994, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 259994
;   LENGTH: 91
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_168732C.1.pep
US-10-425-115-259994

  Query Match             78.0%;  Score 32;  DB 4;  Length 91;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYR 7
              ||||||
Db          1 QYSLYR 6


RESULT 36
US-10-184-300A-4
; Sequence 4, Application US/10184300A
; Publication No. US20030124056A1
; GENERAL INFORMATION:
;  APPLICANT: Carr, Francis J.
;  APPLICANT:  Hamilton, Anita A.
;  TITLE OF INVENTION: Carrier molecules
;  FILE REFERENCE: 229752001700
;  CURRENT APPLICATION NUMBER: US/10/184,300A
;  CURRENT FILING DATE:  2002-10-29
;  PRIOR APPLICATION NUMBER: PCT/AU02/00827
;  PRIOR FILING DATE: 2002-10-26
;  PRIOR APPLICATION NUMBER: US 60/301,154
;  PRIOR FILING DATE: 2001-06-26
;  PRIOR APPLICATION NUMBER: US 60/300,947
;  PRIOR FILING DATE: 2001-06-27
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Synthetic construct of 3B6DIVKv1
US-10-184-300A-4

  Query Match             78.0%;  Score 32;  DB 4;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              ||||||
Db         89 QQYSLY 94


RESULT 37
US-10-184-300A-5
; Sequence 5, Application US/10184300A
; Publication No. US20030124056A1
; GENERAL INFORMATION:
;  APPLICANT: Carr, Francis J.
;  APPLICANT:  Hamilton, Anita A.
;  TITLE OF INVENTION: Carrier molecules
;  FILE REFERENCE: 229752001700
;  CURRENT APPLICATION NUMBER: US/10/184,300A
;  CURRENT FILING DATE:  2002-10-29
;  PRIOR APPLICATION NUMBER: PCT/AU02/00827
;  PRIOR FILING DATE: 2002-10-26
;  PRIOR APPLICATION NUMBER: US 60/301,154
;  PRIOR FILING DATE: 2001-06-26
;  PRIOR APPLICATION NUMBER: US 60/300,947
;  PRIOR FILING DATE: 2001-06-27
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Synthetic construct of 3B6DIVKv4
US-10-184-300A-5

  Query Match             78.0%;  Score 32;  DB 4;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              ||||||
Db         89 QQYSLY 94
```

```
RESULT 38
US-10-184-300A-6
; Sequence 6, Application US/10184300A
; Publication No. US20030124056A1
; GENERAL INFORMATION:
;  APPLICANT: Carr, Francis J.
;  APPLICANT:  Hamilton, Anita A.
;  TITLE OF INVENTION: Carrier molecules
;  FILE REFERENCE: 229752001700
;  CURRENT APPLICATION NUMBER: US/10/184,300A
;  CURRENT FILING DATE:  2002-10-29
;  PRIOR APPLICATION NUMBER: PCT/AU02/00827
;  PRIOR FILING DATE: 2002-10-26
;  PRIOR APPLICATION NUMBER: US 60/301,154
;  PRIOR FILING DATE: 2001-06-26
;  PRIOR APPLICATION NUMBER: US 60/300,947
;  PRIOR FILING DATE: 2001-06-27
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ()..()
;   OTHER INFORMATION: Synthetic construct of 3B6DIVKv7
US-10-184-300A-6

  Query Match             78.0%;  Score 32;  DB 4;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              ||||||
Db         89 QQYSLY 94


RESULT 39
US-10-424-599-277659
; Sequence 277659, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 277659
;   LENGTH: 138
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_9274C.1.pep
US-10-424-599-277659

  Query Match             78.0%;  Score 32;  DB 4;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              ||||||
Db        115 QQYSLY 120


RESULT 40
US-10-424-599-235054
; Sequence 235054, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa Thomas J
;  APPLICANT:  Kovalic David K
;  APPLICANT:  Zhou Yihua
;  APPLICANT:  Cao Yongwei
;  TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants and Uses Thereof for Plant Improvement
;  FILE REFERENCE: 38-21(53223)B
;  CURRENT APPLICATION NUMBER: US/10/424,599
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 235054
;   LENGTH: 160
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (1)..(160)
;   OTHER INFORMATION: unsure at all Xaa locations
;   FEATURE:
;   OTHER INFORMATION: Clone ID: PAT_MRT3847_54282C.1.pep
US-10-424-599-235054

  Query Match             78.0%;  Score 32;  DB 4;  Length 160;
  Best Local Similarity   85.7%;  Pred. No. 2.2e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              ||| |||
Db         84 QQYRLYR 90


RESULT 41
US-10-281-479A-72
; Sequence 72, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  Oshumi, Jun
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERA
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 21085.0029U6
;  CURRENT APPLICATION NUMBER: US/10/281,479A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 60/391,478
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 72
;   LENGTH: 212
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthet
US-10-281-479A-72

  Query Match             78.0%;  Score 32;  DB 4;  Length 212;
  Best Local Similarity   75.0%;  Pred. No. 3e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          1 QQYSLYRS 8
              |||| ||:
Db         89 QQYSSYRT 96


RESULT 42
US-10-275-180A-72
; Sequence 72, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 72
;   LENGTH: 212
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-275-180A-72

  Query Match             78.0%;  Score 32;  DB 4;  Length 212;
  Best Local Similarity   75.0%;  Pred. No. 3e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
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Db         89 QQYSSYRT 96


RESULT 43
US-10-286-132A-72
; Sequence 72, Application US/10286132A
; Publication No. US20030198637A1
; GENERAL INFORMATION:
;  APPLICANT: Zhou, Tong
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
;  TITLE OF INVENTION:  APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U7
;  CURRENT APPLICATION NUMBER: US/10/286,132A
;  CURRENT FILING DATE:  2003-01-22
;  PRIOR APPLICATION NUMBER: US 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: US 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 72
;   LENGTH: 212
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030198637A1e = Synthe
US-10-286-132A-72

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  Best Local Similarity   75.0%;  Pred. No. 3e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| ||:
Db         89 QQYSSYRT 96


RESULT 44
US-10-281-479A-46
; Sequence 46, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  Oshumi, Jun
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERA
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 21085.0029U6
;  CURRENT APPLICATION NUMBER: US/10/281,479A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 60/391,478
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthet
US-10-281-479A-46

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  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| ||:
Db         89 QQYSSYRT 96


RESULT 45
US-10-281-479A-73
; Sequence 73, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  Oshumi, Jun
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERA
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 21085.0029U6
;  CURRENT APPLICATION NUMBER: US/10/281,479A
;  CURRENT FILING DATE:  2003-01-28
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;  PRIOR APPLICATION NUMBER: 60/391,478
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe
US-10-281-479A-73

  Query Match             78.0%;  Score 32;  DB 4;  Length 213;
  Best Local Similarity   75.0%;  Pred. No. 3e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| ||:
Db         89 QQYSSYRT 96


RESULT 46
US-10-281-479A-74
; Sequence 74, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  Oshumi, Jun
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THER
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 21085.0029U6
;  CURRENT APPLICATION NUMBER: US/10/281,479A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 60/391,478
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe
US-10-281-479A-74

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  Best Local Similarity   75.0%;  Pred. No. 3e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| ||:
Db         89 QQYSSYRT 96


RESULT 47
US-10-281-479A-75
; Sequence 75, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  Oshumi, Jun
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERA
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 21085.0029U6
;  CURRENT APPLICATION NUMBER: US/10/281,479A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 60/391,478
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,344
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 75
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthet
US-10-281-479A-75

  Query Match             78.0%;  Score 32;  DB 4;  Length 213;
  Best Local Similarity   75.0%;  Pred. No. 3e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| ||:
Db         89 QQYSSYRT 96


RESULT 48
US-10-281-479A-76
; Sequence 76, Application US/10281479A
; Publication No. US20030133932A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  APPLICANT:  Oshumi, Jun
;  APPLICANT:  LoBuglio, Albert S.
;  APPLICANT:  Buchsbaum, Donald J.
;  TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
;  TITLE OF INVENTION:  FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERA
;  TITLE OF INVENTION:  AGENTS
;  FILE REFERENCE: 21085.0029U6
;  CURRENT APPLICATION NUMBER: US/10/281,479A
;  CURRENT FILING DATE:  2003-01-28
;  PRIOR APPLICATION NUMBER: 60/391,478
;  PRIOR FILING DATE: 2002-06-24
;  PRIOR APPLICATION NUMBER: 60/346,402
;  PRIOR FILING DATE: 2001-11-01
;  PRIOR APPLICATION NUMBER: PCT/US01/14151
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,344
;  PRIOR FILING DATE: 2000-05-02
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;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 76
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030133932A1e = Synthe
US-10-281-479A-76

  Query Match             78.0%;  Score 32;  DB 4;  Length 213;
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  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| ||:
Db         89 QQYSSYRT 96


RESULT 49
US-10-275-180A-46
; Sequence 46, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 46
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-275-180A-46

  Query Match             78.0%;  Score 32;  DB 4;  Length 213;
  Best Local Similarity   75.0%;  Pred. No. 3e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
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Db         89 QQYSSYRT 96


RESULT 50
US-10-275-180A-73
; Sequence 73, Application US/10275180A
; Publication No. US20030190687A1
; GENERAL INFORMATION:
;  APPLICANT: The UAB Research Foundation
;  APPLICANT:  Zhou, Tong
;  APPLICANT:  Ichikawa, Kimihisa
;  APPLICANT:  Kimberly, Robert P.
;  APPLICANT:  Koopman, William J.
;  TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOS
;  TITLE OF INVENTION:  INDUCING LIGAND RECEPTOR AND USES THEREOF
;  FILE REFERENCE: 21085.0029U5
;  CURRENT APPLICATION NUMBER: US/10/275,180A
;  CURRENT FILING DATE:  2002-10-31
;  NUMBER OF SEQ ID NOS: 102
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
;   LENGTH: 213
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
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;   OTHER INFORMATION: Description of Artificial Sequence:/No. US20030190687A1e =
;   OTHER INFORMATION: Synthetic Construct
US-10-275-180A-73

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  Best Local Similarity   75.0%;  Pred. No. 3e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| ||:
Db         89 QQYSSYRT 96


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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:44:01 ; Search time 6.79452 Seconds
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Title: US-10-755-382-22
Perfect score: 41
Sequence: 1 QQYSLYRS 8

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Searched: 169630 seqs, 28622889 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	30	73.2	343	7	US-11-087-099-1522	Sequence 1522, Ap
2	30	73.2	1296	6	US-10-615-668-3	Sequence 3, Appli
3	29	70.7	72	6	US-10-467-657-4880	Sequence 4880, Ap
4	29	70.7	431	7	US-11-198-819-14	Sequence 14, Appl
5	29	70.7	431	7	US-11-198-819-20	Sequence 20, Appl
6	29	70.7	439	7	US-11-198-819-12	Sequence 12, Appl
7	29	70.7	597	6	US-10-884-730-381	Sequence 381, App
8	29	70.7	615	7	US-11-198-819-16	Sequence 16, Appl
9	29	70.7	615	7	US-11-198-819-18	Sequence 18, Appl
10	29	70.7	651	7	US-11-198-819-22	Sequence 22, Appl
11	29	70.7	654	6	US-10-528-031-1	Sequence 1, Appli
12	29	70.7	914	6	US-10-491-468-47	Sequence 47, Appl
13	29	70.7	1381	6	US-10-467-657-178	Sequence 178, App
14	29	70.7	1381	6	US-10-467-657-3726	Sequence 3726, Ap
15	29	70.7	1767	7	US-11-052-554A-372	Sequence 372, App
16	28	68.3	110	7	US-11-096-568A-34065	Sequence 34065, A
17	28	68.3	160	7	US-11-087-099-5754	Sequence 5754, Ap
18	28	68.3	215	6	US-10-793-626-528	Sequence 528, App
19	28	68.3	288	7	US-11-096-568A-23199	Sequence 23199, A
20	28	68.3	446	7	US-11-119-351-8	Sequence 8, Appli
21	28	68.3	476	7	US-11-072-512-3659	Sequence 3659, Ap
22	28	68.3	499	7	US-11-096-568A-25749	Sequence 25749, A
23	28	68.3	558	7	US-11-096-568A-25748	Sequence 25748, A
24	28	68.3	603	7	US-11-096-568A-25747	Sequence 25747, A
25	27	65.9	76	7	US-11-054-281-300	Sequence 300, App
26	27	65.9	103	6	US-10-771-257-99	Sequence 99, Appl
27	27	65.9	103	6	US-10-771-257-110	Sequence 110, App
28	27	65.9	103	6	US-10-771-257-111	Sequence 111, App
29	27	65.9	103	6	US-10-771-257-113	Sequence 113, App
30	27	65.9	148	6	US-10-530-253-22	Sequence 22, Appl
31	27	65.9	148	7	US-11-072-512-2902	Sequence 2902, Ap
32	27	65.9	292	7	US-11-096-568A-34286	Sequence 34286, A
33	27	65.9	324	7	US-11-096-568A-34285	Sequence 34285, A
34	27	65.9	350	7	US-11-096-568A-34284	Sequence 34284, A
35	27	65.9	384	7	US-11-087-099-6378	Sequence 6378, Ap
36	27	65.9	387	7	US-11-202-731-33	Sequence 33, Appl
37	27	65.9	398	6	US-10-821-234-1583	Sequence 1583, Ap
38	27	65.9	409	7	US-11-096-568A-33433	Sequence 33433, A
39	27	65.9	410	7	US-11-096-568A-33432	Sequence 33432, A
40	27	65.9	427	7	US-11-096-568A-33431	Sequence 33431, A
41	27	65.9	442	7	US-11-018-868-49	Sequence 49, Appl
42	27	65.9	485	7	US-11-087-099-398	Sequence 398, App
43	27	65.9	488	7	US-11-010-239-14	Sequence 14, Appl
44	27	65.9	672	6	US-10-499-290-2	Sequence 2, Appli
45	27	65.9	697	7	US-11-052-554A-110	Sequence 110, App
46	27	65.9	841	7	US-11-052-554A-102	Sequence 102, App
47	27	65.9	852	6	US-10-517-939-120	Sequence 120, App
48	27	65.9	915	7	US-11-144-987-16	Sequence 16, Appl
49	27	65.9	915	7	US-11-144-987-22	Sequence 22, Appl
50	27	65.9	915	7	US-11-205-935-16	Sequence 16, Appl
51	27	65.9	915	7	US-11-205-935-22	Sequence 22, Appl
52	27	65.9	917	7	US-11-144-987-18	Sequence 18, Appl
53	27	65.9	917	7	US-11-144-987-20	Sequence 20, Appl
54	27	65.9	917	7	US-11-144-987-24	Sequence 24, Appl
55	27	65.9	917	7	US-11-144-987-26	Sequence 26, Appl
56	27	65.9	917	7	US-11-205-935-18	Sequence 18, Appl
57	27	65.9	917	7	US-11-205-935-20	Sequence 20, Appl
58	27	65.9	917	7	US-11-205-935-24	Sequence 24, Appl
59	27	65.9	917	7	US-11-205-935-26	Sequence 26, Appl
60	27	65.9	1078	7	US-11-165-211-43	Sequence 43, Appl
61	27	65.9	1078	7	US-11-165-226-53	Sequence 53, Appl
62	27	65.9	1288	7	US-11-052-554A-93	Sequence 93, Appl
63	27	65.9	1495	7	US-11-019-711-111	Sequence 111, App
64	27	65.9	2871	7	US-11-124-367A-264	Sequence 264, App
65	26	63.4	9	6	US-10-982-357-20	Sequence 20, Appl
66	26	63.4	9	6	US-10-982-357-37	Sequence 37, Appl
67	26	63.4	9	7	US-11-097-812-59	Sequence 59, Appl
68	26	63.4	9	7	US-11-097-812-122	Sequence 122, App
69	26	63.4	45	6	US-10-467-657-7816	Sequence 7816, Ap
70	26	63.4	101	5	US-09-978-360A-685	Sequence 685, App
71	26	63.4	105	7	US-11-097-812-53	Sequence 53, Appl
72	26	63.4	107	6	US-10-982-357-6	Sequence 6, Appli
73	26	63.4	107	6	US-10-982-357-42	Sequence 42, Appl
74	26	63.4	107	6	US-10-982-357-44	Sequence 44, Appl
75	26	63.4	107	6	US-10-982-357-48	Sequence 48, Appl
76	26	63.4	107	6	US-10-982-357-50	Sequence 50, Appl
77	26	63.4	108	7	US-11-097-812-45	Sequence 45, Appl
78	26	63.4	108	7	US-11-097-812-46	Sequence 46, Appl
79	26	63.4	108	7	US-11-097-812-50	Sequence 50, Appl
80	26	63.4	108	7	US-11-097-812-51	Sequence 51, Appl
81	26	63.4	108	7	US-11-097-812-52	Sequence 52, Appl
82	26	63.4	109	7	US-11-097-812-37	Sequence 37, Appl
83	26	63.4	109	7	US-11-097-812-42	Sequence 42, Appl
84	26	63.4	109	7	US-11-097-812-43	Sequence 43, Appl
85	26	63.4	109	7	US-11-097-812-48	Sequence 48, Appl
86	26	63.4	109	7	US-11-097-812-54	Sequence 54, Appl
87	26	63.4	109	7	US-11-097-812-113	Sequence 113, App
88	26	63.4	115	7	US-11-097-812-38	Sequence 38, Appl
89	26	63.4	127	6	US-10-982-357-28	Sequence 28, Appl
90	26	63.4	174	5	US-09-978-360A-556	Sequence 556, App
91	26	63.4	219	7	US-11-096-568A-12944	Sequence 12944, A
92	26	63.4	229	6	US-10-501-035-231	Sequence 231, App
93	26	63.4	229	6	US-10-501-035-232	Sequence 232, App
94	26	63.4	233	7	US-11-022-562-226	Sequence 226, App
95	26	63.4	235	7	US-11-096-568A-12943	Sequence 12943, A
96	26	63.4	285	7	US-11-096-568A-4297	Sequence 4297, Ap
97	26	63.4	297	7	US-11-096-568A-12942	Sequence 12942, A
98	26	63.4	336	6	US-10-499-715-8	Sequence 8, Appli

99	26	63.4	344	6	US-10-995-561-524	Sequence 524, App
100	26	63.4	344	6	US-10-995-561-525	Sequence 525, App
101	26	63.4	355	7	US-11-096-568A-20983	Sequence 20983, A
102	26	63.4	355	7	US-11-096-568A-21509	Sequence 21509, A
103	26	63.4	359	7	US-11-232-405A-4	Sequence 4, Appli
104	26	63.4	360	7	US-11-082-389-90	Sequence 90, Appl
105	26	63.4	360	7	US-11-082-389-92	Sequence 92, Appl
106	26	63.4	367	7	US-11-096-568A-4296	Sequence 4296, Ap
107	26	63.4	382	5	US-09-978-360A-425	Sequence 425, App
108	26	63.4	383	6	US-10-467-657-554	Sequence 554, App
109	26	63.4	395	7	US-11-053-185-8	Sequence 8, Appli
110	26	63.4	417	7	US-11-096-568A-32727	Sequence 32727, A
111	26	63.4	419	7	US-11-096-568A-32726	Sequence 32726, A
112	26	63.4	439	7	US-11-096-568A-32725	Sequence 32725, A
113	26	63.4	448	7	US-11-087-099-1272	Sequence 1272, Ap
114	26	63.4	448	7	US-11-087-099-7016	Sequence 7016, Ap
115	26	63.4	448	7	US-11-096-568A-20982	Sequence 20982, A
116	26	63.4	448	7	US-11-096-568A-21508	Sequence 21508, A
117	26	63.4	488	6	US-10-793-626-2308	Sequence 2308, Ap
118	26	63.4	542	7	US-11-098-686-11331	Sequence 11331, A
119	26	63.4	664	6	US-10-793-626-1258	Sequence 1258, Ap
120	26	63.4	665	6	US-10-491-468-10	Sequence 10, Appl
121	26	63.4	677	7	US-11-010-239-48	Sequence 48, Appl
122	26	63.4	730	7	US-11-113-424-50	Sequence 50, Appl
123	26	63.4	754	7	US-11-098-686-10899	Sequence 10899, A
124	26	63.4	872	7	US-11-077-550-145	Sequence 145, App
125	26	63.4	879	7	US-11-077-550-143	Sequence 143, App
126	26	63.4	887	7	US-11-077-550-147	Sequence 147, App
127	26	63.4	1045	7	US-11-113-424-54	Sequence 54, Appl
128	26	63.4	1094	6	US-10-821-234-1097	Sequence 1097, Ap
129	26	63.4	1122	6	US-10-821-234-1657	Sequence 1657, Ap
130	26	63.4	1122	6	US-10-964-313-4	Sequence 4, Appli
131	26	63.4	1315	7	US-11-077-550-141	Sequence 141, App
132	26	63.4	2333	6	US-10-453-372-170	Sequence 170, App
133	26	63.4	2376	7	US-11-096-051-4	Sequence 4, Appli
134	26	63.4	2591	6	US-10-453-372-718	Sequence 718, App
135	26	63.4	2602	6	US-10-453-372-716	Sequence 716, App
136	26	63.4	2617	6	US-10-453-372-666	Sequence 666, App
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139	26	63.4	2617	6	US-10-453-372-736	Sequence 736, App
140	26	63.4	2617	6	US-10-453-372-738	Sequence 738, App
141	26	63.4	2617	6	US-10-453-372-740	Sequence 740, App
142	26	63.4	2617	6	US-10-453-372-742	Sequence 742, App
143	26	63.4	2617	6	US-10-453-372-744	Sequence 744, App
144	26	63.4	2617	6	US-10-453-372-746	Sequence 746, App
145	26	63.4	2617	6	US-10-453-372-748	Sequence 748, App
146	26	63.4	2617	6	US-10-453-372-750	Sequence 750, App
147	26	63.4	2662	6	US-10-453-372-114	Sequence 114, App
148	26	63.4	2715	7	US-11-096-051-2	Sequence 2, Appli
149	26	63.4	2715	7	US-11-113-424-51	Sequence 51, Appl
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151	26	63.4	2724	6	US-10-453-372-148	Sequence 148, App
152	26	63.4	2725	7	US-11-096-051-8	Sequence 8, Appli
153	26	63.4	2733	6	US-10-453-372-136	Sequence 136, App
154	26	63.4	2733	6	US-10-453-372-142	Sequence 142, App
155	26	63.4	2733	6	US-10-453-372-146	Sequence 146, App
156	26	63.4	2733	6	US-10-453-372-150	Sequence 150, App
157	26	63.4	2733	6	US-10-453-372-154	Sequence 154, App
158	26	63.4	2759	6	US-10-453-372-168	Sequence 168, App
159	26	63.4	2765	6	US-10-453-372-116	Sequence 116, App
160	26	63.4	2769	7	US-11-113-424-14	Sequence 14, Appl
161	26	63.4	2897	6	US-10-499-715-2	Sequence 2, Appli
162	25.5	62.2	1565	6	US-10-467-657-2704	Sequence 2704, Ap
163	25	61.0	9	6	US-10-989-767A-305	Sequence 305, App
164	25	61.0	10	6	US-10-989-767A-271	Sequence 271, App
165	25	61.0	10	6	US-10-989-767A-373	Sequence 373, App
166	25	61.0	10	6	US-10-989-767A-605	Sequence 605, App
167	25	61.0	10	7	US-11-107-096-33	Sequence 33, Appl
168	25	61.0	93	6	US-10-821-234-1335	Sequence 1335, Ap
169	25	61.0	98	6	US-10-505-263-70	Sequence 70, Appl
170	25	61.0	107	7	US-11-112-240-12	Sequence 12, Appl
171	25	61.0	107	7	US-11-112-304A-12	Sequence 12, Appl
172	25	61.0	108	5	US-09-978-360A-440	Sequence 440, App
173	25	61.0	108	7	US-11-049-536-244	Sequence 244, App
174	25	61.0	132	6	US-10-504-389A-53	Sequence 53, Appl
175	25	61.0	136	7	US-11-072-512-3737	Sequence 3737, Ap
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178	25	61.0	167	6	US-10-931-198-46	Sequence 46, Appl
179	25	61.0	201	7	US-11-082-389-138	Sequence 138, App
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182	25	61.0	227	6	US-10-467-657-1514	Sequence 1514, Ap
183	25	61.0	237	7	US-11-096-568A-12231	Sequence 12231, A
184	25	61.0	239	7	US-11-054-515-1882	Sequence 1882, Ap
185	25	61.0	239	7	US-11-054-515-1922	Sequence 1922, Ap
186	25	61.0	241	7	US-11-054-515-1889	Sequence 1889, Ap
187	25	61.0	241	7	US-11-054-515-1901	Sequence 1901, Ap
188	25	61.0	241	7	US-11-054-515-1948	Sequence 1948, Ap
189	25	61.0	243	7	US-11-054-515-1883	Sequence 1883, Ap
190	25	61.0	243	7	US-11-054-515-1935	Sequence 1935, Ap
191	25	61.0	243	7	US-11-054-515-1945	Sequence 1945, Ap
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199	25	61.0	247	7	US-11-054-515-1177	Sequence 1177, Ap
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206	25	61.0	248	7	US-11-054-515-1778	Sequence 1778, Ap
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208	25	61.0	249	7	US-11-054-515-919	Sequence 919, App
209	25	61.0	249	7	US-11-054-515-926	Sequence 926, App
210	25	61.0	249	7	US-11-054-515-1188	Sequence 1188, Ap
211	25	61.0	250	7	US-11-054-515-932	Sequence 932, App
212	25	61.0	251	6	US-10-467-657-3134	Sequence 3134, Ap
213	25	61.0	251	7	US-11-054-515-922	Sequence 922, App
214	25	61.0	251	7	US-11-054-515-1320	Sequence 1320, Ap
215	25	61.0	254	7	US-11-072-512-2701	Sequence 2701, Ap
216	25	61.0	255	7	US-11-054-515-1603	Sequence 1603, Ap
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218	25	61.0	276	7	US-11-038-901-19	Sequence 19, Appl
219	25	61.0	277	6	US-10-996-007B-13	Sequence 13, Appl
220	25	61.0	277	6	US-10-996-007B-14	Sequence 14, Appl
221	25	61.0	277	6	US-10-996-007B-16	Sequence 16, Appl
222	25	61.0	277	7	US-11-140-416-34	Sequence 34, Appl
223	25	61.0	284	7	US-11-096-568A-15523	Sequence 15523, A
224	25	61.0	293	7	US-11-096-568A-15522	Sequence 15522, A
225	25	61.0	294	7	US-11-096-568A-12229	Sequence 12229, A
226	25	61.0	297	7	US-11-096-568A-30442	Sequence 30442, A
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232	25	61.0	314	7	US-11-156-084-159	Sequence 159, App
233	25	61.0	314	7	US-11-169-041-237	Sequence 237, App
234	25	61.0	318	7	US-11-087-099-4152	Sequence 4152, Ap
235	25	61.0	320	7	US-11-087-099-2146	Sequence 2146, Ap
236	25	61.0	330	6	US-10-453-372-572	Sequence 572, App
237	25	61.0	335	6	US-10-467-657-8238	Sequence 8238, Ap
238	25	61.0	339	6	US-10-517-939-154	Sequence 154, App
239	25	61.0	339	7	US-11-156-084-177	Sequence 177, App
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241	25	61.0	347	6	US-10-931-198-44	Sequence 44, Appl
242	25	61.0	347	7	US-11-096-568A-26732	Sequence 26732, A
243	25	61.0	357	7	US-11-096-568A-15521	Sequence 15521, A
244	25	61.0	358	6	US-10-467-657-3446	Sequence 3446, Ap

245	25	61.0	370	6	US-10-793-626-696	Sequence 696, App
246	25	61.0	370	6	US-10-793-626-1328	Sequence 1328, Ap
247	25	61.0	411	7	US-11-072-512-2989	Sequence 2989, Ap
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249	25	61.0	428	7	US-11-096-568A-30441	Sequence 30441, A
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251	25	61.0	442	7	US-11-102-240-76	Sequence 76, Appl
252	25	61.0	442	7	US-11-103-195-76	Sequence 76, Appl
253	25	61.0	444	7	US-11-098-686-11033	Sequence 11033, A
254	25	61.0	468	7	US-11-072-512-3829	Sequence 3829, Ap
255	25	61.0	469	6	US-10-063-703-58	Sequence 58, Appl
256	25	61.0	469	7	US-11-102-240-58	Sequence 58, Appl
257	25	61.0	469	7	US-11-103-195-58	Sequence 58, Appl
258	25	61.0	471	6	US-10-336-263A-6	Sequence 6, Appli
259	25	61.0	499	7	US-11-024-959-276	Sequence 276, App
260	25	61.0	505	7	US-11-096-568A-26731	Sequence 26731, A
261	25	61.0	508	7	US-11-096-568A-26730	Sequence 26730, A
262	25	61.0	542	6	US-10-131-826A-188	Sequence 188, App
263	25	61.0	542	6	US-10-973-115B-188	Sequence 188, App
264	25	61.0	552	6	US-10-793-626-1182	Sequence 1182, Ap
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266	25	61.0	553	6	US-10-636-716-14	Sequence 14, Appl
267	25	61.0	553	6	US-10-636-716-16	Sequence 16, Appl
268	25	61.0	553	6	US-10-636-716-18	Sequence 18, Appl
269	25	61.0	553	6	US-10-636-716-20	Sequence 20, Appl
270	25	61.0	553	6	US-10-636-716-22	Sequence 22, Appl
271	25	61.0	553	6	US-10-636-716-24	Sequence 24, Appl
272	25	61.0	553	6	US-10-636-716-26	Sequence 26, Appl
273	25	61.0	553	6	US-10-636-716-28	Sequence 28, Appl
274	25	61.0	553	6	US-10-636-716-30	Sequence 30, Appl
275	25	61.0	553	6	US-10-636-716-32	Sequence 32, Appl
276	25	61.0	553	6	US-10-636-716-34	Sequence 34, Appl
277	25	61.0	553	6	US-10-636-716-36	Sequence 36, Appl
278	25	61.0	553	6	US-10-636-716-38	Sequence 38, Appl
279	25	61.0	553	6	US-10-636-716-40	Sequence 40, Appl
280	25	61.0	553	6	US-10-636-716-42	Sequence 42, Appl
281	25	61.0	553	6	US-10-636-716-44	Sequence 44, Appl
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283	25	61.0	553	6	US-10-636-716-48	Sequence 48, Appl
284	25	61.0	553	7	US-11-124-925-7	Sequence 7, Appli
285	25	61.0	564	6	US-10-517-939-318	Sequence 318, App
286	25	61.0	572	6	US-10-878-556A-47	Sequence 47, Appl
287	25	61.0	577	7	US-11-082-389-134	Sequence 134, App
288	25	61.0	621	7	US-11-096-568A-2529	Sequence 2529, Ap
289	25	61.0	629	6	US-10-453-372-576	Sequence 576, App
290	25	61.0	629	6	US-10-453-372-578	Sequence 578, App
291	25	61.0	639	7	US-11-124-367A-379	Sequence 379, App
292	25	61.0	642	6	US-10-453-372-568	Sequence 568, App
293	25	61.0	645	7	US-11-087-099-2510	Sequence 2510, Ap
294	25	61.0	653	7	US-11-087-099-8946	Sequence 8946, Ap
295	25	61.0	663	7	US-11-024-959-314	Sequence 314, App
296	25	61.0	704	6	US-10-505-263-10	Sequence 10, Appl
297	25	61.0	719	6	US-10-505-263-87	Sequence 87, Appl
298	25	61.0	745	6	US-10-532-153-15	Sequence 15, Appl
299	25	61.0	782	7	US-11-124-367A-380	Sequence 380, App
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301	25	61.0	795	6	US-10-532-153-21	Sequence 21, Appl
302	25	61.0	798	6	US-10-453-372-570	Sequence 570, App
303	25	61.0	798	6	US-10-877-346-28	Sequence 28, Appl
304	25	61.0	798	6	US-10-989-767A-658	Sequence 658, App
305	25	61.0	799	7	US-11-124-367A-378	Sequence 378, App
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307	25	61.0	801	6	US-10-532-153-18	Sequence 18, Appl
308	25	61.0	808	6	US-10-532-153-6	Sequence 6, Appli
309	25	61.0	811	6	US-10-453-372-580	Sequence 580, App
310	25	61.0	821	6	US-10-453-372-600	Sequence 600, App
311	25	61.0	837	6	US-10-453-372-594	Sequence 594, App
312	25	61.0	837	6	US-10-877-346-5	Sequence 5, Appli
313	25	61.0	839	7	US-11-124-367A-377	Sequence 377, App
314	25	61.0	841	6	US-10-453-372-586	Sequence 586, App
315	25	61.0	841	6	US-10-453-372-592	Sequence 592, App
316	25	61.0	841	6	US-10-453-372-602	Sequence 602, App
317	25	61.0	841	6	US-10-877-346-2	Sequence 2, Appli
318	25	61.0	841	6	US-10-989-767A-657	Sequence 657, App
319	25	61.0	879	6	US-10-858-730-10	Sequence 10, Appl
320	25	61.0	883	6	US-10-858-730-207	Sequence 207, App
321	25	61.0	1085	6	US-10-523-477-13	Sequence 13, Appl
322	25	61.0	1155	7	US-11-098-686-10550	Sequence 10550, A
323	25	61.0	2399	7	US-11-052-554A-92	Sequence 92, Appl
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326	25	61.0	4473	6	US-10-895-064-460	Sequence 460, App
327	25	61.0	4473	7	US-11-129-741-460	Sequence 460, App
328	24.5	59.8	434	7	US-11-237-600-6	Sequence 6, Appli
329	24	58.5	9	6	US-10-510-101-13	Sequence 13, Appl
330	24	58.5	9	7	US-11-125-837-9	Sequence 9, Appli
331	24	58.5	9	7	US-11-097-812-118	Sequence 118, App
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333	24	58.5	9	7	US-11-097-812-124	Sequence 124, App
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340	24	58.5	12	7	US-11-021-305-36	Sequence 36, Appl
341	24	58.5	25	6	US-10-895-064-1894	Sequence 1894, Ap
342	24	58.5	25	7	US-11-129-741-1894	Sequence 1894, Ap
343	24	58.5	26	7	US-11-158-723-1	Sequence 1, Appli
344	24	58.5	31	7	US-11-004-399-3203	Sequence 3203, Ap
345	24	58.5	41	6	US-10-330-773-344	Sequence 344, App
346	24	58.5	47	7	US-11-096-568A-12245	Sequence 12245, A
347	24	58.5	48	6	US-10-467-657-5558	Sequence 5558, Ap
348	24	58.5	107	7	US-11-154-337-1	Sequence 1, Appli
349	24	58.5	107	7	US-11-154-337-3	Sequence 3, Appli
350	24	58.5	107	7	US-11-182-908-1	Sequence 1, Appli
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362	24	58.5	110	7	US-11-097-812-174	Sequence 174, App
363	24	58.5	111	7	US-11-097-812-107	Sequence 107, App
364	24	58.5	111	7	US-11-097-812-178	Sequence 178, App
365	24	58.5	111	7	US-11-097-812-180	Sequence 180, App
366	24	58.5	113	7	US-11-097-812-108	Sequence 108, App
367	24	58.5	126	6	US-10-467-657-2340	Sequence 2340, Ap
368	24	58.5	130	7	US-11-125-837-21	Sequence 21, Appl
369	24	58.5	138	7	US-11-096-568A-4375	Sequence 4375, Ap
370	24	58.5	143	7	US-11-096-568A-10168	Sequence 10168, A
371	24	58.5	152	7	US-11-096-568A-10167	Sequence 10167, A
372	24	58.5	163	6	US-10-793-626-2330	Sequence 2330, Ap
373	24	58.5	167	7	US-11-072-512-3129	Sequence 3129, Ap
374	24	58.5	173	7	US-11-087-099-7617	Sequence 7617, Ap
375	24	58.5	174	6	US-10-793-626-1520	Sequence 1520, Ap
376	24	58.5	175	7	US-11-072-512-2261	Sequence 2261, Ap
377	24	58.5	177	7	US-11-096-568A-5577	Sequence 5577, Ap
378	24	58.5	191	7	US-11-087-099-2604	Sequence 2604, Ap
379	24	58.5	207	6	US-10-467-657-314	Sequence 314, App
380	24	58.5	207	6	US-10-467-657-3272	Sequence 3272, Ap
381	24	58.5	213	7	US-11-087-099-2022	Sequence 2022, Ap
382	24	58.5	213	7	US-11-096-568A-4374	Sequence 4374, Ap
383	24	58.5	214	7	US-11-154-337-16	Sequence 16, Appl
384	24	58.5	214	7	US-11-182-908-15	Sequence 15, Appl
385	24	58.5	214	7	US-11-096-568A-4373	Sequence 4373, Ap
386	24	58.5	217	7	US-11-182-908-23	Sequence 23, Appl
387	24	58.5	221	7	US-11-087-099-2792	Sequence 2792, Ap
388	24	58.5	231	7	US-11-087-099-1588	Sequence 1588, Ap
389	24	58.5	233	7	US-11-182-908-17	Sequence 17, Appl
390	24	58.5	234	7	US-11-098-686-10787	Sequence 10787, A

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392	24	58.5	243	7	US-11-054-515-1943	Sequence 1943, Ap
393	24	58.5	243	7	US-11-054-515-2064	Sequence 2064, Ap
394	24	58.5	244	7	US-11-096-568A-24638	Sequence 24638, A
395	24	58.5	251	7	US-11-096-568A-5268	Sequence 5268, Ap
396	24	58.5	253	6	US-10-485-517-373	Sequence 373, App
397	24	58.5	258	6	US-10-878-556A-195	Sequence 195, App
398	24	58.5	258	7	US-11-096-568A-5576	Sequence 5576, Ap
399	24	58.5	261	5	US-09-995-493-126	Sequence 126, App
400	24	58.5	267	7	US-11-096-568A-32695	Sequence 32695, A
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402	24	58.5	284	7	US-11-096-568A-16432	Sequence 16432, A
403	24	58.5	284	7	US-11-096-568A-18530	Sequence 18530, A
404	24	58.5	286	7	US-11-087-099-268	Sequence 268, App
405	24	58.5	286	7	US-11-096-568A-5575	Sequence 5575, Ap
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408	24	58.5	313	7	US-11-087-099-11524	Sequence 11524, A
409	24	58.5	322	7	US-11-098-686-11313	Sequence 11313, A
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412	24	58.5	339	7	US-11-087-099-9221	Sequence 9221, Ap
413	24	58.5	343	7	US-11-096-568A-16431	Sequence 16431, A
414	24	58.5	343	7	US-11-096-568A-18529	Sequence 18529, A
415	24	58.5	352	5	US-09-978-360A-437	Sequence 437, App
416	24	58.5	354	7	US-11-096-568A-3310	Sequence 3310, Ap
417	24	58.5	355	6	US-10-517-939-206	Sequence 206, App
418	24	58.5	355	7	US-11-096-568A-33234	Sequence 33234, A
419	24	58.5	356	7	US-11-096-568A-33233	Sequence 33233, A
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423	24	58.5	362	6	US-10-793-626-3120	Sequence 3120, Ap
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426	24	58.5	376	7	US-11-082-389-124	Sequence 124, App
427	24	58.5	377	6	US-10-467-657-7508	Sequence 7508, Ap
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429	24	58.5	383	7	US-11-087-099-4880	Sequence 4880, Ap
430	24	58.5	385	5	US-09-995-493-212	Sequence 212, App
431	24	58.5	391	7	US-11-087-099-10428	Sequence 10428, A
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433	24	58.5	406	7	US-11-096-568A-16557	Sequence 16557, A
434	24	58.5	408	7	US-11-082-389-164	Sequence 164, App
435	24	58.5	411	7	US-11-087-099-7055	Sequence 7055, Ap
436	24	58.5	416	7	US-11-087-099-8746	Sequence 8746, Ap
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438	24	58.5	446	7	US-11-096-568A-32693	Sequence 32693, A
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442	24	58.5	453	6	US-10-931-198-36	Sequence 36, Appl
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457	24	58.5	513	7	US-11-087-099-7975	Sequence 7975, Ap
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459	24	58.5	528	7	US-11-118-809-2	Sequence 2, Appli
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464	24	58.5	585	7	US-11-096-568A-31084	Sequence 31084, A
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466	24	58.5	622	6	US-10-973-115B-180	Sequence 180, App
467	24	58.5	630	6	US-10-893-584-274	Sequence 274, App
468	24	58.5	635	6	US-10-821-234-927	Sequence 927, App
469	24	58.5	677	6	US-10-982-545-12	Sequence 12, Appl
470	24	58.5	682	6	US-10-956-026-14	Sequence 14, Appl
471	24	58.5	686	7	US-11-072-175-225	Sequence 225, App
472	24	58.5	687	7	US-11-087-099-8764	Sequence 8764, Ap
473	24	58.5	693	6	US-10-131-826A-406	Sequence 406, App
474	24	58.5	693	6	US-10-973-115B-406	Sequence 406, App
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476	24	58.5	753	7	US-11-087-099-2868	Sequence 2868, Ap
477	24	58.5	756	6	US-10-956-026-13	Sequence 13, Appl
478	24	58.5	764	7	US-11-072-512-2379	Sequence 2379, Ap
479	24	58.5	766	6	US-10-793-626-2578	Sequence 2578, Ap
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481	24	58.5	787	7	US-11-154-227-110	Sequence 110, App
482	24	58.5	824	6	US-10-330-773-110	Sequence 110, App
483	24	58.5	834	6	US-10-131-826A-148	Sequence 148, App
484	24	58.5	834	6	US-10-928-446A-188	Sequence 188, App
485	24	58.5	834	6	US-10-928-446A-192	Sequence 192, App
486	24	58.5	834	6	US-10-928-446A-194	Sequence 194, App
487	24	58.5	834	6	US-10-928-446A-196	Sequence 196, App
488	24	58.5	834	6	US-10-928-446A-198	Sequence 198, App
489	24	58.5	834	6	US-10-928-446A-200	Sequence 200, App
490	24	58.5	834	6	US-10-928-446A-202	Sequence 202, App
491	24	58.5	834	6	US-10-973-115B-148	Sequence 148, App
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494	24	58.5	841	6	US-10-624-932-8	Sequence 8, Appli
495	24	58.5	925	6	US-10-453-372-1124	Sequence 1124, Ap
496	24	58.5	933	6	US-10-330-773-106	Sequence 106, App
497	24	58.5	942	6	US-10-928-446A-190	Sequence 190, App
498	24	58.5	946	6	US-10-330-773-101	Sequence 101, App
499	24	58.5	947	6	US-10-928-446A-182	Sequence 182, App
500	24	58.5	948	6	US-10-330-773-104	Sequence 104, App
501	24	58.5	950	6	US-10-928-446A-184	Sequence 184, App
502	24	58.5	955	6	US-10-928-446A-186	Sequence 186, App
503	24	58.5	966	6	US-10-877-346-32	Sequence 32, Appl
504	24	58.5	972	6	US-10-453-372-1128	Sequence 1128, Ap
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506	24	58.5	979	7	US-11-072-512-2446	Sequence 2446, Ap
507	24	58.5	990	6	US-10-330-773-108	Sequence 108, App
508	24	58.5	1027	6	US-10-793-626-3106	Sequence 3106, Ap
509	24	58.5	1236	6	US-10-873-528-109	Sequence 109, App
510	24	58.5	1332	7	US-11-091-643-18	Sequence 18, Appl
511	24	58.5	1372	7	US-11-087-099-3054	Sequence 3054, Ap
512	24	58.5	1479	7	US-11-019-711-36	Sequence 36, Appl
513	24	58.5	3003	6	US-10-453-372-1080	Sequence 1080, Ap
514	24	58.5	3361	6	US-10-453-372-1082	Sequence 1082, Ap
515	24	58.5	4544	6	US-10-501-035-214	Sequence 214, App
516	24	58.5	4544	7	US-11-076-427A-32	Sequence 32, Appl
517	23	56.1	9	6	US-10-839-799-120	Sequence 120, App
518	23	56.1	9	6	US-10-850-635-56	Sequence 56, Appl
519	23	56.1	9	6	US-10-850-635-68	Sequence 68, Appl
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522	23	56.1	9	7	US-11-096-046-9	Sequence 9, Appli
523	23	56.1	15	7	US-11-004-399-1735	Sequence 1735, Ap
524	23	56.1	16	6	US-10-895-064-2183	Sequence 2183, Ap
525	23	56.1	16	7	US-11-129-741-2183	Sequence 2183, Ap
526	23	56.1	17	6	US-10-834-397-222	Sequence 222, App
527	23	56.1	18	7	US-11-021-305-3	Sequence 3, Appli
528	23	56.1	18	7	US-11-021-305-14	Sequence 14, Appl
529	23	56.1	20	6	US-10-895-064-2141	Sequence 2141, Ap
530	23	56.1	20	7	US-11-129-741-2141	Sequence 2141, Ap
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533	23	56.1	30	7	US-11-021-305-2	Sequence 2, Appli
534	23	56.1	33	6	US-10-895-064-2077	Sequence 2077, Ap
535	23	56.1	33	7	US-11-129-741-2077	Sequence 2077, Ap
536	23	56.1	37	7	US-11-129-741-3675	Sequence 3675, Ap

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538	23	56.1	44	6	US-10-895-064-341	Sequence 341, App
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540	23	56.1	44	7	US-11-129-741-3272	Sequence 3272, Ap
541	23	56.1	46	6	US-10-895-064-1666	Sequence 1666, Ap
542	23	56.1	46	7	US-11-129-741-1666	Sequence 1666, Ap
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544	23	56.1	51	7	US-11-096-568A-14481	Sequence 14481, A
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548	23	56.1	63	7	US-11-129-741-653	Sequence 653, App
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552	23	56.1	95	7	US-11-054-669-62	Sequence 62, Appl
553	23	56.1	95	7	US-11-054-669-72	Sequence 72, Appl
554	23	56.1	95	7	US-11-084-554-121	Sequence 121, App
555	23	56.1	95	7	US-11-084-554-124	Sequence 124, App
556	23	56.1	95	7	US-11-084-554-126	Sequence 126, App
557	23	56.1	95	7	US-11-061-848-35	Sequence 35, Appl
558	23	56.1	95	7	US-11-061-848-39	Sequence 39, Appl
559	23	56.1	95	7	US-11-061-848-59	Sequence 59, Appl
560	23	56.1	95	7	US-11-061-848-60	Sequence 60, Appl
561	23	56.1	95	7	US-11-061-848-70	Sequence 70, Appl
562	23	56.1	95	7	US-11-004-590-54	Sequence 54, Appl
563	23	56.1	95	7	US-11-004-590-63	Sequence 63, Appl
564	23	56.1	95	7	US-11-004-590-64	Sequence 64, Appl
565	23	56.1	95	7	US-11-136-250-121	Sequence 121, App
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569	23	56.1	107	6	US-10-839-799-131	Sequence 131, App
570	23	56.1	107	6	US-10-850-635-14	Sequence 14, Appl
571	23	56.1	107	6	US-10-850-635-18	Sequence 18, Appl
572	23	56.1	107	7	US-11-051-453-30	Sequence 30, Appl
573	23	56.1	107	7	US-11-051-453-31	Sequence 31, Appl
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576	23	56.1	108	7	US-11-173-071-16	Sequence 16, Appl
577	23	56.1	108	7	US-11-173-071-18	Sequence 18, Appl
578	23	56.1	108	7	US-11-173-071-20	Sequence 20, Appl
579	23	56.1	108	7	US-11-173-071-22	Sequence 22, Appl
580	23	56.1	108	7	US-11-049-536-192	Sequence 192, App
581	23	56.1	108	7	US-11-073-942-20	Sequence 20, Appl
582	23	56.1	109	7	US-11-049-536-532	Sequence 532, App
583	23	56.1	110	7	US-11-087-099-1161	Sequence 1161, Ap
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586	23	56.1	115	7	US-11-217-562-8	Sequence 8, Appli
587	23	56.1	115	7	US-11-107-219-8	Sequence 8, Appli
588	23	56.1	117	7	US-11-009-840A-313	Sequence 313, App
589	23	56.1	117	7	US-11-009-873A-313	Sequence 313, App
590	23	56.1	117	7	US-11-009-769A-313	Sequence 313, App
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592	23	56.1	121	7	US-11-096-568A-9365	Sequence 9365, Ap
593	23	56.1	122	6	US-10-746-909-9	Sequence 9, Appli
594	23	56.1	125	7	US-11-087-099-9510	Sequence 9510, Ap
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596	23	56.1	126	6	US-10-839-799-47	Sequence 47, Appl
597	23	56.1	126	6	US-10-839-799-51	Sequence 51, Appl
598	23	56.1	126	6	US-10-839-799-53	Sequence 53, Appl
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611	23	56.1	126	7	US-11-096-568A-628	Sequence 628, App
612	23	56.1	127	6	US-10-839-799-27	Sequence 27, Appl
613	23	56.1	129	7	US-11-051-453-44	Sequence 44, Appl
614	23	56.1	129	7	US-11-051-453-45	Sequence 45, Appl
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616	23	56.1	129	7	US-11-051-453-47	Sequence 47, Appl
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620	23	56.1	141	6	US-10-475-075-464	Sequence 464, App
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628	23	56.1	150	7	US-11-096-568A-5298	Sequence 5298, Ap
629	23	56.1	155	6	US-10-995-561-953	Sequence 953, App
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632	23	56.1	155	7	US-11-096-568A-627	Sequence 627, App
633	23	56.1	160	7	US-11-087-099-4706	Sequence 4706, Ap
634	23	56.1	162	7	US-11-087-099-2271	Sequence 2271, Ap
635	23	56.1	171	7	US-11-096-568A-7124	Sequence 7124, Ap
636	23	56.1	173	7	US-11-096-568A-5727	Sequence 5727, Ap
637	23	56.1	175	7	US-11-182-016-44	Sequence 44, Appl
638	23	56.1	178	7	US-11-055-822-950	Sequence 950, App
639	23	56.1	180	7	US-11-096-568A-12758	Sequence 12758, A
640	23	56.1	183	7	US-11-087-099-10092	Sequence 10092, A
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642	23	56.1	184	7	US-11-087-099-11086	Sequence 11086, A
643	23	56.1	186	7	US-11-087-099-5268	Sequence 5268, Ap
644	23	56.1	189	6	US-10-793-626-2692	Sequence 2692, Ap
645	23	56.1	189	7	US-11-071-262-1	Sequence 1, Appli
646	23	56.1	192	7	US-11-096-568A-9364	Sequence 9364, Ap
647	23	56.1	192	7	US-11-096-568A-9366	Sequence 9366, Ap
648	23	56.1	194	6	US-10-714-887-6	Sequence 6, Appli
649	23	56.1	194	7	US-11-096-568A-8431	Sequence 8431, Ap
650	23	56.1	195	7	US-11-096-568A-7123	Sequence 7123, Ap
651	23	56.1	196	7	US-11-169-041-154	Sequence 154, App
652	23	56.1	197	7	US-11-096-568A-5726	Sequence 5726, Ap
653	23	56.1	203	6	US-10-467-657-3482	Sequence 3482, Ap
654	23	56.1	204	6	US-10-131-826A-288	Sequence 288, App
655	23	56.1	204	6	US-10-973-115B-288	Sequence 288, App
656	23	56.1	205	6	US-10-501-035-294	Sequence 294, App
657	23	56.1	205	7	US-11-203-251A-91	Sequence 91, Appl
658	23	56.1	206	6	US-10-467-657-3270	Sequence 3270, Ap
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661	23	56.1	212	7	US-11-096-568A-9363	Sequence 9363, Ap
662	23	56.1	216	7	US-11-096-568A-9205	Sequence 9205, Ap
663	23	56.1	217	7	US-11-096-568A-23000	Sequence 23000, A
664	23	56.1	218	6	US-10-467-657-7818	Sequence 7818, Ap
665	23	56.1	218	7	US-11-096-568A-8430	Sequence 8430, Ap
666	23	56.1	219	7	US-11-096-568A-8429	Sequence 8429, Ap
667	23	56.1	222	6	US-10-454-437-380	Sequence 380, App
668	23	56.1	222	7	US-11-096-568A-1841	Sequence 1841, Ap
669	23	56.1	226	7	US-11-096-568A-3448	Sequence 3448, Ap
670	23	56.1	228	6	US-10-517-939-204	Sequence 204, App
671	23	56.1	231	7	US-11-096-568A-17789	Sequence 17789, A
672	23	56.1	231	7	US-11-096-568A-31217	Sequence 31217, A
673	23	56.1	234	7	US-11-041-095-25	Sequence 25, Appl
674	23	56.1	234	7	US-11-098-686-10176	Sequence 10176, A
675	23	56.1	238	7	US-11-203-251A-94	Sequence 94, Appl
676	23	56.1	239	7	US-11-041-095-19	Sequence 19, Appl
677	23	56.1	243	7	US-11-087-099-3396	Sequence 3396, Ap
678	23	56.1	244	6	US-10-821-234-1264	Sequence 1264, Ap
679	23	56.1	244	7	US-11-096-568A-3447	Sequence 3447, Ap
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681	23	56.1	252	7	US-11-087-099-392	Sequence 392, App
682	23	56.1	252	7	US-11-096-568A-17788	Sequence 17788, A

683	23	56.1	252	7	US-11-096-568A-32817	Sequence 32817, A
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686	23	56.1	259	6	US-10-510-386-52	Sequence 52, Appl
687	23	56.1	259	7	US-11-096-568A-3446	Sequence 3446, Ap
688	23	56.1	259	7	US-11-096-568A-32893	Sequence 32893, A
689	23	56.1	260	6	US-10-055-877-166	Sequence 166, App
690	23	56.1	262	7	US-11-096-568A-9204	Sequence 9204, Ap
691	23	56.1	262	7	US-11-096-568A-9206	Sequence 9206, Ap
692	23	56.1	263	7	US-11-098-686-10125	Sequence 10125, A
693	23	56.1	263	7	US-11-098-686-10590	Sequence 10590, A
694	23	56.1	264	7	US-11-072-512-2564	Sequence 2564, Ap
695	23	56.1	267	6	US-10-793-626-882	Sequence 882, App
696	23	56.1	267	7	US-11-096-568A-1840	Sequence 1840, Ap
697	23	56.1	268	6	US-10-055-877-193	Sequence 193, App
698	23	56.1	269	6	US-10-839-799-109	Sequence 109, App
699	23	56.1	270	7	US-11-096-568A-22093	Sequence 22093, A
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706	23	56.1	288	7	US-11-149-462-8	Sequence 8, Appli
707	23	56.1	290	7	US-11-041-095-13	Sequence 13, Appl
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709	23	56.1	300	7	US-11-149-462-10	Sequence 10, Appl
710	23	56.1	306	6	US-10-798-579A-26	Sequence 26, Appl
711	23	56.1	307	7	US-11-087-099-337	Sequence 337, App
712	23	56.1	309	7	US-11-096-568A-21232	Sequence 21232, A
713	23	56.1	309	7	US-11-096-568A-23552	Sequence 23552, A
714	23	56.1	310	7	US-11-053-185-14	Sequence 14, Appl
715	23	56.1	311	6	US-10-467-657-3740	Sequence 3740, Ap
716	23	56.1	312	7	US-11-096-568A-34393	Sequence 34393, A
717	23	56.1	313	7	US-11-000-463-427	Sequence 427, App
718	23	56.1	313	7	US-11-177-506-36	Sequence 36, Appl
719	23	56.1	313	7	US-11-198-728-10	Sequence 10, Appl
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721	23	56.1	313	7	US-11-096-568A-7122	Sequence 7122, Ap
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723	23	56.1	314	6	US-10-467-657-2698	Sequence 2698, Ap
724	23	56.1	314	6	US-10-467-657-5930	Sequence 5930, Ap
725	23	56.1	314	6	US-10-467-657-6496	Sequence 6496, Ap
726	23	56.1	315	6	US-10-467-657-7848	Sequence 7848, Ap
727	23	56.1	315	7	US-11-096-568A-5725	Sequence 5725, Ap
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773	23	56.1	384	7	US-11-108-185-8	Sequence 8, Appli
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775	23	56.1	384	7	US-11-108-185-12	Sequence 12, Appl
776	23	56.1	384	7	US-11-087-099-9360	Sequence 9360, Ap
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784	23	56.1	396	7	US-11-112-882-78	Sequence 78, Appl
785	23	56.1	404	7	US-11-096-568A-5191	Sequence 5191, Ap
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787	23	56.1	410	7	US-11-096-568A-9857	Sequence 9857, Ap
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797	23	56.1	418	6	US-10-995-561-754	Sequence 754, App
798	23	56.1	418	6	US-10-995-561-755	Sequence 755, App
799	23	56.1	418	6	US-10-995-561-756	Sequence 756, App
800	23	56.1	418	6	US-10-995-561-757	Sequence 757, App
801	23	56.1	418	6	US-10-995-561-758	Sequence 758, App
802	23	56.1	418	6	US-10-995-561-759	Sequence 759, App
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804	23	56.1	418	7	US-11-201-443-2	Sequence 2, Appli
805	23	56.1	418	7	US-11-177-506-27	Sequence 27, Appl
806	23	56.1	418	7	US-11-183-205-22	Sequence 22, Appl
807	23	56.1	419	6	US-10-821-234-1556	Sequence 1556, Ap
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812	23	56.1	423	6	US-10-878-556A-176	Sequence 176, App
813	23	56.1	425	6	US-10-793-626-1012	Sequence 1012, Ap
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837	23	56.1	482	7	US-11-096-568A-8410	Sequence 8410, Ap
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839	23	56.1	484	7	US-11-087-099-2542	Sequence 2542, Ap
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841	23	56.1	488	7	US-11-087-099-7125	Sequence 7125, Ap
842	23	56.1	490	7	US-11-087-099-5806	Sequence 5806, Ap
843	23	56.1	491	6	US-10-793-626-2770	Sequence 2770, Ap
844	23	56.1	491	7	US-11-096-568A-9195	Sequence 9195, Ap
845	23	56.1	491	7	US-11-096-568A-9196	Sequence 9196, Ap
846	23	56.1	492	7	US-11-072-512-1974	Sequence 1974, Ap
847	23	56.1	492	7	US-11-072-512-3223	Sequence 3223, Ap
848	23	56.1	493	7	US-11-096-568A-9194	Sequence 9194, Ap
849	23	56.1	495	7	US-11-129-076-8	Sequence 8, Appli
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851	23	56.1	496	7	US-11-129-076-7	Sequence 7, Appli
852	23	56.1	505	7	US-11-096-568A-17181	Sequence 17181, A
853	23	56.1	506	7	US-11-055-822-946	Sequence 946, App
854	23	56.1	509	6	US-10-821-234-1093	Sequence 1093, Ap
855	23	56.1	511	7	US-11-096-568A-9193	Sequence 9193, Ap
856	23	56.1	518	6	US-10-793-626-506	Sequence 506, App
857	23	56.1	520	7	US-11-096-568A-30752	Sequence 30752, A
858	23	56.1	521	7	US-11-096-568A-31589	Sequence 31589, A
859	23	56.1	526	7	US-11-096-568A-31588	Sequence 31588, A
860	23	56.1	529	7	US-11-087-099-1103	Sequence 1103, Ap
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862	23	56.1	538	7	US-11-087-099-1023	Sequence 1023, Ap
863	23	56.1	538	7	US-11-087-099-8465	Sequence 8465, Ap
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865	23	56.1	542	7	US-11-096-568A-31587	Sequence 31587, A
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872	23	56.1	561	7	US-11-096-568A-9122	Sequence 9122, Ap
873	23	56.1	566	7	US-11-096-568A-8408	Sequence 8408, Ap
874	23	56.1	572	6	US-10-467-657-1022	Sequence 1022, Ap
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877	23	56.1	585	7	US-11-096-568A-9123	Sequence 9123, Ap
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879	23	56.1	608	7	US-11-067-260-1	Sequence 1, Appli
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884	23	56.1	648	6	US-10-501-039-6	Sequence 6, Appli
885	23	56.1	658	7	US-11-087-099-6627	Sequence 6627, Ap
886	23	56.1	672	7	US-11-067-260-36	Sequence 36, Appl
887	23	56.1	675	7	US-11-067-260-34	Sequence 34, Appl
888	23	56.1	681	7	US-11-087-099-7473	Sequence 7473, Ap
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893	23	56.1	698	7	US-11-087-099-9341	Sequence 9341, Ap
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895	23	56.1	710	6	US-10-336-263A-14	Sequence 14, Appl
896	23	56.1	717	7	US-11-033-030-49	Sequence 49, Appl
897	23	56.1	718	7	US-11-096-568A-31008	Sequence 31008, A
898	23	56.1	724	7	US-11-109-156-19	Sequence 19, Appl
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901	23	56.1	751	7	US-11-087-099-3268	Sequence 3268, Ap
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903	23	56.1	751	7	US-11-067-260-48	Sequence 48, Appl
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907	23	56.1	763	6	US-10-821-234-1619	Sequence 1619, Ap
908	23	56.1	765	7	US-11-067-260-54	Sequence 54, Appl
909	23	56.1	771	7	US-11-096-568A-31007	Sequence 31007, A
910	23	56.1	798	6	US-10-514-531-2	Sequence 2, Appli
911	23	56.1	806	7	US-11-067-260-38	Sequence 38, Appl
912	23	56.1	806	7	US-11-067-260-42	Sequence 42, Appl
913	23	56.1	812	7	US-11-120-308-126	Sequence 126, App
914	23	56.1	812	7	US-11-096-568A-31006	Sequence 31006, A
915	23	56.1	829	7	US-11-096-568A-20149	Sequence 20149, A
916	23	56.1	835	6	US-10-501-035-216	Sequence 216, App
917	23	56.1	841	6	US-10-501-035-305	Sequence 305, App
918	23	56.1	843	7	US-11-096-568A-20148	Sequence 20148, A
919	23	56.1	853	6	US-10-877-346-30	Sequence 30, Appl
920	23	56.1	866	7	US-11-147-047-32	Sequence 32, Appl
921	23	56.1	866	7	US-11-052-554A-29	Sequence 29, Appl
922	23	56.1	876	6	US-10-453-372-1202	Sequence 1202, Ap
923	23	56.1	876	6	US-10-453-372-1208	Sequence 1208, Ap
924	23	56.1	876	7	US-11-096-568A-20147	Sequence 20147, A
925	23	56.1	894	7	US-11-202-330-2	Sequence 2, Appli
926	23	56.1	896	7	US-11-192-219-3	Sequence 3, Appli
927	23	56.1	897	6	US-10-336-263A-58	Sequence 58, Appl
928	23	56.1	898	7	US-11-166-730-3	Sequence 3, Appli
929	23	56.1	901	7	US-11-087-099-1506	Sequence 1506, Ap
930	23	56.1	923	7	US-11-192-219-4	Sequence 4, Appli
931	23	56.1	923	7	US-11-087-099-4257	Sequence 4257, Ap
932	23	56.1	923	7	US-11-087-099-6750	Sequence 6750, Ap
933	23	56.1	923	7	US-11-087-099-7810	Sequence 7810, Ap
934	23	56.1	924	7	US-11-087-099-6182	Sequence 6182, Ap
935	23	56.1	924	7	US-11-087-099-10364	Sequence 10364, A
936	23	56.1	925	7	US-11-087-099-1558	Sequence 1558, Ap
937	23	56.1	925	7	US-11-087-099-3884	Sequence 3884, Ap
938	23	56.1	925	7	US-11-087-099-8562	Sequence 8562, Ap
939	23	56.1	944	7	US-11-057-058-68	Sequence 68, Appl
940	23	56.1	950	7	US-11-087-099-4822	Sequence 4822, Ap
941	23	56.1	954	7	US-11-096-568A-31293	Sequence 31293, A
942	23	56.1	963	7	US-11-096-568A-31292	Sequence 31292, A
943	23	56.1	964	7	US-11-096-568A-31291	Sequence 31291, A
944	23	56.1	1006	6	US-10-793-626-154	Sequence 154, App
945	23	56.1	1059	6	US-10-336-263A-54	Sequence 54, Appl
946	23	56.1	1059	6	US-10-336-263A-56	Sequence 56, Appl
947	23	56.1	1068	6	US-10-467-657-2904	Sequence 2904, Ap
948	23	56.1	1124	6	US-10-858-730-12	Sequence 12, Appl
949	23	56.1	1153	7	US-11-096-568A-31530	Sequence 31530, A
950	23	56.1	1161	6	US-10-511-538-99	Sequence 99, Appl
951	23	56.1	1162	7	US-11-202-330-43	Sequence 43, Appl
952	23	56.1	1165	7	US-11-192-219-2	Sequence 2, Appli
953	23	56.1	1165	7	US-11-202-330-4	Sequence 4, Appli
954	23	56.1	1166	6	US-10-501-035-205	Sequence 205, App
955	23	56.1	1207	6	US-10-821-234-1109	Sequence 1109, Ap
956	23	56.1	1294	7	US-11-052-554A-340	Sequence 340, App
957	23	56.1	1436	6	US-10-453-372-1094	Sequence 1094, Ap
958	23	56.1	1461	7	US-11-183-136-28	Sequence 28, Appl
959	23	56.1	1464	6	US-10-912-971-4	Sequence 4, Appli
960	23	56.1	1464	7	US-11-076-074-1	Sequence 1, Appli
961	23	56.1	1464	7	US-11-124-367A-262	Sequence 262, App
962	23	56.1	1474	7	US-11-067-260-18	Sequence 18, Appl
963	23	56.1	1493	7	US-11-183-136-26	Sequence 26, Appl
964	23	56.1	1519	7	US-11-182-016-5	Sequence 5, Appli
965	23	56.1	1571	7	US-11-052-554A-2	Sequence 2, Appli
966	23	56.1	1593	6	US-10-453-372-1092	Sequence 1092, Ap
967	23	56.1	2105	7	US-11-052-554A-173	Sequence 173, App
968	22.5	54.9	162	6	US-10-467-657-6626	Sequence 6626, Ap
969	22	53.7	9	6	US-10-510-101-14	Sequence 14, Appl
970	22	53.7	9	6	US-10-510-101-15	Sequence 15, Appl
971	22	53.7	9	6	US-10-510-101-170	Sequence 170, App
972	22	53.7	9	7	US-11-196-459-8	Sequence 8, Appli
973	22	53.7	9	7	US-11-051-453-24	Sequence 24, Appl
974	22	53.7	9	7	US-11-009-840A-216	Sequence 216, App

975	22	53.7	9	7	US-11-009-873A-216	Sequence 216, App
976	22	53.7	9	7	US-11-009-769A-216	Sequence 216, App
977	22	53.7	10	6	US-10-467-657-8944	Sequence 8944, Ap
978	22	53.7	14	7	US-11-004-399-2287	Sequence 2287, Ap
979	22	53.7	24	6	US-10-895-064-75	Sequence 75, Appl
980	22	53.7	24	7	US-11-129-741-75	Sequence 75, Appl
981	22	53.7	24	7	US-11-129-741-3012	Sequence 3012, Ap
982	22	53.7	29	6	US-10-895-064-2723	Sequence 2723, Ap
983	22	53.7	29	7	US-11-129-741-2723	Sequence 2723, Ap
984	22	53.7	33	7	US-11-096-568A-1132	Sequence 1132, Ap
985	22	53.7	37	7	US-11-143-077-12	Sequence 12, Appl
986	22	53.7	37	7	US-11-096-568A-3714	Sequence 3714, Ap
987	22	53.7	39	7	US-11-004-399-286	Sequence 286, App
988	22	53.7	39	7	US-11-004-399-617	Sequence 617, App
989	22	53.7	39	7	US-11-004-399-3928	Sequence 3928, Ap
990	22	53.7	40	7	US-11-157-930-12	Sequence 12, Appl
991	22	53.7	57	7	US-11-087-099-595	Sequence 595, App
992	22	53.7	59	7	US-11-096-568A-12338	Sequence 12338, A
993	22	53.7	65	7	US-11-004-399-2544	Sequence 2544, Ap
994	22	53.7	76	6	US-10-667-295-31	Sequence 31, Appl
995	22	53.7	76	7	US-11-004-399-1849	Sequence 1849, Ap
996	22	53.7	78	6	US-10-467-657-8126	Sequence 8126, Ap
997	22	53.7	79	6	US-10-667-295-28	Sequence 28, Appl
998	22	53.7	82	6	US-10-667-295-69	Sequence 69, Appl
999	22	53.7	84	6	US-10-667-295-30	Sequence 30, Appl
1000	22	53.7	84	6	US-10-667-295-239	Sequence 239, App

ALIGNMENTS

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RESULT 1
US-11-087-099-1522
; Sequence 1522, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1522
;   LENGTH: 343
;   TYPE: PRT
;   ORGANISM: Antirrhinum majus
US-11-087-099-1522

  Query Match             73.2%;  Score 30;  DB 7;  Length 343;
  Best Local Similarity   71.4%;  Pred. No. 69;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         69 QEYELYR 75


RESULT 2
US-10-615-668-3
; Sequence 3, Application US/10615668
; Publication No. US20050276819A1
; GENERAL INFORMATION:
;  APPLICANT: Covacci, Antonello
;  APPLICANT:  Bugnoli, Massimo
;  APPLICANT:  Telford, John
;  APPLICANT:  Macchia, Giovanni
;  APPLICANT:  Rappuoli, Rino
;  TITLE OF INVENTION: Helicobacter Pylori CAI Antigen Polynucleotides
;  FILE REFERENCE: CHIR0337
;  CURRENT APPLICATION NUMBER: US/10/615,668
;  CURRENT FILING DATE:  2003-07-08
;  PRIOR APPLICATION NUMBER: 08/471,491
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: 08/256,848
;  PRIOR FILING DATE: 1994-10-21
;  PRIOR APPLICATION NUMBER: 09/410,835
;  PRIOR FILING DATE: 1999-10-01
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 1296
;   TYPE: PRT
;   ORGANISM: Helicobacter pylori
US-10-615-668-3

  Query Match             73.2%;  Score 30;  DB 6;  Length 1296;
  Best Local Similarity   62.5%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ::| ||||
Db         96 KEYDLYRS 103


RESULT 3
US-10-467-657-4880
; Sequence 4880, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4880
;   LENGTH: 72
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4880

  Query Match             70.7%;  Score 29;  DB 6;  Length 72;
  Best Local Similarity   62.5%;  Pred. No. 23;
  Matches    5;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ||::|:|| 
Db         51 QQHALFRS 58


RESULT 4
US-11-198-819-14
; Sequence 14, Application US/11198819
; Publication No. US20050287582A1
;  GENERAL INFORMATION:
;    APPLICANT:  Adema, Gosse Jan
;    TITLE OF INVENTION:  Isolated Mammalian Monocyte Cell Genes;
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/198,819
;      FILING DATE:  04-AUG-2005
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,950
;      FILING DATE:  05-DEC-1997
;      APPLICATION NUMBER:  US 60/041,279
;      FILING DATE:  21-MARCH-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,181
;      FILING DATE:  16-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/032,252
;      FILING DATE:  06-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0670K
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1204
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  431 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-11-198-819-14

  Query Match             70.7%;  Score 29;  DB 7;  Length 431;
  Best Local Similarity   71.4%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         73 QEYRLYR 79


RESULT 5
US-11-198-819-20
; Sequence 20, Application US/11198819
; Publication No. US20050287582A1
;  GENERAL INFORMATION:
;    APPLICANT:  Adema, Gosse Jan
;    TITLE OF INVENTION:  Isolated Mammalian Monocyte Cell Genes;
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/198,819
;      FILING DATE:  04-AUG-2005
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,950
;      FILING DATE:  05-DEC-1997
;      APPLICATION NUMBER:  US 60/041,279
;      FILING DATE:  21-MARCH-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,181
;      FILING DATE:  16-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/032,252
;      FILING DATE:  06-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0670K
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1204
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  431 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-11-198-819-20

  Query Match             70.7%;  Score 29;  DB 7;  Length 431;
  Best Local Similarity   71.4%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         73 QEYRLYR 79


RESULT 6
US-11-198-819-12
; Sequence 12, Application US/11198819
; Publication No. US20050287582A1
;  GENERAL INFORMATION:
;    APPLICANT:  Adema, Gosse Jan
;    TITLE OF INVENTION:  Isolated Mammalian Monocyte Cell Genes;
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/198,819
;      FILING DATE:  04-AUG-2005
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,950
;      FILING DATE:  05-DEC-1997
;      APPLICATION NUMBER:  US 60/041,279
;      FILING DATE:  21-MARCH-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,181
;      FILING DATE:  16-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/032,252
;      FILING DATE:  06-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0670K
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1204
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  439 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
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;    MOLECULE TYPE:  protein
US-11-198-819-12

  Query Match             70.7%;  Score 29;  DB 7;  Length 439;
  Best Local Similarity   71.4%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         56 QEYHLYR 62


RESULT 7
US-10-884-730-381
; Sequence 381, Application US/10884730
; Publication No. US20050250161A1
; GENERAL INFORMATION:
;  APPLICANT: Suciu-Foca, Nicole
;  APPLICANT:  Liu, Zhuoro
;  APPLICANT:  Chang, Chih-Chao
;  APPLICANT:  Cortesini, Raffaello
;  TITLE OF INVENTION: Generation of Antigen-Specific T Suppressor Cells For Treatment o
;  TITLE OF INVENTION:  Rejection
;  FILE REFERENCE: 0575/58332-B
;  CURRENT APPLICATION NUMBER: US/10/884,730
;  CURRENT FILING DATE:  2004-07-02
;  PRIOR APPLICATION NUMBER: US/09/746,311
;  PRIOR FILING DATE: 2000-12-21
;  PRIOR APPLICATION NUMBER: PCT/US00/16594
;  PRIOR FILING DATE: 2000-06-15
;  NUMBER OF SEQ ID NOS: 382
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 381
;   LENGTH: 597
;   TYPE: PRT
;   ORGANISM: Human Immunoglobulin-Like Transcript
US-10-884-730-381

  Query Match             70.7%;  Score 29;  DB 6;  Length 597;
  Best Local Similarity   71.4%;  Pred. No. 1.9e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         56 QEYRLYR 62


RESULT 8
US-11-198-819-16
; Sequence 16, Application US/11198819
; Publication No. US20050287582A1
;  GENERAL INFORMATION:
;    APPLICANT:  Adema, Gosse Jan
;    TITLE OF INVENTION:  Isolated Mammalian Monocyte Cell Genes;
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/198,819
;      FILING DATE:  04-AUG-2005
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,950
;      FILING DATE:  05-DEC-1997
;      APPLICATION NUMBER:  US 60/041,279
;      FILING DATE:  21-MARCH-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,181
;      FILING DATE:  16-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/032,252
;      FILING DATE:  06-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0670K
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1204
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  615 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-11-198-819-16

  Query Match             70.7%;  Score 29;  DB 7;  Length 615;
  Best Local Similarity   71.4%;  Pred. No. 2e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         73 QEYRLYR 79


RESULT 9
US-11-198-819-18
; Sequence 18, Application US/11198819
; Publication No. US20050287582A1
;  GENERAL INFORMATION:
;    APPLICANT:  Adema, Gosse Jan
;    TITLE OF INVENTION:  Isolated Mammalian Monocyte Cell Genes;
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/198,819
;      FILING DATE:  04-AUG-2005
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,950
;      FILING DATE:  05-DEC-1997
;      APPLICATION NUMBER:  US 60/041,279
;      FILING DATE:  21-MARCH-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,181
;      FILING DATE:  16-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/032,252
;      FILING DATE:  06-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0670K
;    TELECOMMUNICATION INFORMATION:
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```
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1204
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  615 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-11-198-819-18

  Query Match             70.7%;  Score 29;  DB 7;  Length 615;
  Best Local Similarity   71.4%;  Pred. No. 2e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         73 QEYRLYR 79


RESULT 10
US-11-198-819-22
; Sequence 22, Application US/11198819
; Publication No. US20050287582A1
;  GENERAL INFORMATION:
;    APPLICANT:  Adema, Gosse Jan
;    TITLE OF INVENTION:  Isolated Mammalian Monocyte Cell Genes;
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DNAX Research Institute
;      STREET:  901 California Avenue
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/198,819
;      FILING DATE:  04-AUG-2005
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,950
;      FILING DATE:  05-DEC-1997
;      APPLICATION NUMBER:  US 60/041,279
;      FILING DATE:  21-MARCH-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/033,181
;      FILING DATE:  16-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/032,252
;      FILING DATE:  06-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Ching, Edwin P.
;      REGISTRATION NUMBER:  34,090
;      REFERENCE/DOCKET NUMBER:  DX0670K
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650)852-9196
;      TELEFAX:  (650)496-1204
;  INFORMATION FOR SEQ ID NO:  22:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  651 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-11-198-819-22

  Query Match             70.7%;  Score 29;  DB 7;  Length 651;
  Best Local Similarity   71.4%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db         56 QEYRLYR 62


RESULT 11
US-10-528-031-1
; Sequence 1, Application US/10528031
; Publication No. US20050262577A1
; GENERAL INFORMATION:
;  APPLICANT: ORIDIS BIOMED Forschungs- und Entwicklungs GmbH
;  APPLICANT:  Guelly, Christian
;  APPLICANT:  Buck, Charles R.
;  APPLICANT:  Zatloukal, Kurt
;  TITLE OF INVENTION: Polypeptides and nucleic acids encoding these and their use for th
;  TITLE OF INVENTION:  prevention, diagnosis or treatment of liver disorders and epithel
;  FILE REFERENCE: Oridis Biomed
;  CURRENT APPLICATION NUMBER: US/10/528,031
;  CURRENT FILING DATE:  2005-03-16
;  NUMBER OF SEQ ID NOS: 73
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 654
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-528-031-1

  Query Match             70.7%;  Score 29;  DB 6;  Length 654;
  Best Local Similarity   83.3%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              ||||:|
Db        245 QQYSVY 250


RESULT 12
US-10-491-468-47
; Sequence 47, Application US/10491468
; Publication No. US20060051836A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE CORPORATION; TANG, Y. Tom;
;  APPLICANT:  FORSYTHE, Ian J.; EMERLING, Brooke M.;
;  APPLICANT:  HAFALIA, April J.A.; YUE, Henry;
;  APPLICANT:  XU, Yuming; GIETZEN, Kimberly J.;
;  APPLICANT:  CHAWLA, Narinder K.; BAUGHN, Mariah R.;
;  APPLICANT:  MARQUIS, Joseph P.; BECHA, Shanya D.;
;  APPLICANT:  KABLE, Amy E.; LAL, Preeti G.;
;  APPLICANT:  RICHARDSON, Thomas W.; LEE, Soo Y.;
;  APPLICANT:  LEE, Ernestine A.; TRAN, Bao;
;  APPLICANT:  WARREN, Bridget A.; LU, Dyung Aina M.;
;  APPLICANT:  GURURAJAN, Rajagopal; SPRAGUE, William W.;
;  APPLICANT:  BLAKE, Julie J.; THANGAVELU, Kavitha;
;  APPLICANT:  SWARNAKAR, Anita; GORVAD, Ann E.;
;  APPLICANT:  GRIFFIN, Jennifer A.; LINDQUIST, Erika A.;
;  APPLICANT:  ELLIOTT, Vicki S.; ISON, Craig H.;
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
;  FILE REFERENCE: PF-1232 USN
;  CURRENT APPLICATION NUMBER: US/10/491,468
;  CURRENT FILING DATE:  2004-03-31
;  PRIOR APPLICATION NUMBER: PCT/US02/32852
;  PRIOR FILING DATE: 2002-10-10
;  PRIOR APPLICATION NUMBER: US 60/328,944
;  PRIOR FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: US 60/345,384
;  PRIOR FILING DATE: 2001-10-26
;  PRIOR APPLICATION NUMBER: US 60/343,880
;  PRIOR FILING DATE: 2001-11-02
;  PRIOR APPLICATION NUMBER: US 60/345,143
;  PRIOR FILING DATE: 2001-11-09
;  PRIOR APPLICATION NUMBER: US 60/332,430
;  PRIOR FILING DATE: 2001-11-16
```

```
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: PERL Program
; SEQ ID NO 47
;   LENGTH: 914
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 7766880CD1
US-10-491-468-47

  Query Match             70.7%;  Score 29;  DB 6;  Length 914;
  Best Local Similarity   75.0%;  Pred. No. 3e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              | ||||  |
Db        846 QLYSLYHS 853


RESULT 13
US-10-467-657-178
; Sequence 178, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 178
;   LENGTH: 1381
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-178

  Query Match             70.7%;  Score 29;  DB 6;  Length 1381;
  Best Local Similarity   71.4%;  Pred. No. 4.5e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |||||::
Db       1331 QQYSLFQ 1337


RESULT 14
US-10-467-657-3726
; Sequence 3726, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3726
;   LENGTH: 1381
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3726

  Query Match             70.7%;  Score 29;  DB 6;  Length 1381;
  Best Local Similarity   71.4%;  Pred. No. 4.5e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |||||::
Db       1331 QQYSLFQ 1337


RESULT 15
US-11-052-554A-372
; Sequence 372, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
;  APPLICANT: Sachdeva, et al.
;  TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
;  TITLE OF INVENTION:  PROTEINS OF THERAPEUTIC POTENTIAL
;  FILE REFERENCE: 30853/40359A
;  CURRENT APPLICATION NUMBER: US/11/052,554A
;  CURRENT FILING DATE:  2005-02-07
;  PRIOR APPLICATION NUMBER: US 60/589,227
;  PRIOR FILING DATE: 2004-07-20
;  PRIOR APPLICATION NUMBER: IN 173/DEL/2004
;  PRIOR FILING DATE: 2004-02-06
;  NUMBER OF SEQ ID NOS: 763
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 372
;   LENGTH: 1767
;   TYPE: PRT
;   ORGANISM: Streptococcus pneumoniae R6
US-11-052-554A-372

  Query Match             70.7%;  Score 29;  DB 7;  Length 1767;
  Best Local Similarity   75.0%;  Pred. No. 5.8e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              | |  ||||
Db       1037 QPYVLYRS 1044


RESULT 16
US-11-096-568A-34065
; Sequence 34065, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 34065
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(110)
;   OTHER INFORMATION: Ceres Seq. ID no. 13604966
US-11-096-568A-34065

  Query Match             68.3%;  Score 28;  DB 7;  Length 110;
  Best Local Similarity   85.7%;  Pred. No. 56;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              |||| ||
```

```
Db         16 QYSLLRS 22


RESULT 17
US-11-087-099-5754
; Sequence 5754, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5754
;   LENGTH: 160
;   TYPE: PRT
;   ORGANISM: Pseudomonas putida KT2440
US-11-087-099-5754

  Query Match             68.3%;  Score 28;  DB 7;  Length 160;
  Best Local Similarity   71.4%;  Pred. No. 82;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |::||||
Db        102 QRHSLYR 108


RESULT 18
US-10-793-626-528
; Sequence 528, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 528
;   LENGTH: 215
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-10-793-626-528

  Query Match             68.3%;  Score 28;  DB 6;  Length 215;
  Best Local Similarity   71.4%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              |:| |||
Db        144 QKYRLYR 150


RESULT 19
US-11-096-568A-23199
; Sequence 23199, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 23199
;   LENGTH: 288
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(288)
;   OTHER INFORMATION: Ceres Seq. ID no. 12411598
US-11-096-568A-23199

  Query Match             68.3%;  Score 28;  DB 7;  Length 288;
  Best Local Similarity   71.4%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              |:||||:
Db         36 QWSLYRA 42


RESULT 20
US-11-119-351-8
; Sequence 8, Application US/11119351
; Publication No. US20060010519A1
; GENERAL INFORMATION:
;  APPLICANT: Kadowaki, Koichi
;  APPLICANT:  Takahashi, Sakiko
;  APPLICANT:  Kawamukai, Makoto
;  APPLICANT:  Shimada, Hiroaki
;  TITLE OF INVENTION: Method for Producing Ubiquinone-10 in Plant
;  FILE REFERENCE: 59150-8034
;  CURRENT APPLICATION NUMBER: US/11/119,351
;  CURRENT FILING DATE:  2005-04-29
;  PRIOR APPLICATION NUMBER: JP 2004-136906
;  PRIOR FILING DATE: 2004-04-30
;  PRIOR APPLICATION NUMBER: JP 2005-000984
;  PRIOR FILING DATE: 2005-01-05
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
;   LENGTH: 446
;   TYPE: PRT
;   ORGANISM: Nicotiana tabacum
US-11-119-351-8

  Query Match             68.3%;  Score 28;  DB 7;  Length 446;
  Best Local Similarity   83.3%;  Pred. No. 2.3e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YSLYRS 8
              |:||||
Db        256 YALYRS 261


RESULT 21
US-11-072-512-3659
; Sequence 3659, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
;  APPLICANT: ISOGAI, TAKAO
;  APPLICANT:  SUGIYAMA, TOMOYASU
;  APPLICANT:  OTSUKI, TETSUJI
;  APPLICANT:  WAKAMATSU, AI
;  APPLICANT:  SATO, HIROYUKI
;  APPLICANT:  ISHII, SHIZUKO
;  APPLICANT:  YAMAMOTO, JUN-ICHI
;  APPLICANT:  ISONO, YUUKO
;  APPLICANT:  HIO, YURI
;  APPLICANT:  OTSUKA, KAORU
;  APPLICANT:  NAGAI, KEIICHI
;  APPLICANT:  IRIE, RYOTARO
;  APPLICANT:  TAMECHIKA, ICHIRO
;  APPLICANT:  SEKI, NAOHIKO
;  APPLICANT:  YOSHIKAWA, TSUTOMU
```

; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3659
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-3659

Query Match 68.3%; Score 28; DB 7; Length 476;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQYSLYR 7
| | |||
Db 127 QSYKLYR 133

RESULT 22
US-11-096-568A-25749
; Sequence 25749, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25749
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(499)
; OTHER INFORMATION: Ceres Seq. ID no. 13493254
US-11-096-568A-25749

Query Match 68.3%; Score 28; DB 7; Length 499;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYSLYR 7
|:| :||
Db 184 QEYKIYR 190

RESULT 23
US-11-096-568A-25748
; Sequence 25748, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25748
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(558)
; OTHER INFORMATION: Ceres Seq. ID no. 13493253
US-11-096-568A-25748

Query Match 68.3%; Score 28; DB 7; Length 558;
Best Local Similarity 57.1%; Pred. No. 2.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYSLYR 7
|:| :||
Db 243 QEYKIYR 249

RESULT 24
US-11-096-568A-25747
; Sequence 25747, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 25747
; LENGTH: 603
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(603)
; OTHER INFORMATION: Ceres Seq. ID no. 13493252
US-11-096-568A-25747

Query Match 68.3%; Score 28; DB 7; Length 603;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQYSLYR 7
|:| :||
Db 288 QEYKIYR 294

RESULT 25
US-11-054-281-300
; Sequence 300, Application US/11054281
; Publication No. US20060013813A1
; GENERAL INFORMATION:
; APPLICANT: Mezes et al.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-240CIP
; CURRENT APPLICATION NUMBER: US/11/054,281
; CURRENT FILING DATE: 2005-02-08
; PRIOR APPLICATION NUMBER: 60/261,014
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,018
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/318,410
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/261,013
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,026
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/261,029
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/313,170
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 10/044,564

```
;  PRIOR FILING DATE: 2002-01-11
;  NUMBER OF SEQ ID NOS: 324
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 300
;    LENGTH: 76
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:consensus
;    OTHER INFORMATION: sequence
US-11-054-281-300

  Query Match             65.9%;  Score 27;  DB 7;  Length 76;
  Best Local Similarity   71.4%;  Pred. No. 61;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYR 7
              | ||||:
Db         26 QLYSLYK 32


RESULT 26
US-10-771-257-99
; Sequence 99, Application US/10771257
; Publication No. US20050288864A1
; GENERAL INFORMATION:
;  APPLICANT: Medical Research Council
;  APPLICANT:  SISSA - Scuola Superiore Internazionale di Studi Avanzati
;  APPLICANT:  Cattaneo, Antonino
;  APPLICANT:  Maritan, Amos
;  APPLICANT:  Visintin, Michela
;  APPLICANT:  Rabbitts, Terrence H
;  APPLICANT:  Settanni, Giovanni
;  TITLE OF INVENTION: Intracellular antibodies
;  FILE REFERENCE: 18396/2272
;  CURRENT APPLICATION NUMBER: US/10/771,257
;  CURRENT FILING DATE:  2004-02-03
;  PRIOR APPLICATION NUMBER: PCT/GB02/03512
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: GB 0119004.0
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: GB 0121577.1
;  PRIOR FILING DATE: 2001-09-06
;  PRIOR APPLICATION NUMBER: GB 0200928.0
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: GB 0203569.9
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: IT RM2001A000633
;  PRIOR FILING DATE: 2001-10-25
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
;    LENGTH: 103
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-771-257-99

  Query Match             65.9%;  Score 27;  DB 6;  Length 103;
  Best Local Similarity   83.3%;  Pred. No. 83;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              |||| |
Db         89 QQYSTY 94


RESULT 27
US-10-771-257-110
; Sequence 110, Application US/10771257
; Publication No. US20050288864A1
; GENERAL INFORMATION:
;  APPLICANT: Medical Research Council
;  APPLICANT:  SISSA - Scuola Superiore Internazionale di Studi Avanzati
;  APPLICANT:  Cattaneo, Antonino
;  APPLICANT:  Maritan, Amos
;  APPLICANT:  Visintin, Michela
;  APPLICANT:  Rabbitts, Terrence H
;  APPLICANT:  Settanni, Giovanni
;  TITLE OF INVENTION: Intracellular antibodies
;  FILE REFERENCE: 18396/2272
;  CURRENT APPLICATION NUMBER: US/10/771,257
;  CURRENT FILING DATE:  2004-02-03
;  PRIOR APPLICATION NUMBER: PCT/GB02/03512
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: GB 0119004.0
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: GB 0121577.1
;  PRIOR FILING DATE: 2001-09-06
;  PRIOR APPLICATION NUMBER: GB 0200928.0
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: GB 0203569.9
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: IT RM2001A000633
;  PRIOR FILING DATE: 2001-10-25
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 110
;    LENGTH: 103
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-771-257-110

  Query Match             65.9%;  Score 27;  DB 6;  Length 103;
  Best Local Similarity   83.3%;  Pred. No. 83;
  Matches    5;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              |||| |
Db         89 QQYSTY 94


RESULT 28
US-10-771-257-111
; Sequence 111, Application US/10771257
; Publication No. US20050288864A1
; GENERAL INFORMATION:
;  APPLICANT: Medical Research Council
;  APPLICANT:  SISSA - Scuola Superiore Internazionale di Studi Avanzati
;  APPLICANT:  Cattaneo, Antonino
;  APPLICANT:  Maritan, Amos
;  APPLICANT:  Visintin, Michela
;  APPLICANT:  Rabbitts, Terrence H
;  APPLICANT:  Settanni, Giovanni
;  TITLE OF INVENTION: Intracellular antibodies
;  FILE REFERENCE: 18396/2272
;  CURRENT APPLICATION NUMBER: US/10/771,257
;  CURRENT FILING DATE:  2004-02-03
;  PRIOR APPLICATION NUMBER: PCT/GB02/03512
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: GB 0119004.0
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: GB 0121577.1
;  PRIOR FILING DATE: 2001-09-06
;  PRIOR APPLICATION NUMBER: GB 0200928.0
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: GB 0203569.9
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: IT RM2001A000633
;  PRIOR FILING DATE: 2001-10-25
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 111
;    LENGTH: 103
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-771-257-111
```

Query Match 65.9%; Score 27; DB 6; Length 103;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 QQYSLY 6
              |||| |
Db         89 QQYSTY 94
```

RESULT 29
US-10-771-257-113
; Sequence 113, Application US/10771257
; Publication No. US20050288864A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: SISSA - Scuola Superiore Internazionale di Studi Avanzati
; APPLICANT: Cattaneo, Antonino
; APPLICANT: Maritan, Amos
; APPLICANT: Visintin, Michela
; APPLICANT: Rabbitts, Terrence H
; APPLICANT: Settanni, Giovanni
; TITLE OF INVENTION: Intracellular antibodies
; FILE REFERENCE: 18396/2272
; CURRENT APPLICATION NUMBER: US/10/771,257
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: PCT/GB02/03512
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: GB 0119004.0
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: GB 0121577.1
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: GB 0200928.0
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: GB 0203569.9
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: IT RM2001A000633
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 113
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-771-257-113

Query Match 65.9%; Score 27; DB 6; Length 103;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 QQYSLY 6
              |||| |
Db         89 QQYSTY 94
```

RESULT 30
US-10-530-253-22
; Sequence 22, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Cassetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhiney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Human papillomavirus type 52
US-10-530-253-22

Query Match 65.9%; Score 27; DB 6; Length 148;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 QYSLY 6
              |||||
Db         80 QYSLY 84
```

RESULT 31
US-11-072-512-2902
; Sequence 2902, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2902
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2902

Query Match 65.9%; Score 27; DB 7; Length 148;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 QQYSLYRS 8
              ::|||| :
Db         20 EEYSLYEA 27
```

RESULT 32
US-11-096-568A-34286
; Sequence 34286, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides E
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2

```
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 34286
;   LENGTH: 292
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(292)
;   OTHER INFORMATION: Ceres Seq. ID no. 13605711
US-11-096-568A-34286

  Query Match            65.9%;  Score 27;  DB 7;  Length 292;
  Best Local Similarity  62.5%;  Pred. No. 2.4e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ::||| ||
Db         51 EEYSLLRS 58


RESULT 33
US-11-096-568A-34285
; Sequence 34285, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 34285
;   LENGTH: 324
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(324)
;   OTHER INFORMATION: Ceres Seq. ID no. 13605710
US-11-096-568A-34285

  Query Match            65.9%;  Score 27;  DB 7;  Length 324;
  Best Local Similarity  62.5%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ::||| ||
Db         83 EEYSLLRS 90


RESULT 34
US-11-096-568A-34284
; Sequence 34284, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 34284
;   LENGTH: 350
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(350)
;   OTHER INFORMATION: Ceres Seq. ID no. 13605709
US-11-096-568A-34284

  Query Match            65.9%;  Score 27;  DB 7;  Length 350;
  Best Local Similarity  62.5%;  Pred. No. 2.9e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              ::||| ||
Db        109 EEYSLLRS 116


RESULT 35
US-11-087-099-6378
; Sequence 6378, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6378
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Nicotiana tabacum
US-11-087-099-6378

  Query Match            65.9%;  Score 27;  DB 7;  Length 384;
  Best Local Similarity  62.5%;  Pred. No. 3.2e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| |::
Db        320 QQYSGYKA 327


RESULT 36
US-11-202-731-33
; Sequence 33, Application US/11202731
; Publication No. US20060037104A1
; GENERAL INFORMATION:
;  APPLICANT: Green, Allan
;  APPLICANT:  Singh, Surinder
;  APPLICANT:  Liu, Qing
;  TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
;  FILE REFERENCE: 45-00
;  CURRENT APPLICATION NUMBER: US/11/202,731
;  CURRENT FILING DATE:  2005-08-12
;  PRIOR APPLICATION NUMBER: US/09/837,751
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: US 60/198,124
;  PRIOR FILING DATE: 2000-04-18
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Glycine max
US-11-202-731-33

  Query Match            65.9%;  Score 27;  DB 7;  Length 387;
  Best Local Similarity  100.0%;  Pred. No. 3.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 YSLYR 7
              |||||
Db        241 YSLYR 245


RESULT 37
US-10-821-234-1583
; Sequence 1583, Application US/10821234
```

```
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1583
;   LENGTH: 398
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-821-234-1583

  Query Match             65.9%;  Score 27;  DB 6;  Length 398;
  Best Local Similarity   62.5%;  Pred. No. 3.3e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||:: ||
Db        216 QQYNITRS 223


RESULT 38
US-11-096-568A-33433
; Sequence 33433, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 33433
;   LENGTH: 409
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(409)
;   OTHER INFORMATION: Ceres Seq. ID no. 13603086
US-11-096-568A-33433

  Query Match             65.9%;  Score 27;  DB 7;  Length 409;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              ||:|||
Db          8 QQHSLY 13


RESULT 39
US-11-096-568A-33432
; Sequence 33432, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 33432
;   LENGTH: 410
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(410)
;   OTHER INFORMATION: Ceres Seq. ID no. 13603085
US-11-096-568A-33432

  Query Match             65.9%;  Score 27;  DB 7;  Length 410;
  Best Local Similarity   83.3%;  Pred. No. 3.4e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              ||:|||
Db          9 QQHSLY 14


RESULT 40
US-11-096-568A-33431
; Sequence 33431, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 33431
;   LENGTH: 427
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(427)
;   OTHER INFORMATION: Ceres Seq. ID no. 13603084
US-11-096-568A-33431

  Query Match             65.9%;  Score 27;  DB 7;  Length 427;
  Best Local Similarity   83.3%;  Pred. No. 3.5e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 QQYSLY 6
              ||:|||
Db         26 QQHSLY 31


RESULT 41
US-11-018-868-49
; Sequence 49, Application US/11018868
; Publication No. US20060034871A1
; GENERAL INFORMATION:
;  APPLICANT: Chiron Corporation
;  APPLICANT:  Grandi, Guido
;  APPLICANT:  Ratti, Guilio
;  APPLICANT:  Bonci, Alessandro
;  APPLICANT:  Finco, Oretta
;  TITLE OF INVENTION: Immunogenic Compositions for Chlamydia trachomatis
;  FILE REFERENCE: 002441.00099 (PP23152.001)
;  CURRENT APPLICATION NUMBER: US/11/018,868
;  CURRENT FILING DATE:  2004-12-22
;  NUMBER OF SEQ ID NOS: 186
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
;   LENGTH: 442
;   TYPE: PRT
;   ORGANISM: Chlamydia trachomatis
US-11-018-868-49

  Query Match             65.9%;  Score 27;  DB 7;  Length 442;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+02;
```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 QYSLY 6
              |||||
Db        208 QYSLY 212
```

RESULT 42
US-11-087-099-398
; Sequence 398, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 398
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-11-087-099-398

Query Match 65.9%; Score 27; DB 7; Length 485;
Best Local Similarity 62.5%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 QQYSLYRS 8
              :: |||||
Db        179 EEISLYRS 186
```

RESULT 43
US-11-010-239-14
; Sequence 14, Application US/11010239
; Publication No. US20060015970A1
; GENERAL INFORMATION:
; APPLICANT: Roger PENNELL
; APPLICANT: Jack OKAMURO
; APPLICANT: Richard SCHNEEBERGER
; APPLICANT: Yiwen FANG
; APPLICANT: Shing KWOK
; APPLICANT: Diane JOFUKU
; APPLICANT: Edward A. KIEGLE
; APPLICANT: Jonathan DONSON
; APPLICANT: Nestor APUYA
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
; TITLE OF INVENTION: MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1585PUS2
; CURRENT APPLICATION NUMBER: US/11/010,239
; CURRENT FILING DATE: 2004-12-09
; PRIOR APPLICATION NUMBER: US 60/529,352
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(488)
; OTHER INFORMATION: 6795099_protein_ID_6795100
US-11-010-239-14

Query Match 65.9%; Score 27; DB 7; Length 488;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 QYSLY 6
              |||||
Db        179 QYSLY 183
```

RESULT 44
US-10-499-290-2
; Sequence 2, Application US/10499290
; Publication No. US20060051362A1
; GENERAL INFORMATION:
; APPLICANT: Jacques, Mario
; APPLICANT: Coulton, James
; APPLICANT: Mikael, Leonie G.
; APPLICANT: Khamessan, Ali
; APPLICANT: Sirois, Marc
; APPLICANT: Universite de Montreal
; APPLICANT: McGill University
; APPLICANT: Universite du Quebec a Trois-Rivieres
; TITLE OF INVENTION: Antigens for Actinobacillus
; TITLE OF INVENTION: pleuropneumoniae and methods thereof
; FILE REFERENCE: 10662-113ep
; CURRENT APPLICATION NUMBER: US/10/499,290
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US 60/340,483
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A. pleuropneumoniae FhuA sequence
US-10-499-290-2

Query Match 65.9%; Score 27; DB 6; Length 672;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 QYSLY 6
              |||||
Db        361 QYSLY 365
```

RESULT 45
US-11-052-554A-110
; Sequence 110, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
; APPLICANT: Sachdeva, et al.
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 110
; LENGTH: 697
; TYPE: PRT
; ORGANISM: Helicobacter pylori J99
US-11-052-554A-110

Query Match 65.9%; Score 27; DB 7; Length 697;
Best Local Similarity 83.3%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          3 YSLYRS 8
              | ||||
Db        488 YGLYRS 493
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RESULT 46
US-11-052-554A-102
; Sequence 102, Application US/11052554A
; Publication No. US20050288866A1
; GENERAL INFORMATION:
;  APPLICANT: Sachdeva, et al.
;  TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
;  TITLE OF INVENTION:  PROTEINS OF THERAPEUTIC POTENTIAL
;  FILE REFERENCE: 30853/40359A
;  CURRENT APPLICATION NUMBER: US/11/052,554A
;  CURRENT FILING DATE:  2005-02-07
;  PRIOR APPLICATION NUMBER: US 60/589,227
;  PRIOR FILING DATE: 2004-07-20
;  PRIOR APPLICATION NUMBER: IN 173/DEL/2004
;  PRIOR FILING DATE: 2004-02-06
;  NUMBER OF SEQ ID NOS: 763
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 102
;   LENGTH: 841
;   TYPE: PRT
;   ORGANISM: Helicobacter pylori J99
US-11-052-554A-102

  Query Match             65.9%;  Score 27;  DB 7;  Length 841;
  Best Local Similarity   71.4%;  Pred. No. 7e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 QYSLYRS 8
              |||:| |
Db        629 QYSVYTS 635


RESULT 47
US-10-517-939-120
; Sequence 120, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
;  APPLICANT: Steer, Brian
;  APPLICANT:  Callen, Walter
;  APPLICANT:  Healey, Shaun
;  APPLICANT:  Hazlewood, Geoff
;  APPLICANT:  Wu, Di
;  APPLICANT:  Blum, David
;  APPLICANT:  Esteghlalian, Alireza
;  TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
;  TITLE OF INVENTION:  AND METHODS FOR MAKING AND USING THEM
;  FILE REFERENCE: 564462007901
;  CURRENT APPLICATION NUMBER: US/10/517,939
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: PCT/US03/19153
;  PRIOR FILING DATE: 2003-06-16
;  PRIOR APPLICATION NUMBER: 60/389,299
;  PRIOR FILING DATE: 2002-06-14
;  NUMBER OF SEQ ID NOS: 380
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 120
;   LENGTH: 852
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Obtained from an environmental sample
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(33)
US-10-517-939-120

  Query Match             65.9%;  Score 27;  DB 6;  Length 852;
  Best Local Similarity   75.0%;  Pred. No. 7.1e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||| | |
Db        516 QQYSQYFS 523


RESULT 48
US-11-144-987-16
; Sequence 16, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
;  APPLICANT: Mellis, Scott
;  APPLICANT:  Karow, Margaret
;  APPLICANT:  Yancopoulos, George
;  APPLICANT:  Papadopoulos, Joanne
;  TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Diseas
;  FILE REFERENCE: REG 2090A
;  CURRENT APPLICATION NUMBER: US/11/144,987
;  CURRENT FILING DATE:  2005-06-03
;  PRIOR APPLICATION NUMBER: 60/577,023
;  PRIOR FILING DATE: 2004-06-04
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 915
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-144-987-16

  Query Match             65.9%;  Score 27;  DB 7;  Length 915;
  Best Local Similarity   62.5%;  Pred. No. 7.6e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||:: ||
Db        216 QQYNITRS 223


RESULT 49
US-11-144-987-22
; Sequence 22, Application US/11144987
; Publication No. US20050272655A1
; GENERAL INFORMATION:
;  APPLICANT: Mellis, Scott
;  APPLICANT:  Karow, Margaret
;  APPLICANT:  Yancopoulos, George
;  APPLICANT:  Papadopoulos, Joanne
;  TITLE OF INVENTION: Methods of Using IL-1 Antagonists to Treat Autoinflammatory Diseas
;  FILE REFERENCE: REG 2090A
;  CURRENT APPLICATION NUMBER: US/11/144,987
;  CURRENT FILING DATE:  2005-06-03
;  PRIOR APPLICATION NUMBER: 60/577,023
;  PRIOR FILING DATE: 2004-06-04
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
;   LENGTH: 915
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-144-987-22

  Query Match             65.9%;  Score 27;  DB 7;  Length 915;
  Best Local Similarity   62.5%;  Pred. No. 7.6e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||:: ||
Db        554 QQYNITRS 561


RESULT 50
US-11-205-935-16
; Sequence 16, Application US/11205935
; Publication No. US20060040852A1
; GENERAL INFORMATION:
;  APPLICANT: Dix, Daniel
;  APPLICANT:  Bowers, Katherine
```

```
;  TITLE OF INVENTION: IL-1 Antagonist Formulations
;  FILE REFERENCE: 3020A
;  CURRENT APPLICATION NUMBER: US/11/205,935
;  CURRENT FILING DATE:  2005-08-17
;  PRIOR APPLICATION NUMBER: 60/602,137
;  PRIOR FILING DATE: 2004-08-17
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
;   LENGTH: 915
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-205-935-16

  Query Match             65.9%;  Score 27;  DB 7;  Length 915;
  Best Local Similarity   62.5%;  Pred. No. 7.6e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 QQYSLYRS 8
              |||:: ||
Db        216 QQYNITRS 223


Search completed: March 23, 2006, 02:53:03
Job time : 11.7945 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:40:10 ; Search time 43.4931 Seconds
(without alignments)
50.511 Million cell updates/sec

Title: US-10-755-382-23
Perfect score: 32
Sequence: 1 TYWMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	5	2	AAR97316	Aar97316 Humanised
2	32	100.0	5	2	AAY05038	Aay05038 Tumour an
3	32	100.0	5	7	ADC82794	Adc82794 CDR regio
4	32	100.0	5	8	ADM95105	Adm95105 Murine MN
5	32	100.0	5	8	ADM98314	Adm98314 Humanised
6	32	100.0	118	6	ABR42755	Abr42755 Anti-CEA
7	32	100.0	119	2	AAR97334	Aar97334 Murine NE
8	32	100.0	119	8	ADM95101	Adm95101 Humanised
9	32	100.0	119	8	ADM95095	Adm95095 Murine MN
10	32	100.0	119	8	ADM98324	Adm98324 Humanised
11	32	100.0	119	8	ADM98318	Adm98318 Murine MN
12	32	100.0	138	6	ABG76489	Abg76489 Heavy cha
13	32	100.0	236	7	ADF43574	Adf43574 Rice pero
14	32	100.0	256	6	ABR42757	Abr42757 Anti-CEA
15	32	100.0	257	6	ABR42758	Abr42758 Anti-CEA
16	32	100.0	261	6	ABR42289	Abr42289 Diabody 6
17	32	100.0	261	6	ABR42754	Abr42754 Anti-CEA
18	32	100.0	261	6	ABR83645	Abr83645 hMN14-scF
19	32	100.0	267	6	ABR42292	Abr42292 Bispecifi
20	32	100.0	267	6	ABR42299	Abr42299 Bispecifi
21	32	100.0	267	6	ABR42296	Abr42296 Bispecifi
22	32	100.0	267	6	ABR42294	Abr42294 Bispecifi
23	32	100.0	358	8	ADU26571	Adu26571 Chimeric
24	32	100.0	363	8	ADU26561	Adu26561 Chimeric
25	32	100.0	364	8	ADU26570	Adu26570 Chimeric
26	32	100.0	370	8	ADU26560	Adu26560 Chimeric
27	32	100.0	415	6	ABR83648	Abr83648 TS1 VH ch
28	32	100.0	443	6	ABG76488	Abg76488 Humanised
29	32	100.0	443	6	ABG74240	Abg74240 Chimaeric
30	32	100.0	448	8	ADS42718	Ads42718 Bacterial
31	32	100.0	464	8	ADN17753	Adn17753 Bacterial
32	32	100.0	468	7	ADE64201	Ade64201 MN14HCF p
33	32	100.0	468	7	ADF60815	Adf60815 hMN-14 he
34	32	100.0	490	6	ABM66981	Abm66981 Photorhab
35	32	100.0	597	4	ABB63205	Abb63205 Drosophil
36	32	100.0	597	8	ADO07980	Ado07980 Fly polyp
37	32	100.0	669	9	ADY97271	Ady97271 Exemplary
38	29	90.6	5	8	ADU87696	Adu87696 Mouse Luc
39	29	90.6	46	3	AAG16081	Aag16081 Arabidops
40	29	90.6	52	3	AAG16080	Aag16080 Arabidops
41	29	90.6	69	4	AAM06667	Aam06667 Human foe
42	29	90.6	83	6	ABR41152	Abr41152 Human DIT
43	29	90.6	109	6	ABU40094	Abu40094 Protein e
44	29	90.6	114	6	ABR54978	Abr54978 Mouse IgG
45	29	90.6	114	6	ABR54977	Abr54977 Mouse IgG
46	29	90.6	114	6	ABR54979	Abr54979 Mouse IgG
47	29	90.6	115	2	AAW26796	Aaw26796 Anti-gp54
48	29	90.6	115	8	ADQ66863	Adq66863 Novel hum
49	29	90.6	115	9	ADY85022	Ady85022 Monoclona
50	29	90.6	120	8	ADU87690	Adu87690 Mouse Luc
51	29	90.6	124	3	AAG31923	Aag31923 Arabidops
52	29	90.6	125	7	ABO72970	Abo72970 Pseudomon
53	29	90.6	158	9	ADW22661	Adw22661 B. halodu
54	29	90.6	214	8	ADO57604	Ado57604 Actinobac
55	29	90.6	233	6	ABP79500	Abp79500 N. gonorr
56	29	90.6	233	6	ABP76741	Abp76741 N. gonorr
57	29	90.6	240	2	AAW26799	Aaw26799 Anti-gp54
58	29	90.6	261	7	ABO65211	Abo65211 Klebsiell
59	29	90.6	269	2	AAW28052	Aaw28052 Amino aci
60	29	90.6	312	3	AAG59983	Aag59983 Arabidops
61	29	90.6	370	3	AAG59982	Aag59982 Arabidops
62	29	90.6	381	3	AAG59981	Aag59981 Arabidops
63	29	90.6	443	8	ADT58427	Adt58427 Plant pol
64	29	90.6	449	6	ABU00144	Abu00144 Human nov
65	29	90.6	462	5	AAE29156	Aae29156 Human tra
66	29	90.6	462	6	ABU23194	Abu23194 Protein e
67	29	90.6	462	8	ADQ76151	Adq76151 Human nov
68	29	90.6	478	4	AAU36887	Aau36887 Staphyloc
69	29	90.6	478	4	AAU34223	Aau34223 Staphyloc
70	29	90.6	478	6	ABU16061	Abu16061 Protein e
71	29	90.6	478	6	ABM71983	Abm71983 Staphyloc
72	29	90.6	479	7	ABO67461	Abo67461 Klebsiell
73	29	90.6	485	6	ABU30471	Abu30471 Protein e
74	29	90.6	488	4	AAG78335	Aag78335 Maize def
75	29	90.6	508	7	ADG28896	Adg28896 Perennial
76	29	90.6	543	6	ABU41233	Abu41233 Protein e
77	29	90.6	543	7	ADF06616	Adf06616 Bacterial
78	29	90.6	546	7	ABO70343	Abo70343 Pseudomon
79	29	90.6	557	6	ABM68214	Abm68214 Photorhab
80	29	90.6	671	7	ADB70231	Adb70231 C. neofor
81	29	90.6	1081	8	ADN21336	Adn21336 Bacterial
82	29	90.6	1139	8	ADN23559	Adn23559 Bacterial
83	29	90.6	1382	4	ABB64066	Abb64066 Drosophil
84	29	90.6	1382	7	ADD15300	Add15300 Fruitfly
85	29	90.6	1463	4	ABB61943	Abb61943 Drosophil
86	29	90.6	1981	4	ABB61657	Abb61657 Drosophil
87	28	87.5	5	2	AAW24546	Aaw24546 CDR #1 of
88	28	87.5	5	2	AAW44181	Aaw44181 Monoclona
89	28	87.5	5	4	AAB61293	Aab61293 Anti-TANG
90	28	87.5	5	6	ABU11259	Abu11259 Human TAN
91	28	87.5	5	8	ADO36523	Ado36523 Human ant
92	28	87.5	5	8	ADO36535	Ado36535 Human ant
93	28	87.5	5	8	ADP79381	Adp79381 Thyrotrop
94	28	87.5	5	9	ADY70250	Ady70250 Human Mab
95	28	87.5	5	9	ADZ45386	Adz45386 Murine fa
96	28	87.5	5	9	AEA45693	Aea45693 Apolipopr
97	28	87.5	6	8	ADQ91432	Adq91432 CDR1 of t

98	28	87.5	9	7	ADE78686	Ade78686 Interleuk
99	28	87.5	9	7	ADE78853	Ade78853 Interleuk
100	28	87.5	9	7	ADE78946	Ade78946 Interleuk
101	28	87.5	10	7	ADE78854	Ade78854 Interleuk
102	28	87.5	10	7	ADM07751	Adm07751 Canine im
103	28	87.5	10	9	ADY80103	Ady80103 Anti-ghre
104	28	87.5	11	9	ADW95773	Adw95773 Anti-hIL-
105	28	87.5	11	9	ADX15778	Adx15778 Mouse ant
106	28	87.5	14	2	AAR93502	Aar93502 Class II
107	28	87.5	58	9	AEC20858	Aec20858 Human var
108	28	87.5	73	4	ABG04412	Abg04412 Novel hum
109	28	87.5	75	4	ABG21729	Abg21729 Novel hum
110	28	87.5	78	4	AAU49766	Aau49766 Propionib
111	28	87.5	78	6	ABM46285	Abm46285 Propionib
112	28	87.5	88	8	ADY13264	Ady13264 Plant ful
113	28	87.5	94	4	AAM18767	Aam18767 Peptide #
114	28	87.5	94	4	ABB37867	Abb37867 Peptide #
115	28	87.5	94	4	AAM31274	Aam31274 Peptide #
116	28	87.5	94	4	ABB23126	Abb23126 Protein #
117	28	87.5	94	4	AAM70996	Aam70996 Human bon
118	28	87.5	94	4	AAM58498	Aam58498 Human bra
119	28	87.5	94	4	ABG52713	Abg52713 Human liv
120	28	87.5	94	5	ABG40786	Abg40786 Human pep
121	28	87.5	98	2	AAR52066	Aar52066 Heavy cha
122	28	87.5	98	2	AAR72074	Aar72074 DP54 VH r
123	28	87.5	98	3	AAB40138	Aab40138 Anti-hIL1
124	28	87.5	98	3	AAB40140	Aab40140 Anti-hIL1
125	28	87.5	98	4	AAU44076	Aau44076 Propionib
126	28	87.5	98	5	ABG78210	Abg78210 Human Fv
127	28	87.5	98	5	ABG91901	Abg91901 Human ant
128	28	87.5	98	6	ABM40595	Abm40595 Propionib
129	28	87.5	98	6	ABO27082	Abo27082 Human ger
130	28	87.5	98	7	ADD28039	Add28039 Lymphoma
131	28	87.5	98	7	ADF10017	Adf10017 VEGF anti
132	28	87.5	98	7	ADF10119	Adf10119 Antibody
133	28	87.5	98	7	ADF09909	Adf09909 Antibody
134	28	87.5	98	7	ADJ80295	Adj80295 VH gene l
135	28	87.5	98	9	ADY75300	Ady75300 Protein e
136	28	87.5	98	9	ADY93869	Ady93869 Anti-SARS
137	28	87.5	98	9	AEC20847	Aec20847 Human var
138	28	87.5	99	8	ADO36508	Ado36508 Human ant
139	28	87.5	109	6	ABR55320	Abr55320 Amino aci
140	28	87.5	113	8	ADS16561	Ads16561 Human ant
141	28	87.5	114	6	ABR54987	Abr54987 Mouse IgG
142	28	87.5	114	9	ADY80112	Ady80112 Anti-ghre
143	28	87.5	114	9	ADY80111	Ady80111 Anti-ghre
144	28	87.5	117	2	AAR66301	Aar66301 Human imm
145	28	87.5	117	2	AAW00831	Aaw00831 Variable
146	28	87.5	117	2	AAW19017	Aaw19017 Anti-huma
147	28	87.5	117	5	AAE25526	Aae25526 S. aureus
148	28	87.5	117	8	ADO36504	Ado36504 Human ant
149	28	87.5	117	8	ADO36496	Ado36496 Human ant
150	28	87.5	118	4	AAB70168	Aab70168 S19 singl
151	28	87.5	119	2	AAR97336	Aar97336 Humanised
152	28	87.5	119	8	ADP79380	Adp79380 Thyrotrop
153	28	87.5	119	9	ADZ45385	Adz45385 Murine fa
154	28	87.5	119	9	AEA41075	Aea41075 Germline
155	28	87.5	120	7	ADD94123	Add94123 Human VHI
156	28	87.5	120	8	ADG25804	Adg25804 Anti-CD30
157	28	87.5	120	8	ADP03721	Adp03721 Human ant
158	28	87.5	120	9	ADW95772	Adw95772 Mouse ant
159	28	87.5	120	9	ADX15777	Adx15777 Mouse ant
160	28	87.5	123	4	AAB62777	Aab62777 Human HIV
161	28	87.5	123	4	AAB62778	Aab62778 Human HIV
162	28	87.5	123	5	ABG30971	Abg30971 Immunoglo
163	28	87.5	124	8	ADP79384	Adp79384 Thyrotrop
164	28	87.5	125	4	AAB62776	Aab62776 Human HIV
165	28	87.5	128	9	AEA88768	Aea88768 Murine SA
166	28	87.5	129	9	ADY70208	Ady70208 Human mon
167	28	87.5	130	2	AAW24537	Aaw24537 Immunoglo
168	28	87.5	133	5	ABG30972	Abg30972 Immunoglo
169	28	87.5	137	2	AAW44177	Aaw44177 Monoclona
170	28	87.5	140	4	AAO01873	Aao01873 Human pol
171	28	87.5	141	2	AAW01631	Aaw01631 Ber-H2 he
172	28	87.5	157	6	ABR55915	Abr55915 Human mAb
173	28	87.5	157	6	ABR55886	Abr55886 Human mAb
174	28	87.5	161	3	AAG22586	Aag22586 Zea mays
175	28	87.5	163	6	ABJ36937	Abj36937 Anti-CD40
176	28	87.5	192	3	AAG26434	Aag26434 Arabidops
177	28	87.5	198	5	ABB07194	Abb07194 Human Ztg
178	28	87.5	212	5	ABB07193	Abb07193 Human Ztg
179	28	87.5	212	5	AAE22223	Aae22223 Human tra
180	28	87.5	212	6	AAO27010	Aao27010 NSG3 prot
181	28	87.5	213	4	AAG65911	Aag65911 Amino aci
182	28	87.5	236	8	ADN25904	Adn25904 Bacterial
183	28	87.5	240	6	ABU24779	Abu24779 Protein e
184	28	87.5	240	7	ABO79282	Abo79282 Pseudomon
185	28	87.5	241	5	ABP45878	Abp45878 Human BLy
186	28	87.5	241	7	ADG96705	Adg96705 Single ch
187	28	87.5	243	9	ADW95684	Adw95684 Anti-IL-6
188	28	87.5	243	9	ADX15689	Adx15689 Mouse ant
189	28	87.5	247	5	ABP45459	Abp45459 Human BLy
190	28	87.5	247	6	AAO31142	Aao31142 Human CM0
191	28	87.5	247	7	ADG96286	Adg96286 Single ch
192	28	87.5	247	9	ADY34215	Ady34215 TRAIL rec
193	28	87.5	247	9	ABM92236	Abm92236 M. xanthu
194	28	87.5	251	4	AAB70171	Aab70171 Recombina
195	28	87.5	251	4	AAB70173	Aab70173 Recombina
196	28	87.5	251	5	ABP45583	Abp45583 Human BLy
197	28	87.5	251	7	ADG98061	Adg98061 TNF proli
198	28	87.5	251	7	ADG96410	Adg96410 Single ch
199	28	87.5	262	6	ABU41087	Abu41087 Protein e
200	28	87.5	263	7	ADF03925	Adf03925 Bacterial
201	28	87.5	264	4	AAB70170	Aab70170 S19 ScFv
202	28	87.5	264	5	AAU75152	Aau75152 Protein f
203	28	87.5	265	5	AAU75154	Aau75154 Protein f
204	28	87.5	265	5	AAU75149	Aau75149 Amino aci
205	28	87.5	265	5	AAU75153	Aau75153 Protein f
206	28	87.5	269	3	AAG26433	Aag26433 Arabidops
207	28	87.5	269	9	ADY77497	Ady77497 Paraquat
208	28	87.5	271	2	AAW90180	Aaw90180 Human clo
209	28	87.5	273	2	AAW64233	Aaw64233 Murine mM
210	28	87.5	273	2	AAW64235	Aaw64235 Rat homol
211	28	87.5	273	4	ABG04411	Abg04411 Novel hum
212	28	87.5	273	7	ADD47563	Add47563 Rat Prote
213	28	87.5	273	7	ADD47559	Add47559 Rat Prote
214	28	87.5	273	7	ADE62890	Ade62890 Rat Prote
215	28	87.5	280	5	ABB99912	Abb99912 Human mac
216	28	87.5	283	8	ADP03815	Adp03815 Human ant
217	28	87.5	283	8	ADX92031	Adx92031 Plant ful
218	28	87.5	288	3	AAG26432	Aag26432 Arabidops
219	28	87.5	290	8	ADN06987	Adn06987 Human EFG
220	28	87.5	291	7	ADM05075	Adm05075 Human pro
221	28	87.5	294	8	ADN47460	Adn47460 Thermococ
222	28	87.5	296	7	ADH88320	Adh88320 Enterococ
223	28	87.5	303	8	ADR20053	Adr20053 Human imm
224	28	87.5	310	5	AAE14343	Aae14343 Human pro
225	28	87.5	310	8	ADS75553	Ads75553 IL13-R-al
226	28	87.5	312	2	AAW83323	Aaw83323 Single ch
227	28	87.5	312	5	ABB09604	Abb09604 Amino aci
228	28	87.5	312	6	ABG74385	Abg74385 Single ch
229	28	87.5	312	7	ADG98738	Adg98738 Human sin
230	28	87.5	312	8	ADO40447	Ado40447 Human sin
231	28	87.5	315	2	AAW56261	Aaw56261 Mature in
232	28	87.5	317	5	AAE13746	Aae13746 Human sol
233	28	87.5	319	5	ABB55188	Abb55188 Lactococc
234	28	87.5	330	4	AAB70842	Aab70842 SNV-env l
235	28	87.5	359	2	AAW56260	Aaw56260 Construct
236	28	87.5	364	2	AAW01457	Aaw01457 E. coli O
237	28	87.5	364	2	AAY03222	Aay03222 F12 regio
238	28	87.5	366	2	AAW88316	Aaw88316 E. coli O
239	28	87.5	366	7	ADC01225	Adc01225 Enterohae
240	28	87.5	372	2	AAW36616	Aaw36616 Celebus m
241	28	87.5	380	2	AAW36613	Aaw36613 Human Zcy
242	28	87.5	380	2	AAW36614	Aaw36614 Human Zcy
243	28	87.5	380	2	AAW35295	Aaw35295 Human IL-

244	28	87.5	380	2	AAW24972	Aaw24972 Human int
245	28	87.5	380	2	AAW33603	Aaw33603 Homo sapi
246	28	87.5	380	2	AAW41502	Aaw41502 Human cyt
247	28	87.5	380	2	AAW41520	Aaw41520 Human HR-
248	28	87.5	380	3	AAY95296	Aay95296 IL-13 bin
249	28	87.5	380	4	AAG63812	Aag63812 Amino aci
250	28	87.5	380	4	AAY72136	Aay72136 Human int
251	28	87.5	380	4	AAB29748	Aab29748 Human IL-
252	28	87.5	380	5	AAM49201	Aam49201 Human IL-
253	28	87.5	380	6	ABR58523	Abr58523 Human int
254	28	87.5	380	7	ADE78646	Ade78646 Human int
255	28	87.5	380	8	ADJ75305	Adj75305 Marker ge
256	28	87.5	380	8	ADS75556	Ads75556 Full-leng
257	28	87.5	380	9	ADX97892	Adx97892 Human IL-
258	28	87.5	380	9	ADY57304	Ady57304 Human int
259	28	87.5	388	7	ABM86626	Abm86626 Rice abio
260	28	87.5	395	4	AAG90944	Aag90944 C glutami
261	28	87.5	395	7	ADD13735	Add13735 C. glutam
262	28	87.5	402	8	ADN21966	Adn21966 Bacterial
263	28	87.5	402	8	ADN24723	Adn24723 Bacterial
264	28	87.5	429	3	AAB26811	Aab26811 Beta-prim
265	28	87.5	440	6	AAO19845	Aao19845 L pneumop
266	28	87.5	448	5	ABB93325	Abb93325 Herbicida
267	28	87.5	451	4	AAU01689	Aau01689 Gene 31 h
268	28	87.5	454	3	AAG34331	Aag34331 Zea mays
269	28	87.5	455	4	AAU64449	Aau64449 Propionib
270	28	87.5	455	6	ABM60968	Abm60968 Propionib
271	28	87.5	463	9	AEA41021	Aea41021 Human ant
272	28	87.5	476	6	ADA34663	Ada34663 Acinetoba
273	28	87.5	495	3	AAG34330	Aag34330 Zea mays
274	28	87.5	499	6	ABM64775	Abm64775 Propionib
275	28	87.5	507	3	AAB26813	Aab26813 Beta-prim
276	28	87.5	508	7	ADF76572	Adf76572 Novel hum
277	28	87.5	508	8	ABM82045	Abm82045 Tumour-as
278	28	87.5	508	8	ADP55154	Adp55154 Human PRO
279	28	87.5	508	9	ADW08817	Adw08817 Human pro
280	28	87.5	508	9	ADY17188	Ady17188 PRO polyp
281	28	87.5	511	3	AAB43615	Aab43615 Human can
282	28	87.5	512	5	ABB78696	Abb78696 C. elegan
283	28	87.5	515	9	AEB41440	Aeb41440 L. pneumo
284	28	87.5	519	6	ABM68916	Abm68916 Photorhab
285	28	87.5	519	6	ABU30460	Abu30460 Protein e
286	28	87.5	527	3	AAG34329	Aag34329 Zea mays
287	28	87.5	530	9	AEB38151	Aeb38151 L. pneumo
288	28	87.5	534	7	ADG42180	Adg42180 Human bra
289	28	87.5	565	9	ADX97899	Adx97899 Human IL-
290	28	87.5	567	6	ADA55339	Ada55339 Human pro
291	28	87.5	589	4	ABU52814	Abu52814 Human met
292	28	87.5	595	8	ADN22615	Adn22615 Bacterial
293	28	87.5	609	9	AEA16966	Aea16966 Arabidops
294	28	87.5	624	8	ADG93433	Adg93433 Bacillus
295	28	87.5	648	4	AAE02444	Aae02444 Murine be
296	28	87.5	648	7	ADF28924	Adf28924 Murine be
297	28	87.5	648	9	AEB18191	Aeb18191 Mouse bet
298	28	87.5	729	4	ABB59797	Abb59797 Drosophil
299	28	87.5	810	8	ADN21532	Adn21532 Bacterial
300	28	87.5	852	8	ADN18992	Adn18992 Bacterial
301	28	87.5	914	5	AAG66094	Aag66094 Soybean a
302	28	87.5	921	8	ADN73365	Adn73365 Thale cre
303	28	87.5	921	8	ADP88502	Adp88502 Arabidops
304	28	87.5	989	3	AAG33723	Aag33723 Arabidops
305	28	87.5	994	3	AAG33722	Aag33722 Arabidops
306	28	87.5	1006	3	AAG33721	Aag33721 Arabidops
307	28	87.5	1033	8	ADO62841	Ado62841 Transcrip
308	28	87.5	1144	6	ABU40409	Abu40409 Protein e
309	28	87.5	1260	6	ABU22639	Abu22639 Protein e
310	28	87.5	2206	7	ABM90427	Abm90427 Rice abio
311	28	87.5	2364	7	ABM88090	Abm88090 Rice abio
312	27	84.4	5	3	AAY32257	Aay32257 Light cha
313	27	84.4	5	5	AAU75739	Aau75739 Anti-(MCP
314	27	84.4	5	5	AAO17609	Aao17609 Human FAP
315	27	84.4	5	8	ADL27482	Adl27482 CDR from
316	27	84.4	5	8	ADR15171	Adr15171 Anti-prot
317	27	84.4	5	8	ADR15143	Adr15143 Mouse ant
318	27	84.4	5	8	ADU87716	Adu87716 Anti-CS1
319	27	84.4	5	8	ADU87702	Adu87702 Mouse Luc
320	27	84.4	5	9	ADW10770	Adw10770 Heavy cha
321	27	84.4	5	9	ADW04990	Adw04990 PAPP-A im
322	27	84.4	5	9	ADW04958	Adw04958 PAPP-A im
323	27	84.4	10	7	ADD94141	Add94141 Mouse HUI
324	27	84.4	10	7	ADD94158	Add94158 Mouse HUI
325	27	84.4	10	7	ADM07748	Adm07748 Canine im
326	27	84.4	10	7	ADM07744	Adm07744 Canine im
327	27	84.4	10	8	ADU86687	Adu86687 Peptide d
328	27	84.4	31	6	ABU62703	Abu62703 Human MAP
329	27	84.4	31	6	ABU62704	Abu62704 Human MAP
330	27	84.4	55	4	AAU43786	Aau43786 Propionib
331	27	84.4	55	6	ABM40305	Abm40305 Propionib
332	27	84.4	64	4	AAM99630	Aam99630 Human exc
333	27	84.4	64	4	AAM42445	Aam42445 Human kid
334	27	84.4	67	5	ABP32187	Abp32187 Human ORF
335	27	84.4	73	7	ADG30700	Adg30700 Xanthomon
336	27	84.4	84	5	ABP11101	Abp11101 Human ORF
337	27	84.4	85	4	ABG20931	Abg20931 Novel hum
338	27	84.4	98	4	AAE06984	Aae06984 Mouse ger
339	27	84.4	98	4	AAE06989	Aae06989 Mouse ger
340	27	84.4	98	8	ADQ89269	Adq89269 Mouse imm
341	27	84.4	98	8	ADQ89274	Adq89274 Mouse imm
342	27	84.4	98	9	AEB09542	Aeb09542 Murine ge
343	27	84.4	98	9	AEB09547	Aeb09547 Murine ge
344	27	84.4	99	2	AAR38160	Aar38160 Sequence
345	27	84.4	100	4	AAE06973	Aae06973 Mouse ger
346	27	84.4	100	8	ADQ89258	Adq89258 Mouse imm
347	27	84.4	100	9	AEB09531	Aeb09531 Murine ge
348	27	84.4	101	5	ABG67061	Abg67061 Streptavi
349	27	84.4	101	6	ABU57583	Abu57583 Streptavi
350	27	84.4	101	9	ADZ77197	Adz77197 Streptavi
351	27	84.4	101	9	AEB48060	Aeb48060 Streptavi
352	27	84.4	103	8	ADJ65023	Adj65023 Rat anti-
353	27	84.4	107	5	AAE23996	Aae23996 Human MOG
354	27	84.4	108	4	AAO00906	Aao00906 Human pol
355	27	84.4	109	2	AAR52046	Aar52046 Heavy cha
356	27	84.4	113	8	ADS16509	Ads16509 Human ant
357	27	84.4	114	2	AAR75430	Aar75430 Human thy
358	27	84.4	116	3	AAY90820	Aay90820 317G5 hyb
359	27	84.4	117	8	ADG16980	Adg16980 Anti-salm
360	27	84.4	119	8	ADR15132	Adr15132 Mouse ant
361	27	84.4	119	8	ADR15131	Adr15131 Mouse ant
362	27	84.4	119	8	ADU87733	Adu87733 Heavy cha
363	27	84.4	119	8	ADU87692	Adu87692 Mouse Luc
364	27	84.4	119	8	ADU87724	Adu87724 Heavy cha
365	27	84.4	119	8	ADU87727	Adu87727 Humanized
366	27	84.4	119	8	ADU87731	Adu87731 VH region
367	27	84.4	120	7	ADD94119	Add94119 Mouse HUI
368	27	84.4	121	8	ADU86551	Adu86551 Immunoglo
369	27	84.4	121	8	ADU86550	Adu86550 Immunoglo
370	27	84.4	122	2	AAW53172	Aaw53172 Monoclona
371	27	84.4	122	5	AAU75737	Aau75737 AAV293 an
372	27	84.4	123	9	ADZ41228	Adz41228 Anti-HAS
373	27	84.4	126	8	ADU04861	Adu04861 TAg25 mon
374	27	84.4	130	8	ADO05872	Ado05872 C. jacchu
375	27	84.4	132	9	ADW04954	Adw04954 PAPP-A im
376	27	84.4	132	9	ADW04986	Adw04986 PAPP-A im
377	27	84.4	134	2	AAW97112	Aaw97112 Amino aci
378	27	84.4	134	5	AAO14049	Aao14049 Human ant
379	27	84.4	137	3	AAY32260	Aay32260 Mouse ant
380	27	84.4	137	8	ADU87714	Adu87714 Anti-CS1
381	27	84.4	139	8	ADJ48789	Adj48789 Oil-assoc
382	27	84.4	142	4	AAB92630	Aab92630 Human pro
383	27	84.4	142	9	AEB08073	Aeb08073 HLA-DR sp
384	27	84.4	150	8	ADL27481	Adl27481 Amino aci
385	27	84.4	150	8	ADX94905	Adx94905 Plant ful
386	27	84.4	153	2	AAW84148	Aaw84148 Schizochy
387	27	84.4	153	2	AAW95517	Aaw95517 M. alpina
388	27	84.4	153	2	AAW85127	Aaw85127 A putativ
389	27	84.4	153	3	AAY84695	Aay84695 Amino aci

390	27	84.4	153	3	AAY92610
391	27	84.4	153	4	AAU62508
392	27	84.4	153	6	ABM59027
393	27	84.4	156	8	ADS16615
394	27	84.4	163	3	AAG40600
395	27	84.4	163	3	AAG26594
396	27	84.4	163	7	ABM73967
397	27	84.4	170	7	ABO63986
398	27	84.4	171	7	ABO67069
399	27	84.4	180	4	AAG75351
400	27	84.4	183	4	AAE00666
401	27	84.4	185	3	AAY84896
402	27	84.4	185	4	AAM78483
403	27	84.4	185	5	ABB04888
404	27	84.4	185	5	ABB04895
405	27	84.4	185	5	ABB04894
406	27	84.4	185	5	ABB04897
407	27	84.4	185	5	ABB04896
408	27	84.4	185	6	ABP70763
409	27	84.4	185	6	ABP70761
410	27	84.4	185	6	ABO07165
411	27	84.4	185	7	ADC00002
412	27	84.4	185	8	ADT88045
413	27	84.4	185	9	ADX07771
414	27	84.4	188	4	ABB58823
415	27	84.4	191	4	ABB65728
416	27	84.4	192	3	AAG26593
417	27	84.4	192	3	AAG40599
418	27	84.4	196	5	ABP28519
419	27	84.4	207	2	AAW97113
420	27	84.4	210	3	AAG40598
421	27	84.4	211	3	AAG26592
422	27	84.4	220	8	ADU86552
423	27	84.4	223	4	ABB11933
424	27	84.4	223	4	AAM79467
425	27	84.4	224	2	AAW97115
426	27	84.4	239	2	AAY17963
427	27	84.4	243	2	AAR53148
428	27	84.4	251	5	AAU72868
429	27	84.4	252	5	AAU72863
430	27	84.4	252	8	AEB01324
431	27	84.4	254	8	ADN20046
432	27	84.4	256	4	AAO09686
433	27	84.4	256	5	AAU72864
434	27	84.4	258	5	AAU72871
435	27	84.4	262	5	AAO14058
436	27	84.4	262	8	ADG16978
437	27	84.4	268	8	ADY09418
438	27	84.4	276	7	ADH86322
439	27	84.4	278	9	AEA51469
440	27	84.4	278	9	AEA51471
441	27	84.4	286	5	ABB53283
442	27	84.4	299	4	AAB50425
443	27	84.4	301	3	AAB07860
444	27	84.4	306	5	ABP65588
445	27	84.4	314	9	ADY85548
446	27	84.4	342	7	ABO69355
447	27	84.4	345	7	ABM73656
448	27	84.4	348	7	ADB70092
449	27	84.4	352	6	ABR42043
450	27	84.4	352	9	AEA23401
451	27	84.4	353	6	ABJ37892
452	27	84.4	359	6	ABR42044
453	27	84.4	359	9	AEA23403
454	27	84.4	378	8	ADN22955
455	27	84.4	408	6	ABM70496
456	27	84.4	423	4	AAM93853
457	27	84.4	423	5	ABP43750
458	27	84.4	423	8	ADJ93458
459	27	84.4	423	8	ADL31908
460	27	84.4	426	9	AEB76969
461	27	84.4	436	5	ABB90830
462	27	84.4	438	7	ADF74124

Aay92610 Schizochy
Aau62508 Propionib
Abm59027 Propionib
Ads16615 Human ant
Aag40600 Arabidops
Aag26594 Arabidops
Abm73967 DNA clone
Abo63986 Klebsiell
Abo67069 Klebsiell
Aag75351 Human col
Aae00666 Human pro
Aay84896 A human p
Aam78483 Human pro
Abb04888 LDL recep
Abb04895 LDL recep
Abb04894 LDL recep
Abb04897 LDL recep
Abb04896 LDL recep
Abp70763 Anaphase-
Abp70761 Human Ana
Abo07165 Human p53
Adc00002 Enterohae
Adt88045 Human pro
Adx07771 Cyclin-de
Abb58823 Drosophil
Abb65728 Drosophil
Aag26593 Arabidops
Aag40599 Arabidops
Abp28519 Streptoco
Aaw97113 Amino aci
Aag40598 Arabidops
Aag26592 Arabidops
Adu86552 Immunoglo
Abb11933 Human APC
Aam79467 Human pro
Aaw97115 Amino aci
Aay17963 Mouse scF
Aar53148 VH and VL
Aau72868 P5-10 sin
Aau72863 P4-14 sin
Aeb01324 scFv FITC
Adn20046 Bacterial
Aao09686 Human pol
Aau72864 P4-15 sin
Aau72871 3B10xP4-3
Aao14058 Anti-FAPa
Adg16978 Anti-salm
Ady09418 Plant ful
Adh86322 Enterococ
Aea51469 Region of
Aea51471 Peptide,
Abb53283 Human pol
Aab50425 Mouse ant
Aab07860 Amino aci
Abp65588 Bifidobac
Ady85548 Catalytic
Abo69355 Pseudomon
Abm73656 DNA clone
Adb70092 C. neofor
Abr42043 Human ins
Aea23401 Human Maf
Abj37892 NOVX prot
Abr42044 Mouse ins
Aea23403 Mouse Maf
Adn22955 Bacterial
Abm70496 Photorhab
Aam93853 Human pol
Abp43750 Ligase TT
Adj93458 Human tub
Adl31908 Human pro
Aeb76969 Nematode
Abb90830 Herbicida
Adf74124 Human nov

463	27	84.4	439	5	AAE22061
464	27	84.4	439	6	AAE31902
465	27	84.4	439	9	ADU77860
466	27	84.4	439	9	ADW96383
467	27	84.4	444	3	AAY32263
468	27	84.4	460	8	ADJ65026
469	27	84.4	466	7	ABO67808
470	27	84.4	468	9	AEB08072
471	27	84.4	469	5	ABB90833
472	27	84.4	470	4	AAU36485
473	27	84.4	470	6	ABU38843
474	27	84.4	472	6	ABM67410
475	27	84.4	485	7	ABO84135
476	27	84.4	493	5	ABB93470
477	27	84.4	499	5	AAU72872
478	27	84.4	503	5	AAU72873
479	27	84.4	505	5	AAU72875
480	27	84.4	509	7	ADM26699
481	27	84.4	515	6	ABU40548
482	27	84.4	521	6	ABU99126
483	27	84.4	521	8	ADM93817
484	27	84.4	522	5	ABB90905
485	27	84.4	527	5	ABB93903
486	27	84.4	530	5	ABB90904
487	27	84.4	530	6	AAO16177
488	27	84.4	530	6	AAO16333
489	27	84.4	530	8	ADV66290
490	27	84.4	533	5	ABB53284
491	27	84.4	537	8	ADI26097
492	27	84.4	544	4	AAU40519
493	27	84.4	544	6	ABM37038
494	27	84.4	544	8	ADH09570
495	27	84.4	544	8	ADH09572
496	27	84.4	544	8	ADH09573
497	27	84.4	544	8	ADH09571
498	27	84.4	544	8	ADN71926
499	27	84.4	544	9	ADW72034
500	27	84.4	546	6	ABP96072
501	27	84.4	547	5	ABG93114
502	27	84.4	549	2	AAR66030
503	27	84.4	552	8	ADS23588
504	27	84.4	553	4	ABB60028
505	27	84.4	555	4	ABB65546
506	27	84.4	559	8	ADN23087
507	27	84.4	561	7	ABO75040
508	27	84.4	567	2	AAR66031
509	27	84.4	567	8	ADH09629
510	27	84.4	580	7	ABO81434
511	27	84.4	600	6	ABU41290
512	27	84.4	601	9	AEB76973
513	27	84.4	607	6	ADB08362
514	27	84.4	618	4	AAU03598
515	27	84.4	618	7	ADB84593
516	27	84.4	618	8	ADK68582
517	27	84.4	619	2	AAR77545
518	27	84.4	619	2	AAW56162
519	27	84.4	619	2	AAW56158
520	27	84.4	619	2	AAY43319
521	27	84.4	619	2	AAY43323
522	27	84.4	619	2	AAY42108
523	27	84.4	619	2	AAY42105
524	27	84.4	619	2	AAW73532
525	27	84.4	619	3	AAB01221
526	27	84.4	619	3	AAB01217
527	27	84.4	619	5	AAM48937
528	27	84.4	619	5	AAM48936
529	27	84.4	619	7	ADB84596
530	27	84.4	619	7	ADB84594
531	27	84.4	619	7	ADB84590
532	27	84.4	619	7	ADB84598
533	27	84.4	619	8	ADK68587
534	27	84.4	619	8	ADK68579
535	27	84.4	619	8	ADK68583

Aae22061 Thraustoc
Aae31902 Thraustoc
Adu77860 T. aureum
Adw96383 Thraustoc
Aay32263 Humanised
Adj65026 Plasmid p
Abo67808 Klebsiell
Aeb08072 Murine/hu
Abb90833 Herbicida
Aau36485 Pseudomon
Abu38843 Protein e
Abm67410 Photorhab
Abo84135 Pseudomon
Abb93470 Herbicida
Aau72872 3B10xP4-1
Aau72873 3B10xP5-2
Aau72875 Human NKG
Adm26699 Hyperther
Abu40548 Protein e
Abu99126 Novel hum
Adm93817 Human NOV
Abb90905 Herbicida
Abb93903 Herbicida
Abb90904 Herbicida
Aao16177 Human pro
Aao16333 Human sec
Adv66290 Human net
Abb53284 Human pol
Adi26097 Human pro
Aau40519 Propionib
Abm37038 Propionib
Adh09570 Human hos
Adh09572 Human hos
Adh09573 Human hos
Adh09571 Human hos
Adn71926 Human MAP
Adw72034 Retrovira
Abp96072 Human pro
Abg93114 S. cerevi
Aar66030 Mammalian
Ads23588 Bacterial
Abb60028 Drosophil
Abb65546 Drosophil
Adn23087 Bacterial
Abo75040 Pseudomon
Aar66031 Mammalian
Adh09629 Human hos
Abo81434 Pseudomon
Abu41290 Protein e
Aeb76973 Nematode
Adb08362 Alloiococ
Aau03598 Human MEK
Adb84593 Human mit
Adk68582 Human MEK
Aar77545 MEKK2 pro
Aaw56162 A mitogen
Aaw56158 A mitogen
Aay43319 Mitogen E
Aay43323 Mitogen E
Aay42108 Murine ME
Aay42105 Human MEK
Aaw73532 MEKK2 pro
Aab01221 Murine ME
Aab01217 Murine ME
Aam48937 Murine ME
Aam48936 Murine ME
Adb84596 Human mit
Adb84594 Human mit
Adb84590 Human mit
Adb84598 Human mit
Adk68587 Human MEK
Adk68579 Human MEK
Adk68583 Human MEK

536	27	84.4	619	8	ADK68585	Adk68585 Human MEK
537	27	84.4	620	9	AEA51461	Aea51461 MAPKK kin
538	27	84.4	625	4	ABG07837	Abg07837 Novel hum
539	27	84.4	626	2	AAR77546	Aar77546 MEKK3 pro
540	27	84.4	626	2	AAW56159	Aaw56159 A mitogen
541	27	84.4	626	2	AAY43320	Aay43320 Mitogen E
542	27	84.4	626	2	AAY42106	Aay42106 Human MEK
543	27	84.4	626	2	AAY42109	Aay42109 Murine ME
544	27	84.4	626	2	AAW73533	Aaw73533 MEKK3 pro
545	27	84.4	626	3	AAB01218	Aab01218 Murine ME
546	27	84.4	626	3	AAB42659	Aab42659 Human ORF
547	27	84.4	626	5	AAM48938	Aam48938 Murine ME
548	27	84.4	626	5	AAE21447	Aae21447 Human MAP
549	27	84.4	626	7	ADE60403	Ade60403 Rat Prote
550	27	84.4	626	7	ADJ68645	Adj68645 Human hea
551	27	84.4	626	8	ADH56273	Adh56273 Human MAP
552	27	84.4	626	8	ADI26103	Adi26103 Human pro
553	27	84.4	626	8	ADN71932	Adn71932 Human MEK
554	27	84.4	626	8	ABM81921	Abm81921 Tumour-as
555	27	84.4	626	8	ADS88372	Ads88372 Human pro
556	27	84.4	626	9	AEA51463	Aea51463 MAPKK kin
557	27	84.4	630	7	ABO82518	Abo82518 Pseudomon
558	27	84.4	635	8	ADH23360	Adh23360 Fruit fly
559	27	84.4	639	8	ADH23364	Adh23364 Fruit fly
560	27	84.4	641	7	ADF04074	Adf04074 Bacterial
561	27	84.4	646	9	AEB76970	Aeb76970 Nematode
562	27	84.4	646	9	AEB76971	Aeb76971 Nematode
563	27	84.4	647	7	ADC37177	Adc37177 Nuclear f
564	27	84.4	647	8	ADI26099	Adi26099 Human pro
565	27	84.4	648	9	AEB76972	Aeb76972 Nematode
566	27	84.4	648	9	AEB76974	Aeb76974 Nematode
567	27	84.4	653	8	ADN61477	Adn61477 Human KPP
568	27	84.4	657	7	ADC37179	Adc37179 Nuclear f
569	27	84.4	657	8	ADH56271	Adh56271 Human MAP
570	27	84.4	657	8	ADI26101	Adi26101 Human pro
571	27	84.4	657	8	ADN71924	Adn71924 Human DKF
572	27	84.4	657	8	ADR39755	Adr39755 Human kin
573	27	84.4	696	2	AAR75366	Aar75366 Adhesin.
574	27	84.4	696	4	AAB83203	Aab83203 Human tyr
575	27	84.4	696	7	ADC00149	Adc00149 Enterohae
576	27	84.4	739	7	ADF06403	Adf06403 Bacterial
577	27	84.4	809	6	ABU26581	Abu26581 Protein e
578	27	84.4	829	8	ADS99456	Ads99456 Human kin
579	27	84.4	830	8	ADS99459	Ads99459 Murine ki
580	27	84.4	945	4	AAU03538	Aau03538 Human pro
581	27	84.4	945	5	AAE19157	Aae19157 Human kin
582	27	84.4	965	9	ADV97905	Adv97905 Murine pr
583	27	84.4	982	8	ADJ96663	Adj96663 Human tyr
584	27	84.4	1034	4	AAG91031	Aag91031 C glutami
585	27	84.4	1034	9	AEB15199	Aeb15199 C glutami
586	27	84.4	1036	5	ABB93295	Abb93295 Herbicida
587	27	84.4	1096	8	ADP99004	Adp99004 C. albica
588	27	84.4	1130	4	ABG10256	Abg10256 Novel hum
589	27	84.4	1254	4	ABB62006	Abb62006 Drosophil
590	27	84.4	1254	4	ABG19921	Abg19921 Novel hum
591	27	84.4	1277	5	AAU93150	Aau93150 Arabidops
592	27	84.4	1289	6	ABG71151	Abg71151 Protein u
593	27	84.4	1297	4	AAB62491	Aab62491 P. chryso
594	27	84.4	1304	4	ABG14789	Abg14789 Novel hum
595	27	84.4	1305	4	ABB67631	Abb67631 Drosophil
596	27	84.4	1305	5	ABB92378	Abb92378 Herbicida
597	27	84.4	1325	4	ABG14552	Abg14552 Novel hum
598	27	84.4	1330	7	ADE61063	Ade61063 Rat Prote
599	27	84.4	1376	7	ABM90474	Abm90474 Rice abio
600	27	84.4	1474	7	ABM86643	Abm86643 Rice abio
601	27	84.4	2108	8	ADN18884	Adn18884 Bacterial
602	27	84.4	2129	4	AAU48629	Aau48629 Propionib
603	27	84.4	2129	6	ABM45148	Abm45148 Propionib
604	27	84.4	2272	4	ABB70004	Abb70004 Drosophil
605	27	84.4	3269	6	ABP54436	Abp54436 Papaya le
606	27	84.4	3587	2	AAR34713	Aar34713 Bacillus
607	26	81.2	55	4	AAU53567	Aau53567 Propionib
608	26	81.2	55	6	ABM50086	Abm50086 Propionib
609	26	81.2	59	4	AAM24252	Aam24252 Arabidops
610	26	81.2	59	8	ADS12065	Ads12065 Human the
611	26	81.2	70	5	ABP06865	Abp06865 Human ORF
612	26	81.2	77	3	AAG03385	Aag03385 Human sec
613	26	81.2	79	5	ABP32982	Abp32982 Human ORF
614	26	81.2	80	4	AAM84337	Aam84337 Human imm
615	26	81.2	91	5	ABP31592	Abp31592 Human ORF
616	26	81.2	93	4	AAU57591	Aau57591 Propionib
617	26	81.2	93	6	ABM54110	Abm54110 Propionib
618	26	81.2	101	5	ABP31441	Abp31441 Human ORF
619	26	81.2	110	6	ABR57090	Abr57090 MLHR comp
620	26	81.2	111	4	AAM89930	Aam89930 Human imm
621	26	81.2	117	7	ADB65003	Adb65003 Human pro
622	26	81.2	120	4	AAU48267	Aau48267 Propionib
623	26	81.2	120	6	ABM44786	Abm44786 Propionib
624	26	81.2	121	4	AAU58119	Aau58119 Propionib
625	26	81.2	121	6	ABM54638	Abm54638 Propionib
626	26	81.2	127	4	AAM95510	Aam95510 Human rep
627	26	81.2	127	4	ABB96193	Abb96193 Human tes
628	26	81.2	135	5	ABB89998	Abb89998 Human pol
629	26	81.2	136	4	AAG92562	Aag92562 C glutami
630	26	81.2	138	4	ABG18401	Abg18401 Novel hum
631	26	81.2	143	4	AAU29278	Aau29278 Human PRO
632	26	81.2	143	6	ABU58654	Abu58654 Human PRO
633	26	81.2	143	6	ABU88202	Abu88202 Novel hum
634	26	81.2	143	6	ABU84517	Abu84517 Human sec
635	26	81.2	143	6	ABR66391	Abr66391 Human sec
636	26	81.2	143	6	ABR65781	Abr65781 Human sec
637	26	81.2	143	6	ABU99721	Abu99721 Human sec
638	26	81.2	143	6	ABU82960	Abu82960 Human PRO
639	26	81.2	143	6	ABU90081	Abu90081 Novel hum
640	26	81.2	143	6	ABR68330	Abr68330 Human sec
641	26	81.2	143	6	ABU96383	Abu96383 Novel hum
642	26	81.2	143	6	ABU92814	Abu92814 Human sec
643	26	81.2	143	6	ABO08891	Abo08891 Human sec
644	26	81.2	143	6	ABO02943	Abo02943 Human sec
645	26	81.2	143	6	ABR75097	Abr75097 Human sec
646	26	81.2	143	6	ABR94859	Abr94859 Human sec
647	26	81.2	143	6	ABU85832	Abu85832 Human PRO
648	26	81.2	143	6	ABU98992	Abu98992 Novel hum
649	26	81.2	143	6	ABU98207	Abu98207 Novel hum
650	26	81.2	143	6	ABU91913	Abu91913 Novel hum
651	26	81.2	143	6	ABU89606	Abu89606 Human PRO
652	26	81.2	143	6	ABU86447	Abu86447 Human sec
653	26	81.2	143	6	ABU67660	Abu67660 Human sec
654	26	81.2	143	6	ABU80688	Abu80688 Human PRO
655	26	81.2	143	6	ABR99606	Abr99606 Human sec
656	26	81.2	143	6	ABR98996	Abr98996 Human sec
657	26	81.2	143	6	ABO16519	Abo16519 Human sec
658	26	81.2	143	6	ABR92419	Abr92419 Human sec
659	26	81.2	143	6	ABO19060	Abo19060 Human sec
660	26	81.2	143	6	ABR78481	Abr78481 Human sec
661	26	81.2	143	6	ABU85217	Abu85217 Novel hum
662	26	81.2	143	6	ABO00356	Abo00356 Novel hum
663	26	81.2	143	6	ABO11688	Abo11688 Human sec
664	26	81.2	143	6	ABO02333	Abo02333 Human sec
665	26	81.2	143	6	ABU88907	Abu88907 Novel hum
666	26	81.2	143	6	ABU83602	Abu83602 Human sec
667	26	81.2	143	6	ABO06403	Abo06403 Novel hum
668	26	81.2	143	6	ABR59439	Abr59439 Human sec
669	26	81.2	143	6	ABO09501	Abo09501 Human sec
670	26	81.2	143	6	ABO19365	Abo19365 Novel hum
671	26	81.2	143	6	ABO11383	Abo11383 Human sec
672	26	81.2	143	6	ABR67001	Abr67001 Human sec
673	26	81.2	143	6	ABO16214	Abo16214 Human sec
674	26	81.2	143	6	ABO13920	Abo13920 Human sec
675	26	81.2	143	6	ABU65823	Abu65823 Human sec
676	26	81.2	143	6	ABO07671	Abo07671 Human PRO
677	26	81.2	143	6	ABO03858	Abo03858 Human sec
678	26	81.2	143	6	ABR67306	Abr67306 Human sec
679	26	81.2	143	6	ABO15909	Abo15909 Human sec
680	26	81.2	143	6	ABU56190	Abu56190 Human sec
681	26	81.2	143	6	ABU65518	Abu65518 Human PRO

682	26	81.2	143	6	ABU95463	Abu95463 Novel hum
683	26	81.2	143	6	ABU71366	Abu71366 Human PRO
684	26	81.2	143	6	ABO07976	Abo07976 Human PRO
685	26	81.2	143	6	ABR70217	Abr70217 Human sec
686	26	81.2	143	6	ABR69550	Abr69550 Human sec
687	26	81.2	143	6	ABO01691	Abo01691 Human PRO
688	26	81.2	143	6	ABU81493	Abu81493 Human PRO
689	26	81.2	143	6	ABR60290	Abr60290 Human sec
690	26	81.2	143	6	ABR68025	Abr68025 Human sec
691	26	81.2	143	6	ABR65413	Abr65413 Human sec
692	26	81.2	143	6	ABR68635	Abr68635 Human sec
693	26	81.2	143	6	ABR72047	Abr72047 Human sec
694	26	81.2	143	6	ABU85527	Abu85527 Human PRO
695	26	81.2	143	6	ABU89217	Abu89217 Human sec
696	26	81.2	143	6	ABU83297	Abu83297 Human sec
697	26	81.2	143	6	ABU95153	Abu95153 Novel hum
698	26	81.2	143	6	ABU90701	Abu90701 Novel hum
699	26	81.2	143	6	ABU84212	Abu84212 Human sec
700	26	81.2	143	6	ABU93863	Abu93863 Novel hum
701	26	81.2	143	6	ABR65108	Abr65108 Human sec
702	26	81.2	143	6	ABR68940	Abr68940 Human sec
703	26	81.2	143	6	ABO06756	Abo06756 Human sec
704	26	81.2	143	6	ABR99301	Abr99301 Human sec
705	26	81.2	143	6	ABU57185	Abu57185 Human PRO
706	26	81.2	143	6	ABU86137	Abu86137 Novel hum
707	26	81.2	143	6	ABU82424	Abu82424 Novel hum
708	26	81.2	143	6	ABU87435	Abu87435 Human PRO
709	26	81.2	143	6	ABU83907	Abu83907 Human sec
710	26	81.2	143	6	ABO08281	Abo08281 Human PRO
711	26	81.2	143	6	ABU81992	Abu81992 Novel hum
712	26	81.2	143	6	ABU66156	Abu66156 Novel hum
713	26	81.2	143	6	ABR59985	Abr59985 Human sec
714	26	81.2	143	6	ABU94173	Abu94173 Novel hum
715	26	81.2	143	6	ABO00046	Abo00046 Novel hum
716	26	81.2	143	6	ABR66696	Abr66696 Human sec
717	26	81.2	143	6	ABR91114	Abr91114 Human sec
718	26	81.2	143	6	ABU94541	Abu94541 Human PRO
719	26	81.2	143	6	ABU79423	Abu79423 Human PRO
720	26	81.2	143	6	ABU86752	Abu86752 Human sec
721	26	81.2	143	6	ABU87057	Abu87057 Novel hum
722	26	81.2	143	6	ABU94846	Abu94846 Human PRO
723	26	81.2	143	6	ABO04773	Abo04773 Human PRO
724	26	81.2	143	6	ABR70522	Abr70522 Human sec
725	26	81.2	143	6	ABU98687	Abu98687 Human PRO
726	26	81.2	143	6	ABR66086	Abr66086 Human sec
727	26	81.2	143	6	ABR64803	Abr64803 Human sec
728	26	81.2	143	6	ABU79728	Abu79728 Human PRO
729	26	81.2	143	6	ABU93119	Abu93119 Human sec
730	26	81.2	143	6	ABU96078	Abu96078 Human PRO
731	26	81.2	143	6	ABU91298	Abu91298 Novel hum
732	26	81.2	143	6	ABU90391	Abu90391 Novel hum
733	26	81.2	143	6	ABO09806	Abo09806 Human sec
734	26	81.2	143	6	ABO11078	Abo11078 Human sec
735	26	81.2	143	6	ABR71132	Abr71132 Human sec
736	26	81.2	143	6	ABU87740	Abu87740 Human PRO
737	26	81.2	143	6	ABU91608	Abu91608 Human PRO
738	26	81.2	143	6	ABU84822	Abu84822 Human sec
739	26	81.2	143	6	ABR69912	Abr69912 Human sec
740	26	81.2	143	6	ABU80289	Abu80289 Human PRO
741	26	81.2	143	6	ABU93558	Abu93558 Human PRO
742	26	81.2	143	6	ABO10111	Abo10111 Human sec
743	26	81.2	143	6	ABO09196	Abo09196 Human sec
744	26	81.2	143	6	ABU10764	Abu10764 Human sec
745	26	81.2	143	6	ABU95773	Abu95773 Human PRO
746	26	81.2	143	6	ABU96982	Abu96982 Novel hum
747	26	81.2	143	6	ABR70827	Abr70827 Human sec
748	26	81.2	143	6	ABO05178	Abo05178 Novel hum
749	26	81.2	143	6	ABO08586	Abo08586 Human sec
750	26	81.2	143	6	ABO05793	Abo05793 Human sec
751	26	81.2	143	6	ABR74182	Abr74182 Human sec
752	26	81.2	143	6	ABR95774	Abr95774 Human sec
753	26	81.2	143	6	ABR81071	Abr81071 Human sec
754	26	81.2	143	6	ABR81376	Abr81376 Human sec
755	26	81.2	143	6	ABM01072	Abm01072 Human sec
756	26	81.2	143	6	ABR88674	Abr88674 Human sec
757	26	81.2	143	6	ABM77495	Abm77495 Human sec
758	26	81.2	143	6	ABO28979	Abo28979 Human sec
759	26	81.2	143	6	ABO31724	Abo31724 Human sec
760	26	81.2	143	6	ABM08141	Abm08141 Human sec
761	26	81.2	143	6	ABO40621	Abo40621 Human sec
762	26	81.2	143	6	ABO36046	Abo36046 Human PRO
763	26	81.2	143	6	ABO44185	Abo44185 Human PRO
764	26	81.2	143	6	ADA78262	Ada78262 Human sec
765	26	81.2	143	6	ABM24980	Abm24980 Human sec
766	26	81.2	143	6	ABO03248	Abo03248 Human sec
767	26	81.2	143	6	ABR90504	Abr90504 Human sec
768	26	81.2	143	6	ABM17418	Abm17418 Human sec
769	26	81.2	143	6	ABR95164	Abr95164 Human sec
770	26	81.2	143	6	ABR95469	Abr95469 Human sec
771	26	81.2	143	6	ABO21707	Abo21707 Human sec
772	26	81.2	143	6	ABR97971	Abr97971 Human sec
773	26	81.2	143	6	ABR87759	Abr87759 Human sec
774	26	81.2	143	6	ABM77800	Abm77800 Human sec
775	26	81.2	143	6	ABM28030	Abm28030 Human sec
776	26	81.2	143	6	ABM06311	Abm06311 Human sec
777	26	81.2	143	6	ABM03817	Abm03817 Human sec
778	26	81.2	143	6	ABM35268	Abm35268 Human sec
779	26	81.2	143	6	ABM26505	Abm26505 Human sec
780	26	81.2	143	6	ABO48287	Abo48287 Human sec
781	26	81.2	143	6	ABR93029	Abr93029 Human sec
782	26	81.2	143	6	ABO24790	Abo24790 Human sec
783	26	81.2	143	6	ABM11801	Abm11801 Human sec
784	26	81.2	143	6	ABM02902	Abm02902 Human sec
785	26	81.2	143	6	ABM16198	Abm16198 Human sec
786	26	81.2	143	6	ABO27759	Abo27759 Human sec
787	26	81.2	143	6	ABM29250	Abm29250 Human sec
788	26	81.2	143	6	ABM07226	Abm07226 Human sec
789	26	81.2	143	6	ABM21320	Abm21320 Human sec
790	26	81.2	143	6	ABM09666	Abm09666 Human sec
791	26	81.2	143	6	ABO41536	Abo41536 Human sec
792	26	81.2	143	6	ABO36351	Abo36351 Human PRO
793	26	81.2	143	6	ABO43880	Abo43880 Human PRO
794	26	81.2	143	6	ABM76580	Abm76580 Human sec
795	26	81.2	143	6	ABM76276	Abm76276 Human sec
796	26	81.2	143	6	ABM25895	Abm25895 Human sec
797	26	81.2	143	6	ABM26200	Abm26200 Human sec
798	26	81.2	143	6	ABO03553	Abo03553 Human sec
799	26	81.2	143	6	ABO02638	Abo02638 Human sec
800	26	81.2	143	6	ABR90809	Abr90809 Human sec
801	26	81.2	143	6	ABR73877	Abr73877 Human sec
802	26	81.2	143	6	ABO17129	Abo17129 Human sec
803	26	81.2	143	6	ABR94554	Abr94554 Human sec
804	26	81.2	143	6	ABR76061	Abr76061 Human sec
805	26	81.2	143	6	ABR71437	Abr71437 Human sec
806	26	81.2	143	6	ABR93334	Abr93334 Human sec
807	26	81.2	143	6	ABR93639	Abr93639 Human sec
808	26	81.2	143	6	ABR88064	Abr88064 Human sec
809	26	81.2	143	6	ABO28064	Abo28064 Human sec
810	26	81.2	143	6	ABO30199	Abo30199 Human sec
811	26	81.2	143	6	ABO33408	Abo33408 Human PRO
812	26	81.2	143	6	ABM05096	Abm05096 Human sec
813	26	81.2	143	6	ABM09056	Abm09056 Human sec
814	26	81.2	143	6	ABO36656	Abo36656 Human sec
815	26	81.2	143	6	ABO35741	Abo35741 Human PRO
816	26	81.2	143	6	ABO39706	Abo39706 Human sec
817	26	81.2	143	6	ABM10581	Abm10581 Human sec
818	26	81.2	143	6	ABM12106	Abm12106 Human sec
819	26	81.2	143	6	ABO52252	Abo52252 Human PRO
820	26	81.2	143	6	ABO52557	Abo52557 Human PRO
821	26	81.2	143	6	ABO23875	Abo23875 Human sec
822	26	81.2	143	6	ABR97361	Abr97361 Human sec
823	26	81.2	143	6	ABR87149	Abr87149 Human sec
824	26	81.2	143	6	ABM11191	Abm11191 Human sec
825	26	81.2	143	6	ABM28335	Abm28335 Human sec
826	26	81.2	143	6	ABO32334	Abo32334 Human sec
827	26	81.2	143	6	ABM15461	Abm15461 Human sec

828	26	81.2	143	6	ABM06616	Abm06616 Human sec
829	26	81.2	143	6	ABM04427	Abm04427 Human sec
830	26	81.2	143	6	ABM22540	Abm22540 Human sec
831	26	81.2	143	6	ABM07836	Abm07836 Human sec
832	26	81.2	143	6	ABO40926	Abo40926 Human sec
833	26	81.2	143	6	ABM35573	Abm35573 Human sec
834	26	81.2	143	6	ABM33336	Abm33336 Human sec
835	26	81.2	143	6	ABO52862	Abo52862 Human PRO
836	26	81.2	143	6	ABO50422	Abo50422 Human sec
837	26	81.2	143	6	ABU99416	Abu99416 Human sec
838	26	81.2	143	6	ABO04468	Abo04468 Human sec
839	26	81.2	143	6	ABM18638	Abm18638 Human sec
840	26	81.2	143	6	ABR97666	Abr97666 Human sec
841	26	81.2	143	6	ABR80766	Abr80766 Human sec
842	26	81.2	143	6	ABM01377	Abm01377 Human sec
843	26	81.2	143	6	ABR88979	Abr88979 Human sec
844	26	81.2	143	6	ABM13631	Abm13631 Human sec
845	26	81.2	143	6	ABM21015	Abm21015 Human sec
846	26	81.2	143	6	ABO42146	Abo42146 Human sec
847	26	81.2	143	6	ABO42756	Abo42756 Human sec
848	26	81.2	143	6	ABM10276	Abm10276 Human sec
849	26	81.2	143	6	ABO38791	Abo38791 Human sec
850	26	81.2	143	6	ABM33031	Abm33031 Human sec
851	26	81.2	143	6	ABM22845	Abm22845 Human sec
852	26	81.2	143	6	ABM75056	Abm75056 Human sec
853	26	81.2	143	6	ADA80054	Ada80054 Human sec
854	26	81.2	143	6	ABR96446	Abr96446 Human sec
855	26	81.2	143	6	ABM02597	Abm02597 Human sec
856	26	81.2	143	6	ABR86539	Abr86539 Human sec
857	26	81.2	143	6	ABR86844	Abr86844 Human sec
858	26	81.2	143	6	ABM16808	Abm16808 Human sec
859	26	81.2	143	6	ABM29860	Abm29860 Human sec
860	26	81.2	143	6	ABO29284	Abo29284 Human sec
861	26	81.2	143	6	ABM24065	Abm24065 Human sec
862	26	81.2	143	6	ABM23455	Abm23455 Human sec
863	26	81.2	143	6	ABM22235	Abm22235 Human sec
864	26	81.2	143	6	ABO37876	Abo37876 Human sec
865	26	81.2	143	6	ABM28640	Abm28640 Human sec
866	26	81.2	143	6	ABM28945	Abm28945 Human sec
867	26	81.2	143	6	ABM66589	Abm66589 Human sec
868	26	81.2	143	6	ABM75971	Abm75971 Human sec
869	26	81.2	143	6	ABM34251	Abm34251 Human sec
870	26	81.2	143	6	ABM34556	Abm34556 Human sec
871	26	81.2	143	6	ABO20487	Abo20487 Human sec
872	26	81.2	143	6	ABO21402	Abo21402 Human sec
873	26	81.2	143	6	ABO22317	Abo22317 Human sec
874	26	81.2	143	6	ABR96751	Abr96751 Human sec
875	26	81.2	143	6	ABR85929	Abr85929 Human sec
876	26	81.2	143	6	ABR99911	Abr99911 Human sec
877	26	81.2	143	6	ABM00462	Abm00462 Human sec
878	26	81.2	143	6	ABM00767	Abm00767 Human sec
879	26	81.2	143	6	ABO29894	Abo29894 Human sec
880	26	81.2	143	6	ABM23760	Abm23760 Human sec
881	26	81.2	143	6	ABM29555	Abm29555 Human sec
882	26	81.2	143	6	ABO38486	Abo38486 Human sec
883	26	81.2	143	6	ABO45786	Abo45786 Human PRO
884	26	81.2	143	6	ABM20710	Abm20710 Human sec
885	26	81.2	143	6	ADA81781	Ada81781 Human sec
886	26	81.2	143	6	ABO16824	Abo16824 Human sec
887	26	81.2	143	6	ABO18450	Abo18450 Human sec
888	26	81.2	143	6	ABO22877	Abo22877 Human PRO
889	26	81.2	143	6	ABO23182	Abo23182 Human PRO
890	26	81.2	143	6	ABR92724	Abr92724 Human sec
891	26	81.2	143	6	ABR81681	Abr81681 Human sec
892	26	81.2	143	6	ABM78105	Abm78105 Human sec
893	26	81.2	143	6	ABR89894	Abr89894 Human sec
894	26	81.2	143	6	ABM26810	Abm26810 Human sec
895	26	81.2	143	6	ABM13936	Abm13936 Human sec
896	26	81.2	143	6	ABO28674	Abo28674 Human sec
897	26	81.2	143	6	ABO30504	Abo30504 Human sec
898	26	81.2	143	6	ABM07531	Abm07531 Human sec
899	26	81.2	143	6	ABM04122	Abm04122 Human sec
900	26	81.2	143	6	ABO37266	Abo37266 Human sec
901	26	81.2	143	6	ABO41841	Abo41841 Human sec
902	26	81.2	143	6	ABO35436	Abo35436 Human PRO
903	26	81.2	143	6	ABM25285	Abm25285 Human sec
904	26	81.2	143	6	ABO47677	Abo47677 Human sec
905	26	81.2	143	6	ABO47982	Abo47982 Human sec
906	26	81.2	143	6	ABO48592	Abo48592 Human sec
907	26	81.2	143	6	ABO51642	Abo51642 Human PRO
908	26	81.2	143	6	ABO51947	Abo51947 Human PRO
909	26	81.2	143	6	ABO50727	Abo50727 Human sec
910	26	81.2	143	6	ABR79851	Abr79851 Human sec
911	26	81.2	143	6	ABM17113	Abm17113 Human sec
912	26	81.2	143	6	ABO18145	Abo18145 Human sec
913	26	81.2	143	6	ABO21097	Abo21097 Human sec
914	26	81.2	143	6	ABR97056	Abr97056 Human sec
915	26	81.2	143	6	ABM12411	Abm12411 Human sec
916	26	81.2	143	6	ABM16503	Abm16503 Human sec
917	26	81.2	143	6	ABM24370	Abm24370 Human sec
918	26	81.2	143	6	ABM14851	Abm14851 Human sec
919	26	81.2	143	6	ABM04732	Abm04732 Human sec
920	26	81.2	143	6	ABM06921	Abm06921 Human sec
921	26	81.2	143	6	ABM09361	Abm09361 Human sec
922	26	81.2	143	6	ABO39401	Abo39401 Human sec
923	26	81.2	143	6	ABM75666	Abm75666 Human sec
924	26	81.2	143	6	ABM25590	Abm25590 Human sec
925	26	81.2	143	6	ABM20100	Abm20100 Human sec
926	26	81.2	143	6	ABO47006	Abo47006 Human PRO
927	26	81.2	143	6	ABO47311	Abo47311 Human PRO
928	26	81.2	143	6	ADA83579	Ada83579 Human sec
929	26	81.2	143	6	ABR71742	Abr71742 Human sec
930	26	81.2	143	6	ABR72352	Abr72352 Human sec
931	26	81.2	143	6	ABR98691	Abr98691 Human sec
932	26	81.2	143	6	ABO07061	Abo07061 Human sec
933	26	81.2	143	6	ABR85014	Abr85014 Human sec
934	26	81.2	143	6	ABR73572	Abr73572 Human sec
935	26	81.2	143	6	ABR76666	Abr76666 Human sec
936	26	81.2	143	6	ABR73267	Abr73267 Human sec
937	26	81.2	143	6	ABM18333	Abm18333 Human sec
938	26	81.2	143	6	ABO20792	Abo20792 Human sec
939	26	81.2	143	6	ABO25535	Abo25535 Human PRO
940	26	81.2	143	6	ABO25840	Abo25840 Human PRO
941	26	81.2	143	6	ABR94249	Abr94249 Human sec
942	26	81.2	143	6	ABR80156	Abr80156 Human sec
943	26	81.2	143	6	ABM11496	Abm11496 Human sec
944	26	81.2	143	6	ABO33103	Abo33103 Human PRO
945	26	81.2	143	6	ABO30809	Abo30809 Human sec
946	26	81.2	143	6	ABO31114	Abo31114 Human sec
947	26	81.2	143	6	ABM27420	Abm27420 Human sec
948	26	81.2	143	6	ABM30165	Abm30165 Human sec
949	26	81.2	143	6	ABM05701	Abm05701 Human sec
950	26	81.2	143	6	ABM15766	Abm15766 Human sec
951	26	81.2	143	6	ABM08751	Abm08751 Human sec
952	26	81.2	143	6	ABO42451	Abo42451 Human sec
953	26	81.2	143	6	ABO38181	Abo38181 Human sec
954	26	81.2	143	6	ABO46091	Abo46091 Human PRO
955	26	81.2	143	6	ABM66894	Abm66894 Human sec
956	26	81.2	143	6	ADB20622	Adb20622 Human sec
957	26	81.2	143	6	ABM19795	Abm19795 Human sec
958	26	81.2	143	6	ABO49507	Abo49507 Human sec
959	26	81.2	143	6	ABO49812	Abo49812 Human sec
960	26	81.2	143	6	ADA78874	Ada78874 Human sec
961	26	81.2	143	6	ABR88369	Abr88369 Human sec
962	26	81.2	143	6	ABM27115	Abm27115 Human sec
963	26	81.2	143	6	ABM03512	Abm03512 Human sec
964	26	81.2	143	6	ABO40011	Abo40011 Human sec
965	26	81.2	143	7	ABO50117	Abo50117 Human sec
966	26	81.2	143	7	ABO51032	Abo51032 Human sec
967	26	81.2	143	7	ABO05488	Abo05488 Human sec
968	26	81.2	143	7	ABR74792	Abr74792 Human sec
969	26	81.2	143	7	ABR77271	Abr77271 Human sec
970	26	81.2	143	7	ABM18028	Abm18028 Human sec
971	26	81.2	143	7	ABR96079	Abr96079 Human sec
972	26	81.2	143	7	ABO22012	Abo22012 Human sec
973	26	81.2	143	7	ABO20182	Abo20182 Human sec

974	26	81.2	143	7	ABO24485	Abo24485 Human sec
975	26	81.2	143	7	ABR86234	Abr86234 Human sec
976	26	81.2	143	7	ABM10886	Abm10886 Human sec
977	26	81.2	143	7	ABM76885	Abm76885 Human sec
978	26	81.2	143	7	ABR89589	Abr89589 Human sec
979	26	81.2	143	7	ABM12716	Abm12716 Human sec
980	26	81.2	143	7	ABM06006	Abm06006 Human sec
981	26	81.2	143	7	ABO35131	Abo35131 Human PRO
982	26	81.2	143	7	ABM03207	Abm03207 Human sec
983	26	81.2	143	7	ABM19185	Abm19185 Human sec
984	26	81.2	143	7	ABM19490	Abm19490 Human sec
985	26	81.2	143	7	ABO46701	Abo46701 Human PRO
986	26	81.2	143	7	ABO49202	Abo49202 Human sec
987	26	81.2	143	7	ABR69245	Abr69245 Human sec
988	26	81.2	143	7	ABR89284	Abr89284 Human sec
989	26	81.2	143	7	ABR72657	Abr72657 Human sec
990	26	81.2	143	7	ABR74487	Abr74487 Human sec
991	26	81.2	143	7	ABO18755	Abo18755 Human sec
992	26	81.2	143	7	ABR80461	Abr80461 Human sec
993	26	81.2	143	7	ABM01682	Abm01682 Human sec
994	26	81.2	143	7	ABM02292	Abm02292 Human sec
995	26	81.2	143	7	ABR87454	Abr87454 Human sec
996	26	81.2	143	7	ABM13021	Abm13021 Human sec
997	26	81.2	143	7	ABM30775	Abm30775 Human sec
998	26	81.2	143	7	ABM24675	Abm24675 Human sec
999	26	81.2	143	7	ABO29589	Abo29589 Human sec
1000	26	81.2	143	7	ABO31419	Abo31419 Human sec

ALIGNMENTS

RESULT 1
AAR97316
ID AAR97316 standard; peptide; 5 AA.
XX
AC AAR97316;
XX
DT 15-OCT-1996 (first entry)
XX
DE Humanised monoclonal antibody heavy chain CDR.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Mus musculus.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Claim 5; Page 38; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. This sequence is a murine derived CDR region which corresponds
CC to CDR 1 in the heavy chain of the humanised MAb. See AAR97313-97333
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 32; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 1 TYWMS 5

RESULT 2
AAY05038
ID AAY05038 standard; peptide; 5 AA.
XX
AC AAY05038;
XX
DT 16-JUN-1999 (first entry)
XX
DE Tumour antigen antibody heavy chain CDR1 clone F15.
XX
KW Tumour antigen; antibody; CDR; complementarity determining region;
KW binding molecule identification; tumour-specific binding polypeptide;
KW cancer therapy; heavy chain.
XX
OS Homo sapiens.
XX
PN WO9906834-A2.
XX
PD 11-FEB-1999.
XX
PF 04-AUG-1998; 98WO-US016280.
XX
PR 04-AUG-1997; 97US-00905825.
XX
PA (IXSY-) IXSYS INC.
XX
PI Watkins JD, Huse WD, Wu H;
XX
DR WPI; 1999-153951/13.
DR N-PSDB; AAX28215.
XX
PT Identifying binding molecules for ligands, particularly tumour antigens -
PT by selectively immobilising a population of binding molecules to a solid
PT support and screening for binding to two or more ligands.
XX
PS Claim 15; Page 60; 80pp; English.
XX
CC This sequence represents a heavy chain complementarity determining region
CC (CDR) from a tumour antigen specific antibody. The invention relates to a
CC method for identifying a binding molecule having selective affinity for a
CC ligand comprising: (a) selectively immobilising a diverse population of
CC binding molecules to a solid support; (b) simultaneously contacting the
CC diverse population immobilised on the solid support with 2 or more
CC ligands; and (c) determining at least one binding molecule which
CC selectively binds to one or more of the ligands. The method allows for
CC the rapid and efficient methods for the identification of binding
CC molecules which exhibit selective affinity for one or more ligands of
CC interest. They are used particularly for identifying tumour-specific
CC binding polypeptides which can be used as targeting agents for cancer
CC therapy that minimises impact on non-tumour tissues
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 32; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
Db 1 TYWMS 5

RESULT 3
ADC82794
ID ADC82794 standard; peptide; 5 AA.
XX
AC ADC82794;
XX
DT 01-JAN-2004 (first entry)
XX
DE CDR region #3 in heavy chain of human Fab fragment.
XX
KW Binding molecule; selective affinity; ligand;
KW anti-immunoglobulin reagent; phage expressed antibody library;
KW tumour antigen; complementarity determining region; CDR; human disease;
KW cellular pathology; human; Fab; heavy chain.
XX
OS Homo sapiens.
XX
PN US2003044772-A1.
XX
PD 06-MAR-2003.
XX
PF 15-OCT-2001; 2001US-00977797.
XX
PR 04-AUG-1997; 97US-0113667P.
PR 04-AUG-1998; 98US-00129026.
XX
PA (MOLE-) APPLIED MOLECULAR EVOLUTION.
XX
PI Watkins JD, Huse WD, Wu H;
XX
DR WPI; 2003-625402/59.
DR N-PSDB; ADC82793.
XX
PT Identifying binding molecules having selective affinity for ligands for
PT discovering reagents for treating diseases, by contacting solid support
PT coated with anti-immunoglobulin reagent to a phage expressed antibody
PT library.
XX
PS Example 5; Page 16; 26pp; English.
XX
CC The present invention relates to a method for identifying a binding
CC molecule having selective affinity for a ligand. The method involves
CC providing a solid support coated with an anti-immunoglobulin reagent, and
CC a phage expressed antibody library, and contacting the solid support to
CC the phage expressed antibody library. The invention also discloses a
CC method for identifying an antibody having selective affinity for a
CC tumour, and a complementarity determining region (CDR) of an antibody
CC selective for a tumour antigen. The methods of the invention are useful
CC for identifying a binding molecule having selective affinity for a
CC ligand, for the discovery of specific reagents for diagnosis and
CC treatment of human diseases, for identifying binding molecules to, for
CC example tumour cells or other cellular pathologies for the selective
CC targeting of therapeutic agents, or for the identification of binding
CC molecules to normal or diseased tissues for the selective targeting of,
CC for example diagnostic agents such as imaging reagents. The methods are
CC rapid and efficient for the identification of binding molecules which
CC exhibit selective affinity for one or more ligands of interest. The
CC methods allow the simultaneous screening of multiple binding molecules
CC against multiple ligands of interest. Moreover, very little information
CC is required regarding the identity or function of either the binding
CC molecule or the ligand. For example diverse populations of binding
CC molecules can be simultaneously screened against diverse populations of
CC ligands to rapidly identify numerous molecules exhibiting a desired
CC binding specificity. The methods provide improved sensitivity and
CC specificity of detection through the selective immobilisation of the
CC binding molecule population on a solid support. The present sequence
CC represents a CDR region in the heavy chain of human Fab fragment.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 32; DB 7; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
Db 1 TYWMS 5

RESULT 4
ADM95105
ID ADM95105 standard; peptide; 5 AA.
XX
AC ADM95105;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 MAb heavy chain variable region CDR1.
XX
KW non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW complementarity determining region; pancreatic cancer; breast cancer;
KW ovarian cancer.
XX
OS Mus sp.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-364813/34.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Claim 6; SEQ ID NO 23; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the CDR1 of
CC the murine MN-14 antibody heavy chain variable region and used to
CC generate the humanised/chimeric antibody of the invention.
XX
SQ Sequence 5 AA;

Query Match 100.0%; Score 32; DB 8; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
Db 1 TYWMS 5

```
RESULT 5
ADM98314
ID   ADM98314 standard; peptide; 5 AA.
XX
AC   ADM98314;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 antibody heavy chain variable region CDR1 peptide.
XX
KW   carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; humanised;
KW   murine; mouse; antibody; MN-14; non-medullary thyroid carcinoma;
KW   medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW   hepatocellular carcinoma; breast cancer; lung cancer;
KW   antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW   apoptosis.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   WO2004032857-A2.
XX
PD   22-APR-2004.
XX
PF   08-OCT-2003; 2003WO-US031801.
XX
PR   08-OCT-2002; 2002US-0416531P.
PR   11-OCT-2002; 2002WO-US032307.
PR   02-MAY-2003; 2003US-0467161P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-340797/31.
XX
PT   Treating non-medullary or medullary thyroid carcinoma, involves
PT   administering to subject, either concurrently or sequentially, anti-
PT   carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS   Claim 8; Page 76; 122pp; English.
XX
CC   This invention relates to methods for treating cancers that express
CC   carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC   therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC   antibodies that can be used following administration of an agent that
CC   will increase antibody effector functions or following administration of
CC   an amount of interferon effective to upregulate CEA expression in tumour
CC   cells. The present invention describes the anti-CEA antibody as a class
CC   III humanised murine monoclonal antibody that retains specificity for CEA
CC   binding and is preferably an MN-14 antibody or fragment thereof.
CC   Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC   composition useful for the treatment of non-medullary or medullary
CC   thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC   carcinoma, as well as breast or lung cancer. Furthermore, it can
CC   stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC   mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC   cell growth and angiogenesis. This peptide sequence is a CDR region of
CC   the humanised murine MN-14 antibody of the invention.
XX
SQ   Sequence 5 AA;

  Query Match             100.0%;  Score 32;  DB 8;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 2e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db          1 TYWMS 5


RESULT 6
ABR42755
ID   ABR42755 standard; protein; 118 AA.
XX
AC   ABR42755;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14 VH region.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Disclosure; Fig 12; 62pp; English.
XX
CC   The present sequence is the protein sequence of the heavy chain variable
CC   region of anti-carcinoembryonic antigen (CEA) humanized monoclonal
CC   antibody hMN-14. scFv constructs comprising the hMN-14 VH and Vkappa
CC   regions are used in novel multivalent, monospecific binding proteins
CC   (diabody, triabody and tetrabody) of the invention (see also ABR42754,
CC   ABR42757 and ABR42758). Claimed binding proteins are specific for a
CC   tumour-associated antigen, and are used in the diagnosis and treatment of
CC   a tumour, carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma,
CC   lymphoma or myeloma, or a cancer selected from acute lymphoblastic
CC   leukaemia, acute myelogenous leukaemia, biliary, breast, cervical,
CC   chronic lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 118 AA;

  Query Match             100.0%;  Score 32;  DB 6;  Length 118;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 7
AAR97334
ID   AAR97334 standard; protein; 119 AA.
XX
AC   AAR97334;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Murine NEWM MN-14 variable region heavy chain.
```

```
XX
KW   Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW   complementary determining region; anti-carcinoembryonic antigen; CEA;
KW   diagnosis; imaging; therapy; immune response.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    31. .35
FT                   /label= CDR 1.
FT   Binding-site    50. .66
FT                   /label= CDR 2.
FT   Binding-site    99. .108
FT                   /label= CDR 3.
XX
PN   WO9611013-A1.
XX
PD   18-APR-1996.
XX
PF   28-SEP-1995;   95WO-US011964.
XX
PR   05-OCT-1994;   94US-00318157.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Hansen HJ,  Armour KL;
XX
DR   WPI; 1996-209653/21.
DR   N-PSDB; AAT29010.
XX
PT   New humanised anti-CEA monoclonal antibody - having engrafted murine
PT   CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS   Example 5; Fig 1; 62pp; English.
XX
CC   New humanised monoclonal antibodies (MAbs) comprising the complementary
CC   determining regions (CDRs) of a parental murine class III anti-
CC   carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC   heterologous antibody which can be derived from any species including
CC   human, retain the anti-CEA binding specificity of the parental murine MAb
CC   but are less immunogenic in a human subject than the parental MAb. The
CC   humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC   -producing cancers and patients receiving the humanised antibodies and
CC   conjugates show improved therapeutic results, decreased immune responses
CC   and decreased immune-mediated adverse effects compared to the parent
CC   antibody. See AAR97313-97333 for the CDR sequence and framework regions
CC   of the humanised MAbs
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 32;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 8
ADM95101
ID   ADM95101 standard; protein; 119 AA.
XX
AC   ADM95101;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 MAb heavy chain variable region coding sequence.
XX
KW   non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW   complementarity determining region; pancreatic cancer; breast cancer;
KW   ovarian cancer.
XX
OS   Mus sp.
OS   Homo sapiens.
XX
PN   WO2004032962-A1.
XX
PD   22-APR-2004.
XX
PF   11-OCT-2002; 2002WO-US032307.
XX
PR   08-OCT-2002; 2002US-0416531P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-364813/34.
DR   N-PSDB; ADM95099.
XX
PT   Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT   comprises administering, either concurrently or sequentially, Class III
PT   anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT   therapeutic agent(s).
XX
PS   Claim 14; Fig 16B; 88pp; English.
XX
CC   The invention relates to a method of treating a non-medullary thyroid
CC   carcinoma or treating medullary thyroid carcinoma involves administering
CC   to a subject, either concurrently or sequentially, a Class III anti-CEA
CC   (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC   least one therapeutic agent. The antibody or its fragment comprises the
CC   complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC   antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC   medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC   ovarian cancer, in a subject. This sequence corresponds to the humanised
CC   murine MN-14 antibody heavy chain variable region.
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 32;  DB 8;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 9
ADM95095
ID   ADM95095 standard; protein; 119 AA.
XX
AC   ADM95095;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Murine MN-14 MAb heavy chain variable region.
XX
KW   non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW   complementarity determining region; pancreatic cancer; breast cancer;
KW   ovarian cancer.
XX
OS   Mus sp.
XX
PN   WO2004032962-A1.
XX
PD   22-APR-2004.
XX
PF   11-OCT-2002; 2002WO-US032307.
XX
PR   08-OCT-2002; 2002US-0416531P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
```

```
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-364813/34.
XX
PT   Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT   comprises administering, either concurrently or sequentially, Class III
PT   anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT   therapeutic agent(s).
XX
PS   Disclosure; Fig 11A-B; 88pp; English.
XX
CC   The invention relates to a method of treating a non-medullary thyroid
CC   carcinoma or treating medullary thyroid carcinoma involves administering
CC   to a subject, either concurrently or sequentially, a Class III anti-CEA
CC   (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC   least one therapeutic agent. The antibody or its fragment comprises the
CC   complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC   antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC   medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC   ovarian cancer, in a subject. This sequence corresponds to the murine MN-
CC   14 antibody heavy chain variable region.
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 32;  DB 8;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 10
ADM98324
ID   ADM98324 standard; protein; 119 AA.
XX
AC   ADM98324;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 antibody heavy chain variable region protein.
XX
KW   carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW   antibody; MN-14; non-medullary thyroid carcinoma;
KW   medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW   hepatocellular carcinoma; breast cancer; lung cancer;
KW   antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW   apoptosis; humanised.
XX
OS   Mus sp.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 33. .34
FT                   /note= "Encoded by TGGGATAGCAGTACGATTAACTATGCGATG"
FT   Misc-difference 53. .62
FT                   /note= "Encoded by CCACCG"
XX
PN   WO2004032857-A2.
XX
PD   22-APR-2004.
XX
PF   08-OCT-2003; 2003WO-US031801.
XX
PR   08-OCT-2002; 2002US-0416531P.
PR   11-OCT-2002; 2002WO-US032307.
PR   02-MAY-2003; 2003US-0467161P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-340797/31.
DR   N-PSDB; ADM98323.
XX
PT   Treating non-medullary or medullary thyroid carcinoma, involves
PT   administering to subject, either concurrently or sequentially, anti-
PT   carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS   Disclosure; Fig 23b; 122pp; English.
XX
CC   This invention relates to methods for treating cancers that express
CC   carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC   therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC   antibodies that can be used following administration of an agent that
CC   will increase antibody effector functions or following administration of
CC   an amount of interferon effective to upregulate CEA expression in tumour
CC   cells. The present invention describes the anti-CEA antibody as a class
CC   III humanised murine monoclonal antibody that retains specificity for CEA
CC   binding and is preferably an MN-14 antibody or fragment thereof.
CC   Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC   composition useful for the treatment of non-medullary or medullary
CC   thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC   carcinoma, as well as breast or lung cancer. Furthermore, it can
CC   stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC   mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC   cell growth and angiogenesis. This polypeptide sequence is the humanised
CC   murine MN-14 antibody heavy chain variable region protein of the
CC   invention.
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 32;  DB 8;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 11
ADM98318
ID   ADM98318 standard; protein; 119 AA.
XX
AC   ADM98318;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Murine MN-14 antibody heavy chain variable region protein.
XX
KW   carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW   antibody; MN-14; non-medullary thyroid carcinoma;
KW   medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW   hepatocellular carcinoma; breast cancer; lung cancer;
KW   antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW   apoptosis.
XX
OS   Mus sp.
XX
PN   WO2004032857-A2.
XX
PD   22-APR-2004.
XX
PF   08-OCT-2003; 2003WO-US031801.
XX
PR   08-OCT-2002; 2002US-0416531P.
PR   11-OCT-2002; 2002WO-US032307.
PR   02-MAY-2003; 2003US-0467161P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-340797/31.
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```
DR   N-PSDB; ADM98317.
XX
PT   Treating non-medullary or medullary thyroid carcinoma, involves
PT   administering to subject, either concurrently or sequentially, anti-
PT   carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS   Disclosure; Fig 11; 122pp; English.
XX
CC   This invention relates to methods for treating cancers that express
CC   carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC   therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC   antibodies that can be used following administration of an agent that
CC   will increase antibody effector functions or following administration of
CC   an amount of interferon effective to upregulate CEA expression in tumour
CC   cells. The present invention describes the anti-CEA antibody as a class
CC   III humanised murine monoclonal antibody that retains specificity for CEA
CC   binding and is preferably an MN-14 antibody or fragment thereof.
CC   Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC   composition useful for the treatment of non-medullary or medullary
CC   thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC   carcinoma, as well as breast or lung cancer. Furthermore, it can
CC   stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC   mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC   cell growth and angiogenesis. This polypeptide sequence is murine MN-14
CC   antibody heavy chain variable region protein of the invention.
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 32;  DB 8;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 12
ABG76489
ID   ABG76489 standard; protein; 138 AA.
XX
AC   ABG76489;
XX
DT   13-MAY-2003  (first entry)
XX
DE   Heavy chain variable, VH, region of antibody hMN14.
XX
KW   CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW   colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW   human; zeta signalling chain; CD8alpha hinge; humanised antibody;
KW   heavy chain variable region; VH.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT   Protein         20. .138
FT                   /label= Mature_VH_of_hMN14
XX
PN   US2002165360-A1.
XX
PD   07-NOV-2002.
XX
PF   10-DEC-2001; 2001US-00006771.
XX
PR   30-NOV-2000; 2000US-0250087P.
PR   30-NOV-2000; 2000US-0250090P.
XX
PA   (JUNG/) JUNGHANS R P.
XX
PI   Junghans RP;
XX
DR   WPI; 2003-298705/29.
DR   N-PSDB; ABX13169.
XX
PT   New chimeric molecule from humanized antibody against carcinoembryonic
PT   antigen and having signaling molecules of T cells and other effector
PT   cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS   Disclosure; Page 9; 20pp; English.
XX
CC   The invention relates to a chimaeric molecule comprising the
CC   carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC   as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC   chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC   which the cysteine residues have been mutated, with the IgTCR molecule
CC   occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC   appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC   NK (not defined) or other effector cells are useful in treating patients
CC   with cancers expressing the CEA antigen, together with other or with
CC   heterologous constructs to engage additional stimulatory and functional
CC   properties of the effector cells to enhance the anti-tumour therapeutic
CC   efficacy. The cancer disorder includes colorectal, breast and lung
CC   cancers. The present sequence represents the heavy chain variable, VH,
CC   region of antibody hMN14. The VH protein is humanised (complementarity
CC   determining region-grafted) and has a leader peptide
XX
SQ   Sequence 138 AA;

  Query Match             100.0%;  Score 32;  DB 6;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         50 TYWMS 54


RESULT 13
ADF43574
ID   ADF43574 standard; protein; 236 AA.
XX
AC   ADF43574;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Rice peronospora parasitica resistant protein (PPR2) orthologue #2.
XX
KW   transgenic plant; peronospora parasitica resistant; PPR2;
KW   pathogen resistant phenotype; modified pathogen resistance.
XX
OS   Oryza sativa.
XX
PN   WO2003091412-A2.
XX
PD   06-NOV-2003.
XX
PF   24-APR-2003; 2003WO-US012981.
XX
PR   24-APR-2002; 2002US-0375333P.
XX
PA   (AGRI-) AGRINOMICS LLC.
XX
PI   Federspiel N,  Lammers A,  Liu XL,  Bates SR,  Westerlund C;
PI   Fitch JR;
XX
DR   WPI; 2003-865582/80.
XX
PT   New transgenic plants with increased resistance to pathogens due to
PT   altered expression of Peronospora Parasitica Resistant gene (PPR2),
PT   useful for generating plants with a pathogen resistance phenotype.
XX
```

PS Claim 4; SEQ ID NO 10; 36pp; English.
XX
CC The invention relates to a transgenic plant that possesses a plant
CC transformation vector comprising a nucleotide sequence that encodes a
CC peronospora parasitica resistant (PPR2) protein, or a PPR2 orthologue.
CC The transgenic plant is useful in generating plants with a pathogen
CC resistance phenotype. The PPR2 nucleic acids and proteins of the
CC invention are useful in the generation of genetically modified plants
CC having a modified pathogen resistance phenotype. The present amino acid
CC sequence represents a PPR2 orthologue protein of the invention.
XX
SQ Sequence 236 AA;

Query Match 100.0%; Score 32; DB 7; Length 236;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 200 TYWMS 204

RESULT 14
ABR42757
ID ABR42757 standard; protein; 256 AA.
XX
AC ABR42757;
XX
DT 26-AUG-2003 (first entry)
XX
DE Anti-CEA humanized monoclonal antibody hMN-14-0.
XX
KW Humanized; monoclonal antibody; antibody; hMN-14-0;
KW carcinoembryonic antigen; CEA; tumour; cytostatic; triabody.
XX
OS Homo sapiens.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1. .23
FT /label= Signal_peptide
FT /note= "pelB"
FT Region 23. .141
FT /label= hMN-14VH
FT Protein 24. .256
FT /label= hMN-14-0
FT Region 142. .250
FT /label= hMN-14Vkappa
FT Region 251. .256
FT /label= 6xHis_tag
XX
PN WO2003033654-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032718.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
PR 08-JAN-2002; 2002US-0345641P.
PR 22-AUG-2002; 2002US-0404919P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg DM;
XX
DR WPI; 2003-513460/48.
DR N-PSDB; ACC58722.
XX
PT New multivalent, monospecific binding protein comprising two or more
PT binding sites having affinity for the same single target antigen, where
PT each binding site is associated with scFv fragments, useful for
PT diagnosing or treating tumor.
XX
PS Claim 39; Fig 13; 62pp; English.
XX
CC The present sequence is the protein sequence of hMN-14-0, which is
CC designed to form an hMN-14 triabody. The hMN-14-0 polypeptide comprises
CC the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC Vkappa without a peptide linker. The use of the zero linker enables the
CC secreted polypeptide to form a triabody, forming 3 binding sites for CEA.
CC The polypeptide also includes a pelB signal peptide, which precedes the
CC VH moiety to facilitate synthesis of the polypeptide in the periplasmic
CC space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC purification. This monospecific triabody is an example of claimed
CC multivalent binding proteins specific for a tumour-associated antigen.
CC The binding proteins are used in the diagnosis and treatment of a tumour,
CC carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC prostate and bladder
XX
SQ Sequence 256 AA;

Query Match 100.0%; Score 32; DB 6; Length 256;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 54 TYWMS 58

RESULT 15
ABR42758
ID ABR42758 standard; protein; 257 AA.
XX
AC ABR42758;
XX
DT 26-AUG-2003 (first entry)
XX
DE Anti-CEA humanized monoclonal antibody hMN-14-1G.
XX
KW Humanized; monoclonal antibody; antibody; hMN-14-1G;
KW carcinoembryonic antigen; CEA; tumour; cytostatic; tetrabody.
XX
OS Homo sapiens.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1. .23
FT /label= Signal_peptide
FT /note= "pelB"
FT Region 23. .141
FT /label= hMN-14VH
FT Protein 24. .257
FT /label= hMN-14-0
FT Region 142
FT /label= 1G_linker
FT Region 143. .251
FT /label= hMN-14Vkappa
FT Region 252. .257
FT /label= 6xHis_tag
XX
PN WO2003033654-A2.
XX
PD 24-APR-2003.
XX

PF 15-OCT-2002; 2002WO-US032718.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
PR 08-JAN-2002; 2002US-0345641P.
PR 22-AUG-2002; 2002US-0404919P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg DM;
XX
DR WPI; 2003-513460/48.
XX
PT New multivalent, monospecific binding protein comprising two or more
PT binding sites having affinity for the same single target antigen, where
PT each binding site is associated with scFv fragments, useful for
PT diagnosing or treating tumor.
XX
PS Claim 48; Fig 14; 62pp; English.
XX
CC The present sequence is the protein sequence of hMN-14-1G, which is
CC designed to form an hMN-14 tetrabody. The hMN-14-1G polypeptide comprises
CC the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC Vkappa via a single glycine residues. Use of the 1G linker enables some
CC of the the secreted polypeptide to form a tetrabody with 4 binding sites
CC for CEA. The polypeptide also includes a pelB signal peptide, which
CC precedes the VH moiety to facilitate synthesis of the polypeptide in the
CC periplasmic space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC purification. This monospecific tetrabody is an example of claimed
CC multivalent binding proteins specific for a tumour-associated antigen.
CC The binding proteins are used in the diagnosis and treatment of a tumour,
CC carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC prostate and bladder
XX
SQ Sequence 257 AA;

Query Match 100.0%; Score 32; DB 6; Length 257;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 54 TYWMS 58

RESULT 16
ABR42289
ID ABR42289 standard; protein; 261 AA.
XX
AC ABR42289;
XX
DT 11-AUG-2003 (first entry)
XX
DE Diabody 679-scFv-L5 polypeptide (VH-I3Q/C101S mutant).
XX
KW Diabody; antibody; 679-scFv-L5; histamine-succinyl-glycyl; HSG;
KW affinity enhancement system; tumour; targeting; mutant; mutein.
XX
OS Mus sp.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1. .22
FT /label= Signal_peptide
FT /note= "pelB signal peptide"
FT Misc-difference 3
FT /note= "wild-type Ile substituted by Gln"
FT Protein 23. .268
FT /label= 679-scFv-L5
FT Region 23. .142
FT /label= 679VH(I3Q/C101S)
FT Misc-difference 101
FT /note= "wild-type Cys substituted by Ser"
FT Region 143. .147
FT /label= Linker
FT Region 148. .260
FT /label= 679Vk
FT Region 261. .268
FT /label= 6His_tag
XX
PN WO2003033653-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032717.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (IBCP-) IBC PHARM.
XX
PI Chang CK, Rossi E;
XX
DR WPI; 2003-393513/37.
DR N-PSDB; ACC57803.
XX
PT New kit comprising a multivalent, multi-specific binding protein and a
PT carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT for treating cancer, and cardiovascular, immune, inflammatory, or
PT infectious diseases.
XX
PS Disclosure; Fig 28; 87pp; English.
XX
CC The present sequence is the protein sequence of a 679 mutant diabody in
CC which antibody 679 VH has a Gln for Ile amino acid substitution at
CC position 3 and a Ser for Gln amino acid substitution at position 101.
CC Murine monoclonal antibody 679 binds with high affinity to molecules
CC containing the moiety histamine-succinyl-glycyl (HSG). The present
CC polypeptide comprises: 679 VH(I3Q) linked to 679 Vk via a peptide linker
CC (enables the secreted polypeptide to dimerise into a diabody, forming 2
CC sites for HSG); a pelB leader signal peptide (facilitates transport of
CC the polypeptide into the periplasmic space of Escherichia coli); and 6
CC His residues (allows purification by IMAC). The 679 diabody was expressed
CC in E. coli at a level of 10 ug/l of culture, compared with 1 ug/l for the
CC non-mutant polypeptide. The invention provides a bispecific diabody
CC comprising an HSG binding site and a carcinoembryonic antigen (CEA)
CC binding site. The HSG antigen binding site may comprise the VH and Vk
CC polypeptides of 679 MAb. These diabodies are produced via recombinant DNA
CC technology and create a novel affinity enhancement system that shows
CC specific affinity for HSG and CEA. They pre-target CEA positive tumours
CC for subsequent specific delivery of therapeutic radioisotopes carried by
CC HSG-carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC cardiovascular diseases and inflammatory diseases can be detected or
CC treated using the methods of the invention
XX
SQ Sequence 261 AA;

Query Match 100.0%; Score 32; DB 6; Length 261;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 54 TYWMS 58

RESULT 17

```
ABR42754
ID   ABR42754 standard; protein; 261 AA.
XX
AC   ABR42754;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-scFv-L5.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-scFv-15;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .261
FT                   /label= hMN-14-scFv-L5
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .255
FT                   /label= hMN-14Vkappa
FT   Region          256. .261
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
DR   N-PSDB; ACC58721.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 31; Fig 11; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-scFv-L5, which was
CC   designed to form an hMN-14 diabody. The hMN-14-scFv-L5 polypeptide
CC   comprises the C-terminal end of anti-carcinoembryonic antigen (CEA)
CC   humanized monoclonal antibody hMN-14 VH linked to the N-terminal part of
CC   hMN-14 Vkappa by a peptide linker that enables the secreted polypeptide
CC   to dimerize into a diabody, forming 2 binding sites for CEA. The
CC   polypeptide also includes a pelB signal peptide, which precedes the VH
CC   moiety to facilitate synthesis of the polypeptide in the periplasmic
CC   space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. In the claimed monospecific diabody, each scFv comprises
CC   the present sequence. The diabody is an example of claimed multivalent
CC   binding proteins specific for a tumour-associated antigen. The binding
CC   proteins are used in the diagnosis and treatment of a tumour, carcinoma,
CC   melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma or myeloma,
CC   or a cancer selected from acute lymphoblastic leukaemia, acute
CC   myelogenous leukaemia, biliary, breast, cervical, chronic lymphocytic
CC   leukaemia, chronic myelogenous leukaemia, colorectal, endometrial,
CC   oesophageal, gastric, head and neck, Hodgkin's lymphoma, lung, medullary
CC   thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic, prostate and
CC   bladder
XX
SQ   Sequence 261 AA;

  Query Match             100.0%;  Score 32;  DB 6;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         54 TYWMS 58


RESULT 18
ABR83645
ID   ABR83645 standard; protein; 261 AA.
XX
AC   ABR83645;
XX
DT   16-OCT-2003  (first entry)
XX
DE   hMN14-scFv-L5 amino acid sequence.
XX
KW   Multispecific binding protein; multivalent; target antigen; cytostatic;
KW   immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW   immunotherapy; autoimmune disease; infectious disease;
KW   cardiovascular disease; inflammatory disease.
XX
OS   Escherichia coli.
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003057829-A2.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-US038985.
XX
PR   26-DEC-2001; 2001US-0342103P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg D;
XX
DR   WPI; 2003-607997/57.
DR   N-PSDB; ACF57430.
XX
PT   Novel multivalent, multi-specific binding protein useful for treating
PT   cancer, has first binding site having affinity towards hapten group and
PT   second and third binding sites each having affinity towards target
PT   antigen.
XX
PS   Claim 11; Fig 6; 43pp; English.
XX
CC   The present invention describes a multivalent, multi-specific binding
CC   protein (I) comprising a first binding site having an affinity towards a
CC   hapten group and a second and a third binding sites each having affinity
CC   towards a target antigen, which may be the same or a different target
CC   antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC   and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC   useful for delivering a diagnostic agent, a therapeutic agent, or its
CC   combination to a target, which involves administering (I) to a subject,
CC   waiting for a sufficient amount of time for an amount of the non-binding
CC   protein to clear the subject's blood stream, and administering to the
CC   subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC   agent, or its combination, that binds to a binding site of the binding
CC   protein. (I) is also useful for detecting or treating a human disorder,
CC   preferably cancer, autoimmune diseases, infectious diseases,
CC   cardiovascular diseases and inflammatory diseases. The present sequence
CC   represents a hMN14-scFv-L5 amino acid sequence, which is used in the
```

```
CC   exemplification of the present invention
XX
SQ   Sequence 261 AA;

  Query Match            100.0%;  Score 32;  DB 6;  Length 261;
  Best Local Similarity  100.0%;  Pred. No. 6.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         54 TYWMS 58


RESULT 19
ABR42292
ID   ABR42292 standard; protein; 267 AA.
XX
AC   ABR42292;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .267
FT                   /label= BSI_polypeptide#1
FT   Region          24. .141
FT                   /label= hMN14_VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .259
FT                   /label= 679_Vk
FT   Region          262. .267
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57806.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 31; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of a
CC   novel bispecific diabody comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen. The bispecific diabody can be produced using
CC   recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC   a novel affinity enhancement system that shows specific affinity for HSG
CC   and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC   subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC   carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match            100.0%;  Score 32;  DB 6;  Length 267;
  Best Local Similarity  100.0%;  Pred. No. 6.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         54 TYWMS 58


RESULT 20
ABR42299
ID   ABR42299 standard; protein; 267 AA.
XX
AC   ABR42299;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS1.5H polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BS1.5H_polypeptide#2
FT   Region          24. .142
FT                   /label= hMN14_VH
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
FT                   /label= h679_Vk
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
```

DR WPI; 2003-393513/37.
DR N-PSDB; ACC57813.
XX
PT New kit comprising a multivalent, multi-specific binding protein and a
PT carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT for treating cancer, and cardiovascular, immune, inflammatory, or
PT infectious diseases.
XX
PS Claim 14; Fig 38; 87pp; English.
XX
CC The present sequence is the protein sequence for polypeptide #2 of novel
CC bispecific diabody BS1.5H comprising the VH region of monoclonal antibody
CC hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC binds with high affinity to molecules containing the moiety histamine-
CC succinyl-glycyl (HSG). A humanised version of its VH and Vk sequences
CC have been used in BS1.5H. Humanised antibody hMN14 binds specifically to
CC carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC provides a novel affinity enhancement system that shows specific affinity
CC for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC tumours for subsequent specific delivery of therapeutic radioisotopes
CC carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC disease, cardiovascular diseases and inflammatory diseases can be
CC detected or treated using the methods of the invention
XX
SQ Sequence 267 AA;

Query Match 100.0%; Score 32; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 54 TYWMS 58

RESULT 21
ABR42296
ID ABR42296 standard; protein; 267 AA.
XX
AC ABR42296;
XX
DT 11-AUG-2003 (first entry)
XX
DE Bispecific diabody BS2 polypeptide #2.
XX
KW Diabody; antibody; carcinoembryonic antigen; CEA;
KW histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW targeting; mutant; mutein.
XX
OS Homo sapiens.
OS Mus sp.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1. .22
FT /label= Signal_peptide
FT /note= "pelB leader peptide"
FT Protein 23. .267
FT /label= BS2_polypeptide#2
FT Region 24. .141
FT /label= hMN14-VH
FT Region 142. .146
FT /label= Linker
FT Region 147. .259
FT /label= 679_Vk
FT Region 262. .267
FT /label= His_tag
XX
PN WO2003033653-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032717.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (IBCP-) IBC PHARM.
XX
PI Chang CK, Rossi E;
XX
DR WPI; 2003-393513/37.
DR N-PSDB; ACC57810.
XX
PT New kit comprising a multivalent, multi-specific binding protein and a
PT carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT for treating cancer, and cardiovascular, immune, inflammatory, or
PT infectious diseases.
XX
PS Claim 14; Fig 35; 87pp; English.
XX
CC The present sequence is the protein sequence for polypeptide #2 of novel
CC bispecific diabody BS2 comprising the VH region of monoclonal antibody
CC hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC binds with high affinity to molecules containing the moiety histamine-
CC succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC provides a novel affinity enhancement system that shows specific affinity
CC for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC tumours for subsequent specific delivery of therapeutic radioisotopes
CC carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC disease, cardiovascular diseases and inflammatory diseases can be
CC detected or treated using the methods of the invention
XX
SQ Sequence 267 AA;

Query Match 100.0%; Score 32; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 54 TYWMS 58

RESULT 22
ABR42294
ID ABR42294 standard; protein; 267 AA.
XX
AC ABR42294;
XX
DT 11-AUG-2003 (first entry)
XX
DE Bispecific diabody BS1.5 polypeptide #2.
XX
KW Diabody; antibody; carcinoembryonic antigen; CEA;
KW histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW targeting; mutant; mutein.
XX
OS Homo sapiens.
OS Mus sp.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1. .22
FT /label= Signal_peptide
FT /note= "pelB leader peptide"
FT Protein 23. .267
FT /label= BS1.5_polypeptide#2

```
FT   Region          24. .141
FT                   /label= hMN14_VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .259
FT                   /label= 679_Vk(I3Q)
FT   Region          261. .267
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57808.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 33; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of a
CC   novel bispecific diabody comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen. The bispecific diabody can be produced using
CC   recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC   a novel affinity enhancement system that shows specific affinity for HSG
CC   and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC   subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC   carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             100.0%;  Score 32;  DB 6;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         54 TYWMS 58


RESULT 23
ADU26571
ID   ADU26571 standard; protein; 358 AA.
XX
AC   ADU26571;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric hBS14 polypeptide 2.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26573.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 2; SEQ ID NO 12; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
CC   activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC   site of inflammation (caused by infectious agent). (I) is useful in
CC   antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric hBS14 polypeptide 2 containing heavy and light chain variable
CC   regions.
XX
SQ   Sequence 358 AA;

  Query Match             100.0%;  Score 32;  DB 8;  Length 358;
  Best Local Similarity   100.0%;  Pred. No. 8.5e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        145 TYWMS 149


RESULT 24
ADU26561
ID   ADU26561 standard; protein; 363 AA.
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```
XX
AC   ADU26561;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric BS14hp polypeptide 2.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .6
FT                   /note= "signal peptide"
FT   Protein         7. .363
FT                   /note= "mature protein"
FT   Region          30. .40
FT                   /note= "CDR1hMN14Vk"
FT   Region          56. .62
FT                   /note= "CDR2hMN14Vk"
FT   Region          95. .102
FT                   /note= "CDR3hMN14Vk"
FT   Region          114. .119
FT                   /note= "linker region"
FT   Region          150. .154
FT                   /note= "CDR1hMN14Vh"
FT   Region          169. .185
FT                   /note= "CDR2hMN14Vh"
FT   Region          218. .227
FT                   /note= "CDR3hMN14Vh"
FT   Region          238. .242
FT                   /note= "linker region"
FT   Region          266. .282
FT                   /note= "CDR1h679Vk"
FT   Region          298. .304
FT                   /note= "CDR2h679Vk"
FT   Region          337. .344
FT                   /note= "CDR3h679Vk"
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26569.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 1; SEQ ID NO 2; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
CC   activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC   site of inflammation (caused by infectious agent). (I) is useful in
CC   antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric BS14HP polypeptide 2 containing heavy and light chain variable
CC   regions. The encoded polypeptide is designated alpha-factor-hMN-14Vk-
CC   GGGGS-hMN-14Vh-LEGGGS-h679Vk-6-His where the hMN14 is from a humanized
CC   antibody that binds specifically to the carcinoembryonic antigen and the
CC   h679 is a monoclonal antibody that binds the tri-peptide moiety histamine
CC   -succinyl-glycyl (HSG).
XX
SQ   Sequence 363 AA;

  Query Match             100.0%;  Score 32;  DB 8;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 8.7e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        150 TYWMS 154


RESULT 25
ADU26570
ID   ADU26570 standard; protein; 364 AA.
XX
AC   ADU26570;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric hBS14 polypeptide 1.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
```

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XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26572.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 2; SEQ ID NO 11; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
CC   activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC   site of inflammation (caused by infectious agent). (I) is useful in
CC   antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric hBS14 polypeptide 1 containing heavy and light chain variable
CC   regions.
XX
SQ   Sequence 364 AA;

  Query Match            100.0%;  Score 32;  DB 8;  Length 364;
  Best Local Similarity  100.0%;  Pred. No. 8.7e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        269 TYWMS 273


RESULT 26
ADU26560
ID   ADU26560 standard; protein; 370 AA.
XX
AC   ADU26560;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric  BS14HP polypeptide 1.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .7
FT                   /note= "signal peptide"
FT   Protein         8. .370
FT                   /note= "mature protein"
FT   Region          38. .42
FT                   /note= "CDR1h679Vh"
FT   Region          57. .68
FT                   /note= "CDR2h679Vh"
FT   Region          106. .115
FT                   /note= "CDR3h679Vh"
FT   Region          127. .131
FT                   /note= "linker region"
FT   Region          155. .165
FT                   /note= "CDR1hMN14Vk"
FT   Region          181. .187
FT                   /note= "CDR2hMN14Vk"
FT   Region          220. .227
FT                   /note= "CDR3hMN14Vk"
FT   Region          239. .244
FT                   /note= "linker region"
FT   Region          275. .279
FT                   /note= "CDR1hMN14Vh"
FT   Region          294. .310
FT                   /note= "CDR2hMN14Vh"
FT   Region          343. .352
FT                   /note= "CDR3hMN14Vh"
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26568.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 1; SEQ ID NO 1; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
```

CC infarction, ischemic heart disease, atherosclerotic plaques, graft
CC rejection, Alzheimer's disease or inflammation caused by accretion of
CC activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC site of inflammation (caused by infectious agent). (I) is useful in
CC antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC molecule, and immunostaining technique. This sequence corresponds to the
CC chimeric BS14HP polypeptide 1 containing heavy and light chain variable
CC regions. The encoded polypeptide is designated alpha-factor-h679Vh-GGGGS-
CC hMN-14Vk-LEGGGS-hMN-14Vh-6-His where the hMN14 is from a humanized
CC antibody that binds specifically to the carcinoembryonic antigen and the
CC h679 is a monoclonal antibody that binds the tri-peptide moiety histamine
CC -succinyl-glycyl (HSG).
XX
SQ Sequence 370 AA;

Query Match 100.0%; Score 32; DB 8; Length 370;
Best Local Similarity 100.0%; Pred. No. 8.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 275 TYWMS 279

RESULT 27
ABR83648
ID ABR83648 standard; protein; 415 AA.
XX
AC ABR83648;
XX
DT 16-OCT-2003 (first entry)
XX
DE TS1 VH chain amino acid sequence.
XX
KW Multispecific binding protein; multivalent; target antigen; cytostatic;
KW immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW immunotherapy; autoimmune disease; infectious disease;
KW cardiovascular disease; inflammatory disease.
XX
OS Escherichia coli.
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003057829-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US038985.
XX
PR 26-DEC-2001; 2001US-0342103P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg D;
XX
DR WPI; 2003-607997/57.
DR N-PSDB; ACF57433.
XX
PT Novel multivalent, multi-specific binding protein useful for treating
PT cancer, has first binding site having affinity towards hapten group and
PT second and third binding sites each having affinity towards target
PT antigen.
XX
PS Claim 48; Fig 8A-B; 43pp; English.
XX
CC The present invention describes a multivalent, multi-specific binding
CC protein (I) comprising a first binding site having an affinity towards a
CC hapten group and a second and a third binding sites each having affinity
CC towards a target antigen, which may be the same or a different target
CC antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC useful for delivering a diagnostic agent, a therapeutic agent, or its
CC combination to a target, which involves administering (I) to a subject,
CC waiting for a sufficient amount of time for an amount of the non-binding
CC protein to clear the subject's blood stream, and administering to the
CC subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC agent, or its combination, that binds to a binding site of the binding
CC protein. (I) is also useful for detecting or treating a human disorder,
CC preferably cancer, autoimmune diseases, infectious diseases,
CC cardiovascular diseases and inflammatory diseases. The present sequence
CC represents the TS1 VH chain amino acid sequence, which is used in the
CC exemplification of the present invention
XX
SQ Sequence 415 AA;

Query Match 100.0%; Score 32; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 9.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 54 TYWMS 58

RESULT 28
ABG76488
ID ABG76488 standard; protein; 443 AA.
XX
AC ABG76488;
XX
DT 13-MAY-2003 (first entry)
XX
DE Humanised anti-CEA antibody, hMN14.
XX
KW CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW human; zeta signalling chain; CD8alpha hinge; humanised antibody.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
PN US2002165360-A1.
XX
PD 07-NOV-2002.
XX
PF 10-DEC-2001; 2001US-00006771.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250090P.
XX
PA (JUNG/) JUNGHANS R P.
XX
PI Junghans RP;
XX
DR WPI; 2003-298705/29.
DR N-PSDB; ABX13168.
XX
PT New chimeric molecule from humanized antibody against carcinoembryonic
PT antigen and having signaling molecules of T cells and other effector
PT cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS Disclosure; Page 7-8; 20pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the
CC carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC which the cysteine residues have been mutated, with the IgTCR molecule
CC occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC NK (not defined) or other effector cells are useful in treating patients
CC with cancers expressing the CEA antigen, together with other or with
CC heterologous constructs to engage additional stimulatory and functional
CC properties of the effector cells to enhance the anti-tumour therapeutic

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CC   efficacy. The cancer disorder includes colorectal, breast and lung
CC   cancers. The present sequence represents the chimaeric molecule of the
CC   invention
XX
SQ   Sequence 443 AA;

  Query Match             100.0%;  Score 32;  DB 6;  Length 443;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        172 TYWMS 176


RESULT 29
ABG74240
ID   ABG74240 standard; protein; 443 AA.
XX
AC   ABG74240;
XX
DT   23-OCT-2003  (revised)
DT   22-APR-2003  (first entry)
XX
DE   Chimaeric hMN14/T-cell receptor.
XX
KW   Retroviral vector; T-cell receptor; hMN14; antibody; IgTCR; receptor;
KW   cytostatic; dermatological; neuroprotective; immunostimulant; GD3;
KW   ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4; 3E11;
KW   prostate-specific membrane antigen; zeta signalling chain; human; cancer;
KW   melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer;
KW   mouse; CD8alpha hinge.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
XX
PN   US2002132983-A1.
XX
PD   19-SEP-2002.
XX
PF   10-DEC-2001; 2001US-00006773.
XX
PR   30-NOV-2000; 2000US-0250087P.
PR   30-NOV-2000; 2000US-0250089P.
XX
PA   (JUNG/) JUNGHANS R P.
XX
PI   Junghans RP;
XX
DR   WPI; 2003-208946/20.
DR   N-PSDB; ABX16565.
XX
PT   New chimeric molecule useful in treating patients with disorders, such as
PT   melanoma, neuroendocrine disorders, prostate and small cell lung cancer
PT   comprises GD3 and/or PSMA binding domains of antibody.
XX
PS   Disclosure; Page 7-8; 35pp; English.
XX
CC   The invention relates to a chimaeric molecule comprising the GD3
CC   (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC   variable gene sequences, or the PSMA (prostate-specific membrane antigen)
CC   binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC   sequences, the zeta signalling chain of the T cell receptor and an
CC   intervening CD8alpha hinge in which cysteine residues have been mutated.
CC   The chimaeric molecules expressed in T cells or NK cells or other
CC   effector cells are useful in treating patients with cancers expressing
CC   the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC   and/or together with each other or with heterologous constructs to engage
CC   additional stimulatory and functional properties of the effector cells to
CC   enhance the antitumour therapeutic efficacy (claimed). They are
CC   particularly useful in disorders including melanoma, neuroendocrine
CC   tumours and prostate and small cell lung cancer. The present sequence is
CC   a hMN14 antibody (specific to CEA antigen) in a fusion protein with the
CC   modified CD8alpha hinge and the T-cell receptor zeta chain (IgTCR)
CC   encoded by a retroviral vector. The hMN14 antibody coding region is
CC   replaced with the MB3.6, 3D8, 4D4 or 3E11 genes of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 443 AA;

  Query Match             100.0%;  Score 32;  DB 6;  Length 443;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        172 TYWMS 176


RESULT 30
ADS42718
ID   ADS42718 standard; protein; 448 AA.
XX
AC   ADS42718;
XX
DT   02-DEC-2004  (first entry)
XX
DE   Bacterial polypeptide #21148.
XX
KW   Recombinant DNA construct; transformed plant; improved plant property;
KW   cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW   pathogen tolerance; pest tolerance; plant disease resistance;
KW   cell cycle pathway modification; plant growth regulator;
KW   homologous recombination; seed oil yield; protein yield; carbohydrate;
KW   nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW   bacterial polypeptide.
XX
OS   Bacteria.
XX
PN   US2003233675-A1.
XX
PD   18-DEC-2003.
XX
PF   20-FEB-2003; 2003US-00369493.
XX
PR   21-FEB-2002; 2002US-0360039P.
XX
PA   (CAOY/) CAO Y.
PA   (HINK/) HINKLE G J.
PA   (SLAT/) SLATER S C.
PA   (CHEN/) CHEN X.
PA   (GOLD/) GOLDMAN B S.
XX
PI   Cao Y,  Hinkle GJ,  Slater SC,  Chen X,  Goldman BS;
XX
DR   WPI; 2004-061375/06.
XX
PT   New recombinant DNA construct comprising a promoter positioned to provide
PT   for expression of a polynucleotide encoding a polypeptide from a
PT   microbial source, useful for producing plants with improved properties.
XX
PS   Claim 1; SEQ ID NO 21148; 122pp; English.
XX
CC   The invention relates to a recombinant DNA construct comprising a
CC   promoter functional in a plant cell, where the promoter is positioned to
CC   provide for expression of a polynucleotide encoding a polypeptide from a
CC   microbial source. The invention also relates to a transformed plant
CC   comprising the recombinant DNA construct and a method of producing a
CC   transformed plant having an improved property. The plant is a crop plant
CC   such as maize or soybean. The method of producing a transformed plant
CC   having an improved property comprises transforming a plant with the
CC   recombinant DNA construct and growing the transformed plant, where the
CC   polynucleotide or polypeptide is useful for improving plant properties.
CC   The recombinant DNA construct is useful for producing plants with
CC   improved plant properties, e.g. improved cold, heat or drought tolerance,
```

CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 448 AA;

Query Match 100.0%; Score 32; DB 8; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||||
Db 96 TYWMS 100

RESULT 31
ADN17753
ID ADN17753 standard; protein; 464 AA.
XX
AC ADN17753;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #406.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
DR WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 406; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 464 AA;

Query Match 100.0%; Score 32; DB 8; Length 464;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||||
Db 105 TYWMS 109

RESULT 32
ADE64201
ID ADE64201 standard; protein; 468 AA.
XX
AC ADE64201;
XX
DT 29-JAN-2004 (first entry)
XX
DE MN14HCF protein related to a novel antibody library.
XX
KW antibody library; retroviral vector; antibody light chain;
KW antibody heavy chain; human therapy; multiplicity of infection; MOI;
KW plasmid; GATEWAY vector; MN14HCF.
XX
OS Unidentified.
XX
PN WO2003083077-A2.
XX
PD 09-OCT-2003.
XX
PF 28-MAR-2003; 2003WO-US009662.
XX
PR 28-MAR-2002; 2002US-0368808P.
PR 10-APR-2002; 2002US-0371299P.
PR 28-MAR-2003; 2003US-00371299.
XX
PA (GALA-) GALA DESIGN INC.
XX
PI Bremel RD, Eakle K, Imboden M;
XX
DR WPI; 2003-804051/75.
DR N-PSDB; ADE64206.
XX
PT New antibody library comprising cells comprising at least one integrated
PT retroviral vector expressing an antibody light or heavy chain, useful in
PT preparing a composition for diagnosing or treating disorders.
XX
PS Disclosure; Fig 6; 57pp; English.
XX
CC This invention relates to a new antibody library which comprises at least
CC 100 cells, each of which comprises at least one integrated retroviral
CC vector expressing an antibody light or heavy chain. Antibodies are of

CC increasing importance in human therapy, assay procedures and diagnostic
CC methods and a need exists for efficient methods of generating and
CC screening antibody libraries containing large numbers of antibodies. The
CC antibody library of the invention addresses this need, with the
CC additional advantage of strict control over multiplicity of infection
CC (MOI), and is useful in preparing a composition for diagnosing or
CC treating a wide variety of disorders. The present sequence is the amino
CC acid sequence of the MN14HCF protein, which was encoded by the Gateway
CC retroviral vectors used in the exemplification of the invention.
XX
SQ Sequence 468 AA;

Query Match 100.0%; Score 32; DB 7; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 50 TYWMS 54

RESULT 33
ADF60815
ID ADF60815 standard; protein; 468 AA.
XX
AC ADF60815;
XX
DT 12-FEB-2004 (first entry)
XX
DE hMN-14 heavy chain amino acid sequence.
XX
KW Immunomodulatory; antidiabetic; immunosuppressive; cardiovascular;
KW neuroprotective; nootropic; fungicide; virucide; antimalarial;
KW antihelmintic; antiparasitic; haemostatic; muscular; antiinflammatory;
KW dermatological; antipyretic; antirheumatic; cytostatic; mutant;
KW bispecific antibody; immunoglobulin G; IgG; scFvs; Fvs; CH2 domain;
KW immune; autoimmune; disease; organ graft rejection; cardiovascular;
KW neurological; Alzheimer's disease; graft vs host disease;
KW systemic lupus erythematosus; diabetes mellitus.
XX
OS Homo sapiens.
XX
PN WO2003074569-A2.
XX
PD 12-SEP-2003.
XX
PF 03-MAR-2003; 2003WO-GB000871.
XX
PR 01-MAR-2002; 2002US-0361037P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (MCCA/) MCCALL J D.
XX
PI Qu Z, Hansen H, Goldenberg DM;
XX
DR WPI; 2003-902725/82.
DR N-PSDB; ADF60814.
XX
PT Mutant bispecific antibody which is rapidly cleared from a patient's
PT body, useful as a pretargeting agent in methods for diagnosing or
PT treating diseases, such as autoimmune disease, and disease caused by
PT infectious agents.
XX
PS Example; Fig 1; 68pp; English.
XX
CC The invention relates to a mutant bispecific antibody (mbAb1) comprising
CC at least a human hinge constant region from immunoglobulin G (IgG), two
CC single chain variable fragments (scFvs), and two variable fragments
CC (Fvs), where the constant region contains one or more amino acid
CC mutations in the heavy chain 2 (CH2) domain. The methods and antibody of
CC the invention are used to diagnose or treat an immune dysregulation
CC disease, an autoimmune disease, organ graft rejection, cardiovascular
CC disease, neurological disease (Alzheimer's disease) or graft vs. host
CC disease. The methods are also useful for treating a disease caused by a
CC fungus, virus, parasite, or bacterium. The methods may also be used for
CC intraoperative or endoscopic diagnosis to identify diseased tissue. The
CC autoimmune diseases that may be diagnosed or treated include acute or
CC chronic idiopathic thrombocytopenic purpura, dermatomyositis, Sydenham's
CC chorea, myasthenia gravis, systemic lupus erythematosus, lupus nephritis,
CC rheumatic fever, polyglandular syndromes and diabetes mellitus. The
CC current sequence represents the hMN-14 heavy chain amino acid sequence.
XX
SQ Sequence 468 AA;

Query Match 100.0%; Score 32; DB 7; Length 468;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 50 TYWMS 54

RESULT 34
ABM66981
ID ABM66981 standard; protein; 490 AA.
XX
AC ABM66981;
XX
DT 20-NOV-2003 (first entry)
XX
DE Photorhabdus luminescens protein sequence #78.
XX
KW Antibacterial; fungicide; insecticide; polymorphism; genetic analysis;
KW detection; food; gene expression; plant; animal; microorganism; toxin;
KW antibiotic; biopesticide; virulence factor; disease model; plague;
KW whooping cough.
XX
OS Photorhabdus luminescens.
XX
PN WO200294867-A2.
XX
PD 28-NOV-2002.
XX
PF 07-FEB-2002; 2002WO-IB003040.
XX
PR 07-FEB-2001; 2001FR-00001659.
XX
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Duchaud E, Taourit S, Glaser P, Frangeul L, Kunst F, Danchin A;
PI Buchrieser C;
XX
DR WPI; 2003-148459/14.
XX
PT Genomic sequence of Photorhabdus luminescens and encoded polypeptides,
PT useful e.g. as therapeutic antimicrobials and agricultural pesticides.
XX
PS Claim 2; SEQ ID NO 78; 1205pp; French.
XX
CC The invention relates to the isolation of genes and their encoded
CC proteins from Photorhabdus luminescens. The isolated sequences are
CC sources of probes and primers for detecting the genome of P. luminescens
CC and related species; to study polymorphisms; for gene analysis and for
CC detection/amplification of the genes. Antibodies (Ab) raised against the
CC polypeptides encoded by the genes are used for detection/identification
CC of P. luminescens, e.g. in foods. The genes, proteins, Ab and cells that
CC carry a gene-containing vector are used to select compounds that
CC modulate, regulate, induce or inhibit expression of the genes in plants,
CC animals or microorganisms other than P. luminescens and are able to alter
CC response or sensitivity to toxins and antibiotics produced by P.
CC luminescens. Cells transformed to express the genes are useful for
CC recombinant production of the proteins, particularly toxins and
CC antibacterials useful as insecticides, bactericides and fungicides. The
CC genes, proteins, vectors containing the genes and Ab are also useful

```
CC   therapeutically (to treat microbial infection by bacteria or fungi that
CC   are sensitive to P. luminescens-encoded toxins or antibiotics) and as
CC   biopesticides. Other uses of the genes and the proteins are as virulence
CC   factors and for identifying targets of human diseases for which P.
CC   luminescens is a model (particularly plague and whooping cough). This
CC   sequence represents one of the isolated P. luminescens proteins
XX
SQ   Sequence 490 AA;

  Query Match             100.0%;  Score 32;  DB 6;  Length 490;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        114 TYWMS 118


RESULT 35
ABB63205
ID   ABB63205 standard; protein; 597 AA.
XX
AC   ABB63205;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster polypeptide SEQ ID NO 16407.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US009231.
XX
PR   23-MAR-2000; 2000US-0191637P.
PR   11-JUL-2000; 2000US-00614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   N-PSDB; ABL07308.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signaling and cell-cell
PT   interactions.
XX
PS   Disclosure; SEQ ID NO 16407; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC   ABB72072). The sequence data for this patent did not form part of the
CC   printed specification, but was obtained in electronic format directly
CC   from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 597 AA;

  Query Match             100.0%;  Score 32;  DB 4;  Length 597;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        443 TYWMS 447


RESULT 36
ADO07980
ID   ADO07980 standard; protein; 597 AA.
XX
AC   ADO07980;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Fly polypeptide #44.
XX
KW   Fly; fat cell number; fat cell size; obesity; diabetes; anorectic;
KW   antidiabetic.
XX
OS   Diptera.
XX
PN   US2004071700-A1.
XX
PD   15-APR-2004.
XX
PF   09-OCT-2002; 2002US-00267502.
XX
PR   09-OCT-2002; 2002US-00267502.
XX
PA   (LIFE-) LIFE SCI DEV CORP.
XX
PI   Kim J,  Galant R;
XX
DR   WPI; 2004-328526/30.
DR   N-PSDB; ADO07763.
XX
PT   Identifying compounds that influence fat cell number or size for treating
PT   or preventing obesity or diabetes by exposing the cell to the agent and
PT   identifying fat cell number or size relative to cells not exposed to the
PT   agent.
XX
PS   Claim 14; SEQ ID NO 306; 275pp; English.
XX
CC   The invention relates to a method of identifying compounds that influence
CC   fat cell number or size comprising providing a cell that expresses a gene
CC   and an agent, exposing the cell to the agent and identifying fat cell
CC   number or size relative to cells not exposed to the agent. The method
CC   also comprises providing an expression vector and an agent, exposing the
CC   vector to the agent, detecting a change in expression of the gene
CC   relative to expression of the gene in an expression vector not exposed to
CC   the agent, treating a subject with the agent and identifying fat cell
CC   number or size in the subject. The agent comprises an antisense
CC   oligonucleotide. The subject comprises a mammal, preferably a human. The
CC   method also comprises providing a polypeptide and an agent, exposing the
CC   polypeptide to the agent, detecting binding of the agent to the
CC   polypeptide or a change in an activity of the polypeptide, treating a
CC   subject with the agent and identifying fat cell number or size in the
CC   subject. The agent comprises an antibody. A method of regulating fat cell
CC   number or size comprises providing a subject containing fat cells and an
CC   agent that changes the expression of a gene, and treating the subject
CC   with the agent under conditions so that fat cell size or number in the
CC   subject is altered. The method is useful for identifying compounds that
CC   influence fat cell number or size, for preparing a composition for
CC   treating or preventing obesity or diabetes. This sequence represents a
CC   fly polypeptide used in the scope of the invention.
XX
SQ   Sequence 597 AA;

  Query Match             100.0%;  Score 32;  DB 8;  Length 597;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        443 TYWMS 447
```

RESULT 37
ADY97271
ID ADY97271 standard; protein; 669 AA.
XX
AC ADY97271;
XX
DT 16-JUN-2005 (first entry)
XX
DE Exemplary antibody fusion protein SEQ ID NO:3.
XX
KW antibody engineering; fusion protein; cytostatic; antimicrobial;
KW virucide; antibacterial; cancer; infection.
XX
OS Synthetic.
XX
PN US2005069552-A1.
XX
PD 31-MAR-2005.
XX
PF 28-JUL-2004; 2004US-00900928.
XX
PR 28-JUL-2003; 2003US-0490569P.
XX
PA (BLEC/) BLECK G T.
PA (YORK/) YORK D.
PA (COLL/) COLLINS I.
XX
PI Bleck GT, York D, Collins I;
XX
DR WPI; 2005-261600/27.
DR N-PSDB; ADY97269.
XX
PT Composition useful as cancer vaccine, comprises polypeptide having
PT antibody heavy chain fused to antibody light chain, or multivalent
PT antibody having two polypeptides with antibody heavy chain fused to
PT antibody light chain.
XX
PS Disclosure; SEQ ID NO 3; 101pp; English.
XX
CC The invention describes a composition (I) comprising: (a) a polypeptide
CC comprising at least one antibody heavy chain fused to at least one
CC antibody light chain; or (b) a multivalent antibody comprising at least
CC two polypeptides, where each of the polypeptides comprises at least one
CC antibody heavy chain fused to at least one antibody light chain. Also
CC described: (1) a composition (II) comprising a nucleic acid comprising at
CC least one antibody heavy chain gene and at least one antibody light chain
CC gene, where the nucleic acid encodes a polypeptide comprising at least
CC one antibody heavy chain fused to at least one antibody light chain; (2)
CC a method (M1) of binding an antigen, involves providing a polypeptide
CC comprising at least one antibody heavy chain fused to at least one
CC antibody light chain, and contacting the polypeptide with a sample having
CC an antigen under conditions such that the polypeptide binds to the
CC antigen; (3) a method (M2), which involves providing a vector comprising
CC a bicistronic expression construct comprising genes encoding an antibody
CC heavy chain gene and an antibody light chain gene, and altering the
CC nucleic acid sequence of a splice acceptor sequence or a splice donor
CC sequence in the antibody light chain gene or the antibody heavy chain
CC gene under conditions such that splicing is prevented at the splice
CC acceptor sequence or donor sequence; (4) a nucleic acid sequence produced
CC by (M2); (5) a vector (III) comprising a modified antibody heavy or light
CC gene, where modification eliminates a splice donor or acceptor sequence
CC in antibody heavy or light chain gene; and (6) a host cell comprising
CC (III). (I) is useful in in vitro binding assays for identifying antigens
CC in a mixture or determining the presence or absence of expression of a
CC particular protein. (I) is also useful as vaccine for treating cancer and
CC infections caused by pathogens e.g. virus or bacteria. The present
CC sequence represents an exemplary antibody fusion protein from the present
CC invention.
XX
SQ Sequence 669 AA;

Query Match 100.0%; Score 32; DB 9; Length 669;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||||
Db 31 TYWMS 35

RESULT 38
ADU87696
ID ADU87696 standard; peptide; 5 AA.
XX
AC ADU87696;
XX
DT 10-FEB-2005 (first entry)
XX
DE Mouse Luc90 heavy chain variable region, CDR1.
XX
KW Antibody; CS1; SLAM family member 7; SLAMF7; immunoglobulin;
KW pharmaceutical; antibody-dependent cellular cytotoxicity;
KW FcgammaR receptor; cell proliferation; leukocyte; cancer;
KW multiple myeloma; multiple myeloma-related bone disorder; plasmacytoma;
KW macroglobulinemia; amyloidosis; chronic lymphocytic leukemia;
KW autoimmune disease; inflammatory bowel disease;
KW systemic lupus erythematosus; cytostatic; immunosuppressive;
KW antiinflammatory; gastrointestinal-gen.; dermatological; luc90;
KW heavy chain variable region; complementarity determining region; CDR.
XX
OS Mus sp.
XX
PN WO2004100898-A2.
XX
PD 25-NOV-2004.
XX
PF 10-MAY-2004; 2004WO-US014866.
XX
PR 08-MAY-2003; 2003US-0469211P.
PR 29-MAR-2004; 2004US-0557620P.
PR 29-MAR-2004; 2004US-0557621P.
PR 29-MAR-2004; 2004US-0557622P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Williams M, Tso YJ, Landolfi NF;
XX
DR WPI; 2004-821790/81.
XX
PT New anti-CS1 antibodies, useful for diagnosing, preventing or treating
PT cancer, myeloma, autoimmune disorder, inflammatory bowel disease, or
PT systemic lupus erythematosus.
XX
PS Claim 12; SEQ ID NO 9; 151pp; English.
XX
CC The invention relates to an antibody or its antigen-binding fragment,
CC which binds to CS1 (also known as SLAM family member 7, SLAMF7) and
CC inhibits immunoglobulin secretion, where the antibody binds to
CC substantially the same epitope as an antibody comprising an amino acid
CC sequence of any one of SEQ ID NOS: 3-26, the antibody comprises an amino
CC acid sequence of SEQ ID NOS: 27-44, and where the heavy chain variable
CC region comprises a complementarity determining region (CDR) of SEQ ID NO:
CC 33. Also disclosed are (i) a heavy chain CDR of an antibody comprising an
CC amino acid sequence of SEQ ID NOS: 9-11, 15-17, 21-23, 29-33, (ii) a
CC light chain CDR of an antibody comprising an amino acid sequence of SEQ
CC ID NOS: 12-14, 18-20, 24-26, 34-370, (iii) a pharmaceutical composition
CC comprising a pharmaceutical carrier and the antibody described above,
CC (iv) a method of inhibiting proliferation of CS1 expressing cells, (v)
CC inhibiting immunoglobulin secretion, and (vi) increasing antibody-
CC dependent cellular cytotoxicity (ADCC) activity of the antibody described
CC above, where the antibody has decreased levels of fucose or is mutated to
CC increase antibody affinity for a FcgammaR receptor. The antibody of the
CC invention inhibits the proliferation of leukocytes or cancer cells. The
CC antibody triggers cytotoxic effects on cells expressing CS1 or enhances

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CC   cytotoxicity mediated by immune cells, or triggers ADCC-mediated
CC   cytotoxicity of cells expressing CS1. The antibody binds to substantially
CC   the same epitope as the antibody produced by a hybridoma cell line having
CC   ATCC accession number PTA-5091 or a Luc63 antibody. The antibody is
CC   produced by a hybridoma cell line having ATCC accession number PTA-5091
CC   or by a hybridoma cell line expressing Luc63 antibody. The antibody is a
CC   monoclonal antibody, e.g. a chimeric antibody, a humanized antibody, or a
CC   fully human antibody. The antibody is conjugated with a cytotoxic agent.
CC   The antibody comprises a heavy chain variable region comprising amino
CC   acid sequences of SEQ ID NOS: 3, 5, 7, or 27, and a light chain variable
CC   region comprising amino acid sequences of SEQ ID NOS: 4, 6, 8, or 28. The
CC   antibody, compositions, and methods are useful for diagnosing, preventing
CC   or treating plasma cell cancer, e.g. myeloma, multiple myeloma, myeloma
CC   of bone, extramedullary plasmacytoma, macroglobulinemia (including
CC   Waldenstrom's macroglobulinemia), heavy-chain disease, primary
CC   amyloidosis or monoclonal gammopathy of unknown significance, non-plasma
CC   cell cancer (chronic lymphocytic leukemia), autoimmune disorder,
CC   inflammatory bowel disease (IBD), or systemic lupus erythematosus (SLE).
CC   This sequence represents a CDR from a CS1 antibody.
XX
SQ   Sequence 5 AA;

  Query Match             90.6%;  Score 29;  DB 8;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 2e+06;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db          1 TYWMN 5


RESULT 39
AAG16081
ID   AAG16081 standard; protein; 46 AA.
XX
AC   AAG16081;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 16584.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-00301439.
XX
PR   25-FEB-1999;   99US-0121825P.
PR   05-MAR-1999;   99US-0123180P.
PR   09-MAR-1999;   99US-0123548P.
PR   23-MAR-1999;   99US-0125788P.
PR   25-MAR-1999;   99US-0126264P.
PR   29-MAR-1999;   99US-0126785P.
PR   01-APR-1999;   99US-0127462P.
PR   06-APR-1999;   99US-0128234P.
PR   08-APR-1999;   99US-0128714P.
PR   16-APR-1999;   99US-0129845P.
PR   19-APR-1999;   99US-0130077P.
PR   21-APR-1999;   99US-0130449P.
PR   23-APR-1999;   99US-0130510P.
PR   23-APR-1999;   99US-0130891P.
PR   28-APR-1999;   99US-0131449P.
PR   30-APR-1999;   99US-0132048P.
PR   30-APR-1999;   99US-0132407P.
PR   04-MAY-1999;   99US-0132484P.
PR   05-MAY-1999;   99US-0132485P.
PR   06-MAY-1999;   99US-0132486P.
PR   06-MAY-1999;   99US-0132487P.
PR   07-MAY-1999;   99US-0132863P.
PR   11-MAY-1999;   99US-0134256P.
PR   14-MAY-1999;   99US-0134218P.
PR   14-MAY-1999;   99US-0134219P.
PR   14-MAY-1999;   99US-0134221P.
PR   14-MAY-1999;   99US-0134370P.
PR   18-MAY-1999;   99US-0134768P.
PR   19-MAY-1999;   99US-0134941P.
PR   20-MAY-1999;   99US-0135124P.
PR   21-MAY-1999;   99US-0135353P.
PR   24-MAY-1999;   99US-0135629P.
PR   25-MAY-1999;   99US-0136021P.
PR   27-MAY-1999;   99US-0136392P.
PR   28-MAY-1999;   99US-0136782P.
PR   01-JUN-1999;   99US-0137222P.
PR   03-JUN-1999;   99US-0137528P.
PR   04-JUN-1999;   99US-0137502P.
PR   07-JUN-1999;   99US-0137724P.
PR   08-JUN-1999;   99US-0138094P.
PR   10-JUN-1999;   99US-0138540P.
PR   10-JUN-1999;   99US-0138847P.
PR   14-JUN-1999;   99US-0139119P.
PR   16-JUN-1999;   99US-0139452P.
PR   16-JUN-1999;   99US-0139453P.
PR   17-JUN-1999;   99US-0139492P.
PR   18-JUN-1999;   99US-0139454P.
PR   18-JUN-1999;   99US-0139455P.
PR   18-JUN-1999;   99US-0139456P.
PR   18-JUN-1999;   99US-0139457P.
PR   18-JUN-1999;   99US-0139458P.
PR   18-JUN-1999;   99US-0139459P.
PR   18-JUN-1999;   99US-0139460P.
PR   18-JUN-1999;   99US-0139461P.
PR   18-JUN-1999;   99US-0139462P.
PR   18-JUN-1999;   99US-0139463P.
PR   18-JUN-1999;   99US-0139750P.
PR   18-JUN-1999;   99US-0139763P.
PR   21-JUN-1999;   99US-0139817P.
PR   22-JUN-1999;   99US-0139899P.
PR   23-JUN-1999;   99US-0140353P.
PR   23-JUN-1999;   99US-0140354P.
PR   24-JUN-1999;   99US-0140695P.
PR   28-JUN-1999;   99US-0140823P.
PR   29-JUN-1999;   99US-0140991P.
PR   30-JUN-1999;   99US-0141287P.
PR   01-JUL-1999;   99US-0141842P.
PR   01-JUL-1999;   99US-0142154P.
PR   02-JUL-1999;   99US-0142055P.
PR   06-JUL-1999;   99US-0142390P.
PR   08-JUL-1999;   99US-0142803P.
PR   09-JUL-1999;   99US-0142920P.
PR   12-JUL-1999;   99US-0142977P.
PR   13-JUL-1999;   99US-0143542P.
PR   14-JUL-1999;   99US-0143624P.
PR   15-JUL-1999;   99US-0144005P.
PR   16-JUL-1999;   99US-0144085P.
PR   16-JUL-1999;   99US-0144086P.
PR   19-JUL-1999;   99US-0144325P.
PR   19-JUL-1999;   99US-0144331P.
PR   19-JUL-1999;   99US-0144332P.
PR   19-JUL-1999;   99US-0144333P.
PR   19-JUL-1999;   99US-0144334P.
PR   19-JUL-1999;   99US-0144335P.
PR   20-JUL-1999;   99US-0144352P.
PR   20-JUL-1999;   99US-0144632P.
PR   20-JUL-1999;   99US-0144884P.
PR   21-JUL-1999;   99US-0144814P.
PR   21-JUL-1999;   99US-0145086P.
PR   21-JUL-1999;   99US-0145088P.
PR   22-JUL-1999;   99US-0145085P.
PR   22-JUL-1999;   99US-0145087P.
PR   22-JUL-1999;   99US-0145089P.
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PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 90.6%; Score 29; DB 3; Length 46;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TYWMS 5
              |||:|
Db         25 TYWLS 29
```

RESULT 40
AAG16080
ID AAG16080 standard; protein; 52 AA.
XX
AC AAG16080;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16583.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
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PR 21-APR-1999; 99US-0130449P.
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PR 23-APR-1999; 99US-0130891P.
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PR 06-MAY-1999; 99US-0132487P.
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PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
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PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
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PR 16-JUN-1999; 99US-0139452P.
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PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
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PR 18-JUN-1999; 99US-0139763P.
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PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
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PR 24-JUN-1999; 99US-0140695P.
PR 28-JUN-1999; 99US-0140823P.
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PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
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PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
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PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
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PR 27-JUL-1999; 99US-0145918P.
PR 27-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
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PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
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PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
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PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.

PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 90.6%; Score 29; DB 3; Length 52;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:|
Db 31 TYWLS 35

RESULT 41
AAM06667
ID AAM06667 standard; protein; 69 AA.
XX
AC AAM06667;
XX
DT 05-OCT-2001 (first entry)
XX
DE Human foetal protein, SEQ ID NO: 398.
XX
KW Human; foetal protein; cytostatic; immunosuppressive; immunostimulant;
KW nootropic; neuroprotective; thrombolytic; osteopathic; antiinflammatory;
KW gene therapy; antisense therapy; cancer; immune disorder;
KW growth disorder; osteoporosis; thrombolytic disorder;
KW nervous system disorder; inflammation.
XX
OS Homo sapiens.
XX
PN WO200155339-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002723.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 15-SEP-2000; 2000US-00663870.
PR 06-NOV-2000; 2000US-00707351.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Yeung G, Ford JE, Boyle BJ, Arterburn MC, Drmanac RA, Tang YT;
PI Liu C, Asundi V, Zhou P, Werhman T;
XX
DR WPI; 2001-465571/50.
DR N-PSDB; AAH94342.
XX
PT Novel fetal proteins useful for the treatment and diagnosis of diseases
PT associated with dysfunction of the protein e.g. cancers, immune
PT disorders, growth disorders, thrombolytic disorders, nervous system
PT disorders and inflammation.
XX
PS Claim 10; Page 323; 715pp; English.
XX
CC The invention relates to novel foetal polypeptides encoded by
CC polynucleotides comprising one of 477 sequences fully defined in the
CC specification. The foetal polynucleotides and polypeptides are useful in
CC the treatment and diagnosis of diseases such as cancers, immune
CC disorders, growth disorders (e.g. osteoporosis), thrombolytic disorders,
CC nervous system disorders and inflammation. The present sequence is a
CC polypeptide encoded by a cDNA assembled using an expressed sequence tag
CC (EST) found to be expressed in human foetal tissue cDNA libraries
XX
SQ Sequence 69 AA;

Query Match 90.6%; Score 29; DB 4; Length 69;
Best Local Similarity 80.0%; Pred. No. 5.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:|
Db 11 TYWLS 15

RESULT 42
ABR41152
ID ABR41152 standard; protein; 83 AA.
XX
AC ABR41152;
XX
DT 02-JUN-2003 (first entry)
XX
DE Human DITHP enzyme.
XX
KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
KW cancer; cell proliferative disorder; autoimmune disorder;
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
KW neurological disorder; gastrointestinal disorder; transport disorder;
KW connective tissue disorder; drug screening; proteome analysis;
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
KW disease model; toxicological testing; transcript imaging; enzyme.
XX
OS Homo sapiens.
XX
PN WO200297031-A2.
XX
PD 05-DEC-2002.
XX
PF 27-MAR-2002; 2002WO-US010056.
XX
PR 28-MAR-2001; 2001US-0279619P.
PR 29-MAR-2001; 2001US-0280067P.
PR 29-MAR-2001; 2001US-0280068P.
PR 16-MAY-2001; 2001US-0291280P.
PR 17-MAY-2001; 2001US-0291829P.
PR 17-MAY-2001; 2001US-0291849P.
PR 19-JUN-2001; 2001US-0299428P.
PR 20-JUN-2001; 2001US-0299776P.
PR 20-JUN-2001; 2001US-0300001P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX
DR WPI; 2003-129518/12.
DR N-PSDB; ACC46096.
XX
PT Novel human diagnostic and therapeutic polypeptide useful for identifying
PT test compound which specifically binds to a polypeptide encoded by human
PT diagnostic and therapeutic polynucleotide, and to induce antibodies.
XX
PS Claim 27; SEQ ID NO 687; 591pp; English.
XX
CC The invention relates to novel human diagnostic and therapeutic
CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to
CC polynucleotide sequences at least 90% identical to the dithp cDNA
CC sequences of the invention; recombinant vectors, host cells and
CC transgenic organisms comprising a dithp nucleic acid sequence; the
CC recombinant production of DITHP proteins; antibodies specific for DITHP
CC proteins; microarrays comprising dithp nucleic acid sequences; methods of
CC detecting dithp nucleotide and protein sequences; methods of screening
CC for compounds which specifically bind a DITHP protein; and methods of
CC assessing the toxicity of test compounds using a dithp hybridisation
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
CC diagnosis of a wide variety of conditions including cancer and other cell

CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
CC viral, fungal or parasitic infections; hormonal disorders; metabolic
CC disorders; neurological disorders; gastrointestinal disorders; transport
CC disorders; and connective tissue disorders. They may also be used to
CC screen for modulators of protein activity or gene expression. DITHP
CC proteins can additionally be used in analysis of the proteome of a tissue
CC or cell type and to induce antibodies. The dithp nucleic acids are
CC additionally useful in somatic or germline gene therapy of the disorders
CC mentioned above, as a source of antisense sequences, as a source of
CC probes and primers, in genotyping and identification of individuals, in
CC the generation of transgenic animal models of human disease or knock in
CC humanised animals, in toxicological testing, and in transcript imaging.
CC The present sequence represents a DITHP protein which has enzyme
CC activity. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 83 AA;

Query Match 90.6%; Score 29; DB 6; Length 83;
Best Local Similarity 80.0%; Pred. No. 7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:
Db 35 TYWMN 39

RESULT 43
ABU40094
ID ABU40094 standard; protein; 109 AA.
XX
AC ABU40094;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #25621.
XX
KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Pseudomonas putida.
XX
PN WO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACA43964.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 68018; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide;(5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than S. aureus, S. typhimurium,
CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 109 AA;

Query Match 90.6%; Score 29; DB 6; Length 109;
Best Local Similarity 80.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 84 TYWLS 88

RESULT 44
ABR54978
ID ABR54978 standard; protein; 114 AA.
XX
AC ABR54978;
XX
DT 30-JUN-2003 (first entry)
XX
DE Mouse IgG lambda clone to IgE Fc m3G1R3F8 SEQ ID NO:258.
XX
KW Engineered template; single primer amplification; antibody library;
KW nucleic acid amplification.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO2003025202-A2.
XX
PD 27-MAR-2003.
XX
PF 19-SEP-2002; 2002WO-US029889.
XX
PR 19-SEP-2001; 2001US-0323455P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
XX
DR WPI; 2003-313359/30.
XX
PT Amplifying nucleic acid by contacting engineered nucleic acid strand
PT having predetermined sequence at one end and sequence complementary to
PT predetermined sequence at other end, with primer having predetermined
PT sequence.
XX

PS Example 5; Fig 9b-c; 68pp; English.
XX
CC The present invention describes a method (M1) for amplifying a nucleic
CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)
CC having a predetermined sequence at one end and a sequence complementary
CC to the predetermined sequence at the other, and contacting (S) with a
CC primer having the predetermined sequence in the presence of a polymers
CC and nucleotides under conditions suitable for polymerisation of the
CC nucleotides. Also described is an engineered nucleic acid strand (I)
CC having a predetermined sequence at one end and a sequence complementary
CC to the predetermined sequence at the other end. M1 is useful for
CC amplifying a nucleic acid. M1 can be used for producing an antibody
CC library. M1 is useful for preparing amplified products that can be
CC ligated into a suitable expression vector, where the vector can be used
CC to transform an appropriate host organism to produce the polypeptide or
CC protein encoded by the target sequence. M1 is useful to amplify a family
CC of related sequences to build a complex library such as, for example an
CC antibody library. M1 is useful not only for producing large amounts of
CC one target nucleic acid sequence, but also for amplifying simultaneously
CC more than one different target nucleic acid sequence located on the same
CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
CC ABR54998 represent sequence used in the exemplification of the present
CC invention
XX
SQ Sequence 114 AA;

Query Match 90.6%; Score 29; DB 6; Length 114;
Best Local Similarity 80.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:
Db 24 TYWMT 28

RESULT 45
ABR54977
ID ABR54977 standard; protein; 114 AA.
XX
AC ABR54977;
XX
DT 30-JUN-2003 (first entry)
XX
DE Mouse IgG lambda clone to IgE Fc m3G1R3E10 SEQ ID NO:257.
XX
KW Engineered template; single primer amplification; antibody library;
KW nucleic acid amplification.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO2003025202-A2.
XX
PD 27-MAR-2003.
XX
PF 19-SEP-2002; 2002WO-US029889.
XX
PR 19-SEP-2001; 2001US-0323455P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
XX
DR WPI; 2003-313359/30.
XX
PT Amplifying nucleic acid by contacting engineered nucleic acid strand
PT having predetermined sequence at one end and sequence complementary to
PT predetermined sequence at other end, with primer having predetermined
PT sequence.
XX
PS Example 5; Fig 9b-c; 68pp; English.
XX
CC The present invention describes a method (M1) for amplifying a nucleic
CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)
CC having a predetermined sequence at one end and a sequence complementary
CC to the predetermined sequence at the other, and contacting (S) with a
CC primer having the predetermined sequence in the presence of a polymers
CC and nucleotides under conditions suitable for polymerisation of the
CC nucleotides. Also described is an engineered nucleic acid strand (I)
CC having a predetermined sequence at one end and a sequence complementary
CC to the predetermined sequence at the other end. M1 is useful for
CC amplifying a nucleic acid. M1 can be used for producing an antibody
CC library. M1 is useful for preparing amplified products that can be
CC ligated into a suitable expression vector, where the vector can be used
CC to transform an appropriate host organism to produce the polypeptide or
CC protein encoded by the target sequence. M1 is useful to amplify a family
CC of related sequences to build a complex library such as, for example an
CC antibody library. M1 is useful not only for producing large amounts of
CC one target nucleic acid sequence, but also for amplifying simultaneously
CC more than one different target nucleic acid sequence located on the same
CC or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
CC ABR54998 represent sequence used in the exemplification of the present
CC invention
XX
SQ Sequence 114 AA;

Query Match 90.6%; Score 29; DB 6; Length 114;
Best Local Similarity 80.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:
Db 24 TYWMT 28

RESULT 46
ABR54979
ID ABR54979 standard; protein; 114 AA.
XX
AC ABR54979;
XX
DT 30-JUN-2003 (first entry)
XX
DE Mouse IgG lambda clone to IgE Fc m3G1R3G9 SEQ ID NO:259.
XX
KW Engineered template; single primer amplification; antibody library;
KW nucleic acid amplification.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO2003025202-A2.
XX
PD 27-MAR-2003.
XX
PF 19-SEP-2002; 2002WO-US029889.
XX
PR 19-SEP-2001; 2001US-0323455P.
XX
PA (ALEX-) ALEXION PHARM INC.
XX
PI Bowdish KS, Frederickson S, Maruyama T, Lin Y, Renshaw M;
XX
DR WPI; 2003-313359/30.
XX
PT Amplifying nucleic acid by contacting engineered nucleic acid strand
PT having predetermined sequence at one end and sequence complementary to
PT predetermined sequence at other end, with primer having predetermined
PT sequence.
XX
PS Example 5; Fig 9b-c; 68pp; English.
XX
CC The present invention describes a method (M1) for amplifying a nucleic
CC acid strand. M1 comprises providing an engineered nucleic acid strand (S)
CC having a predetermined sequence at one end and a sequence complementary
CC to the predetermined sequence at the other, and contacting (S) with a

```
CC   primer having the predetermined sequence in the presence of a polymers
CC   and nucleotides under conditions suitable for polymerisation of the
CC   nucleotides. Also described is an engineered nucleic acid strand (I)
CC   having a predetermined sequence at one end and a sequence complementary
CC   to the predetermined sequence at the other end. M1 is useful for
CC   amplifying a nucleic acid. M1 can be used for producing an antibody
CC   library. M1 is useful for preparing amplified products that can be
CC   ligated into a suitable expression vector, where the vector can be used
CC   to transform an appropriate host organism to produce the polypeptide or
CC   protein encoded by the target sequence. M1 is useful to amplify a family
CC   of related sequences to build a complex library such as, for example an
CC   antibody library. M1 is useful not only for producing large amounts of
CC   one target nucleic acid sequence, but also for amplifying simultaneously
CC   more than one different target nucleic acid sequence located on the same
CC   or different nucleic acid molecules. ACC62635 to ACC62753 and ABR54841 to
CC   ABR54998 represent sequence used in the exemplification of the present
CC   invention
XX
SQ   Sequence 114 AA;

  Query Match             90.6%;  Score 29;  DB 6;  Length 114;
  Best Local Similarity   80.0%;  Pred. No. 9.5e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         24 TYWLS 28


RESULT 47
AAW26796
ID   AAW26796 standard; protein; 115 AA.
XX
AC   AAW26796;
XX
DT   14-SEP-1998  (first entry)
XX
DE   Anti-gp54 MAb 48-127 heavy chain variable region.
XX
KW   Single chain antibody; scFv; monoclonal antibody; MAb; 48-127; trop-2;
KW   gp54; antigen; cancer marker; bladder cancer; breast cancer;
KW   cervix cancer; prostate cancer; metastasis; diagnosis; therapy;
KW   immunotherapy.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          31. .36
FT                   /label= CDR1
FT   Region          50. .66
FT                   /label= CDR2
FT   Region          89. .94
FT                   /label= CDR3
XX
PN   WO9812227-A1.
XX
PD   26-MAR-1998.
XX
PF   19-SEP-1997;   97WO-CA000690.
XX
PR   19-SEP-1996;   96US-0026320P.
XX
PA   (DIAG-) DIAGNOCURE INC.
XX
PI   Fradet Y,  Darveau A;
XX
DR   WPI; 1998-217211/19.
DR   N-PSDB; AAV26767.
XX
PT   New recombinant antibodies to gp54 antigen - used for the detection of
PT   cancers and metastases and for therapy of cancers expressing the gp54
PT   antigen.
XX
PS   Claim 1; Fig 3; 33pp; English.
XX
CC   This polypeptide comprises the heavy chain variable region of murine
CC   monoclonal antibody (MAb) 48-127. This MAb recognises an epitope of gp54
CC   antigen (trop-2), a cancer marker expressed at the surface of bladder,
CC   breast, uterine and prostate cancers. MAb 48-127 (IgG1) reacts with a
CC   majority of human bladder cell lines and with human breast carcinoma cell
CC   lines. The invention relates to novel single chain antibody (scFv)
CC   molecules, including a 48-127 scFv (see AAW26799) that comprises the 48-
CC   127 VH and VL chains joined via a linker. Such scFvs can be used to
CC   detect cancers and micrometastases, e.g. bladder, prostate, breast or
CC   uterine cervix cancers, and may be linked to specific toxins for use in
CC   cancer therapy. The scFvs are not immunogenic and are distributed and
CC   captured by gp45-bearing target cells more quickly than conventional
CC   antibodies
XX
SQ   Sequence 115 AA;

  Query Match             90.6%;  Score 29;  DB 2;  Length 115;
  Best Local Similarity   80.0%;  Pred. No. 9.6e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db         31 TYWMN 35


RESULT 48
ADQ66863
ID   ADQ66863 standard; protein; 115 AA.
XX
AC   ADQ66863;
XX
DT   07-OCT-2004  (first entry)
XX
DE   Novel human protein sequence #1836.
XX
KW   osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
KW   gene therapy; diagnostic marker; morbid state; osteoporosis;
KW   neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
KW   cancer.
XX
OS   Homo sapiens.
XX
PN   EP1440981-A2.
XX
PD   28-JUL-2004.
XX
PF   21-JAN-2004; 2004EP-00001196.
XX
PR   21-JAN-2003; 2003JP-00102206.
PR   09-MAY-2003; 2003JP-00131392.
XX
PA   (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI   Isogai T,  Sugiyama T,  Otsuki T,  Wakamatsu A,  Sato H,  Ishii S;
PI   Yamamoto J,  Isono Y,  Nagai K,  Irie R;
XX
DR   WPI; 2004-535376/52.
DR   N-PSDB; ADQ64675.
XX
PT   Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,
PT   Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS   Claim 1; SEQ ID NO 4024; 2449pp; English.
XX
CC   The invention relates to 2495 novel polynucleotides (I) and their encoded
CC   polypeptides, sequences hybridizing to these nucleotides, sequences
CC   encoding partial polypeptides and sequences having 70% or 90% identity to
CC   the nucleotide and protein sequences. The nucleotides and polypeptides
CC   are useful as diagnostic markers or therapeutic target for the diseases
CC   or morbid states. They are also useful for treating osteoporosis,
CC   neurological diseases, Alzheimer's diseases, Parkinson's diseases,
```

```
CC   dementia and various cancers. This sequence corresponds to a protein
CC   sequence of the invention.
XX
SQ   Sequence 115 AA;

  Query Match             90.6%;  Score 29;  DB 8;  Length 115;
  Best Local Similarity   80.0%;  Pred. No. 9.6e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         84 TYWLS 88


RESULT 49
ADY85022
ID   ADY85022 standard; protein; 115 AA.
XX
AC   ADY85022;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Monoclonal antibody 2E11 HMGB1 VH domain.
XX
KW   High mobility group box; HMGB1; monoclonal antibody; antibody therapy;
KW   sepsis; antibacterial immunosuppressive; graft rejection; arthritis;
KW   antiarthritic; asthma; antiasthmatic; lupus erythematosus;
KW   antiinflammatory; inflammation; dermatological;
KW   respiratory distress syndrome; respiratory-gen.; psoriasis;
KW   antipsoriatic; chronic obstructive pulmonary disease; pancreatitis;
KW   peritonitis; burns; vulnerary; ischemia; vasotropic; Behcets disease;
KW   graft versus host disease; inflammatory bowel disease;
KW   gastrointestinal-gen.; multiple sclerosis neuroprotective; cachexia;
KW   anabolic; infection; musculoskeletal disease; immune disorder;
KW   heavy chain variable region.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          31. .35
FT                   /label= CDR1
FT   Region          50. .66
FT                   /label= CDR2
FT   Region          99. .104
FT                   /label= CDR3
XX
PN   WO2005026209-A2.
XX
PD   24-MAR-2005.
XX
PF   10-SEP-2004; 2004WO-US029527.
XX
PR   11-SEP-2003; 2003US-0502568P.
XX
PA   (CRIT-) CRITICAL THERAPEUTICS INC.
XX
PI   Newman W,  Qin S,  Okeefe T,  Obar R;
XX
DR   WPI; 2005-233483/24.
DR   N-PSDB; ADY85021.
XX
PT   New antibody or its antigen-binding fragment specific to a vertebrate
PT   high mobility group box (HMGB) A box that inhibits release of a
PT   proinflammatory cytokine from a cell treated with HMGB protein, useful
PT   for treating, e.g. sepsis.
XX
PS   Example 4; SEQ ID NO 11; 123pp; English.
XX
CC   The invention provides antibodies, or their antigen-binding fragments,
CC   that bind to a vertebrate high mobility group box (HMGB) polypeptide, to
CC   methods of detecting and/or identifying an agent that binds to an HMGB
CC   polypeptide, methods of treating a condition in a subject characterized
CC   by activation of an inflammatory cytokine cascade, and methods of
CC   detecting an HMGB polypeptide in a sample. The antibody (or antigen-
CC   binding fragment) binds to a vertebrate HMGB A box but does not
CC   specifically bind to non-A box epitopes of HMGB, and inhibits release of
CC   a proinflammatory cytokine from a vertebrate cell treated with an HMGB
CC   protein. A method of treating a condition characterized by activation of
CC   an inflammatory cytokine cascade comprises administering an antibody of
CC   the invention, or its antigen-binding fragment. The condition is selected
CC   from sepsis, allograft rejection, arthritis, asthma, lupus, adult
CC   respiratory distress syndrome, chronic obstructive pulmonary disease,
CC   psoriasis, pancreatitis, peritonitis, burns, ischemia, Behcet's disease,
CC   graft versus host disease, inflammatory bowel disease, multiple sclerosis
CC   and cachexia, especially sepsis, arthritis, or lupus. The present
CC   sequence is the protein sequence of the heavy chain variable region (VH)
CC   of an anti-HMGB1 monoclonal antibody produced by claimed murine hybridoma
CC   2E11 HMGB1 (ATCC PTA-5431). This monoclonal antibody binds a peptide
CC   corresponding to amino acid residues 151-168 of human HMGB1 ADY85012.
XX
SQ   Sequence 115 AA;

  Query Match             90.6%;  Score 29;  DB 9;  Length 115;
  Best Local Similarity   80.0%;  Pred. No. 9.6e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db         31 TYWMN 35


RESULT 50
ADU87690
ID   ADU87690 standard; protein; 120 AA.
XX
AC   ADU87690;
XX
DT   10-FEB-2005  (first entry)
XX
DE   Mouse Luc90 heavy chain variable region.
XX
KW   Antibody; CS1; SLAM family member 7; SLAMF7; immunoglobulin;
KW   pharmaceutical; antibody-dependent cellular cytotoxicity;
KW   FcgammaR receptor; cell proliferation; leukocyte; cancer;
KW   multiple myeloma; multiple myeloma-related bone disorder; plasmacytoma;
KW   macroglobulinemia; amyloidosis; chronic lymphocytic leukemia;
KW   autoimmune disease; inflammatory bowel disease;
KW   systemic lupus erythematosus; cytostatic; immunosuppressive;
KW   antiinflammatory; gastrointestinal-gen.; dermatological; luc90;
KW   heavy chain variable region.
XX
OS   Mus sp.
XX
PN   WO2004100898-A2.
XX
PD   25-NOV-2004.
XX
PF   10-MAY-2004; 2004WO-US014866.
XX
PR   08-MAY-2003; 2003US-0469211P.
PR   29-MAR-2004; 2004US-0557620P.
PR   29-MAR-2004; 2004US-0557621P.
PR   29-MAR-2004; 2004US-0557622P.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Williams M,  Tso YJ,  Landolfi NF;
XX
DR   WPI; 2004-821790/81.
XX
PT   New anti-CS1 antibodies, useful for diagnosing, preventing or treating
PT   cancer, myeloma, autoimmune disorder, inflammatory bowel disease, or
PT   systemic lupus erythematosus.
XX
PS   Claim 12; SEQ ID NO 3; 151pp; English.
XX
```

CC The invention relates to an antibody or its antigen-binding fragment,
CC which binds to CS1 (also known as SLAM family member 7, SLAMF7) and
CC inhibits immunoglobulin secretion, where the antibody binds to
CC substantially the same epitope as an antibody comprising an amino acid
CC sequence of any one of SEQ ID NOS: 3-26, the antibody comprises an amino
CC acid sequence of SEQ ID NOS: 27-44, and where the heavy chain variable
CC region comprises a complementarity determining region (CDR) of SEQ ID NO:
CC 33. Also disclosed are (i) a heavy chain CDR of an antibody comprising an
CC amino acid sequence of SEQ ID NOS: 9-11, 15-17, 21-23, 29-33, (ii) a
CC light chain CDR of an antibody comprising an amino acid sequence of SEQ
CC ID NOS: 12-14, 18-20, 24-26, 34-370, (iii) a pharmaceutical composition
CC comprising a pharmaceutical carrier and the antibody described above,
CC (iv) a method of inhibiting proliferation of CS1 expressing cells, (v)
CC inhibiting immunoglobulin secretion, and (vi) increasing antibody-
CC dependent cellular cytotoxicity (ADCC) activity of the antibody described
CC above, where the antibody has decreased levels of fucose or is mutated to
CC increase antibody affinity for a FcgammaR receptor. The antibody of the
CC invention inhibits the proliferation of leukocytes or cancer cells. The
CC antibody triggers cytotoxic effects on cells expressing CS1 or enhances
CC cytotoxicity mediated by immune cells, or triggers ADCC-mediated
CC cytotoxicity of cells expressing CS1. The antibody binds to substantially
CC the same epitope as the antibody produced by a hybridoma cell line having
CC ATCC accession number PTA-5091 or a Luc63 antibody. The antibody is
CC produced by a hybridoma cell line having ATCC accession number PTA-5091
CC or by a hybridoma cell line expressing Luc63 antibody. The antibody is a
CC monoclonal antibody, e.g. a chimeric antibody, a humanized antibody, or a
CC fully human antibody. The antibody is conjugated with a cytotoxic agent.
CC The antibody comprises a heavy chain variable region comprising amino
CC acid sequences of SEQ ID NOS: 3, 5, 7, or 27, and a light chain variable
CC region comprising amino acid sequences of SEQ ID NOS: 4, 6, 8, or 28. The
CC antibody, compositions, and methods are useful for diagnosing, preventing
CC or treating plasma cell cancer, e.g. myeloma, multiple myeloma, myeloma
CC of bone, extramedullary plasmacytoma, macroglobulinemia (including
CC Waldenstrom's macroglobulinemia), heavy-chain disease, primary
CC amyloidosis or monoclonal gammopathy of unknown significance, non-plasma
CC cell cancer (chronic lymphocytic leukemia), autoimmune disorder,
CC inflammatory bowel disease (IBD), or systemic lupus erythematosus (SLE).
CC This sequence represents a CS1 antibody.
XX
SQ Sequence 120 AA;

Query Match 90.6%; Score 29; DB 8; Length 120;
Best Local Similarity 80.0%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:
Db 31 TYWMN 35

Search completed: March 23, 2006, 01:52:59
Job time : 73.4931 secs

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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:54:26 ; Search time 6.91781 Seconds
(without alignments)
69.543 Million cell updates/sec

Title: US-10-755-382-23
Perfect score: 32
Sequence: 1 TYWMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	309	2	S43573	C05B5.4 protein (c
2	32	100.0	315	2	B88571	protein C05B5.4 [i
3	32	100.0	454	2	F83760	hypothetical prote
4	32	100.0	2025	2	T21588	hypothetical prote
5	29	90.6	101	2	S42183	Ig gamma chain V r
6	29	90.6	116	2	AE3516	hypothetical prote
7	29	90.6	117	2	S03289	Ig heavy chain pre
8	29	90.6	123	2	S31509	Ig heavy chain - h
9	29	90.6	124	2	G84812	hypothetical prote
10	29	90.6	136	2	B47159	Ig heavy chain V r
11	29	90.6	158	2	A84069	hypothetical prote
12	29	90.6	170	2	S74997	hypothetical prote
13	29	90.6	282	2	T19594	hypothetical prote
14	29	90.6	290	2	AG2812	conserved hypothet
15	29	90.6	298	2	A97591	hypothetical prote
16	29	90.6	347	2	H84673	hypothetical prote
17	29	90.6	386	2	T48821	hypothetical prote
18	29	90.6	395	2	S41035	hypothetical prote
19	29	90.6	454	2	E87571	amine oxidase, fla
20	29	90.6	457	2	AF2819	amine oxidase, fla
21	29	90.6	457	2	F97597	hypothetical prote
22	29	90.6	468	2	AD2395	two-component sens
23	29	90.6	478	2	E89790	6-phospho-beta-glu
24	29	90.6	485	2	F64165	hypothetical prote
25	29	90.6	490	2	AB2335	hypothetical prote
26	29	90.6	571	2	B64469	hypothetical prote
27	29	90.6	587	2	T02829	conserved hypothet
28	29	90.6	635	2	T08934	hypothetical prote
29	29	90.6	933	2	T43201	MutS protein homol
30	29	90.6	1057	2	T15720	hypothetical prote
31	29	90.6	1112	2	T30202	probable chitin sy
32	29	90.6	1139	2	T20660	hypothetical prote
33	29	90.6	1400	2	T20904	hypothetical prote
34	29	90.6	1404	2	H89715	protein F14F4.3 [i
35	29	90.6	1427	2	T20903	hypothetical prote
36	28	87.5	56	2	G81042	hypothetical prote
37	28	87.5	98	2	PL0123	Ig heavy chain V-I
38	28	87.5	101	2	S26460	Ig heavy chain V r
39	28	87.5	110	2	PH1655	Ig heavy chain V r
40	28	87.5	114	2	S36280	Ig heavy chain V r
41	28	87.5	115	2	S38714	Ig heavy chain V r
42	28	87.5	117	2	S17079	Ig heavy chain V-g
43	28	87.5	117	2	S78486	Ig heavy chain V r
44	28	87.5	118	2	S00700	Ig heavy chain V r
45	28	87.5	122	2	S31675	Ig heavy chain V r
46	28	87.5	122	2	A33989	Ig heavy chain V-1
47	28	87.5	126	2	PH1412	Ig heavy chain V r
48	28	87.5	136	2	S31587	Ig heavy chain V r
49	28	87.5	137	2	S78054	Ig heavy chain pre
50	28	87.5	139	2	I37781	Ig variable region
51	28	87.5	139	2	S30984	gene 39 protein -
52	28	87.5	147	2	I37780	Ig variable region
53	28	87.5	177	2	E96938	probable acetyltra
54	28	87.5	186	2	T50361	hypothetical prote
55	28	87.5	207	2	H84273	flagellin A1 precu
56	28	87.5	207	2	F95966	probable aldehyde
57	28	87.5	273	2	A47246	tryptase (EC 3.4.2
58	28	87.5	288	2	I49058	Ly49c - mouse
59	28	87.5	301	2	S45880	SCO1 protein homol
60	28	87.5	302	2	AH3108	conserved hypothet
61	28	87.5	305	2	T05072	hypothetical prote
62	28	87.5	313	2	D98178	hypothetical prote
63	28	87.5	319	2	C53290	oligopeptide trans
64	28	87.5	319	2	G86854	oligopeptide ABC t
65	28	87.5	329	2	C97560	hypothetical prote
66	28	87.5	329	2	AB2781	amidohydrolase [im
67	28	87.5	333	2	H82852	hydroxybenzoate oc
68	28	87.5	364	2	D85829	perosamine synthet
69	28	87.5	366	2	A99984	perosamine synthet
70	28	87.5	448	2	T48214	endo-1,4-beta-mann
71	28	87.5	457	2	AF2158	two-component resp
72	28	87.5	463	2	T45074	probable phenylala
73	28	87.5	471	2	A38262	ribulose-bisphosph
74	28	87.5	472	1	RKKRL1	ribulose-bisphosph
75	28	87.5	515	2	T24781	hypothetical prote
76	28	87.5	517	2	T02403	probable beta-gluc
77	28	87.5	519	2	I64163	hypothetical prote
78	28	87.5	595	2	T26843	hypothetical prote
79	28	87.5	609	2	E96742	probable ABC trans
80	28	87.5	624	2	A84150	hypothetical prote
81	28	87.5	648	2	A32576	beta-glucuronidase
82	28	87.5	650	2	AG0733	probable bacteriop
83	28	87.5	661	2	AE3395	NADH2 dehydrogenas
84	28	87.5	662	2	AD0623	probable bacteriop
85	28	87.5	683	2	B71325	conserved hypothet
86	28	87.5	715	2	AF1829	two-component hybr
87	28	87.5	782	2	T25925	hypothetical prote
88	28	87.5	851	2	T31520	hypothetical prote
89	28	87.5	852	2	S57984	probable membrane
90	28	87.5	939	2	AE2275	hypothetical prote
91	28	87.5	942	2	B84469	Mutator-like trans
92	28	87.5	942	2	T37539	probable guanine n
93	28	87.5	989	2	T02568	hypothetical prote
94	28	87.5	1254	1	A32686	DNA-directed DNA p
95	28	87.5	1539	2	T30037	hypothetical prote
96	28	87.5	1844	2	T51890	related to Nup98-N
97	27	84.4	51	2	B31946	hypothetical prote
98	27	84.4	67	2	A84376	hypothetical prote
99	27	84.4	94	2	I67528	CD33 antigen homol
100	27	84.4	95	2	I67527	CD33 antigen homol
101	27	84.4	116	1	HVMS44	Ig heavy chain pre
102	27	84.4	117	1	G2MS73	Ig heavy chain V r

103	27	84.4	117	1	G2MSU1	Ig heavy chain V r
104	27	84.4	118	2	A47329	Ig heavy chain V r
105	27	84.4	119	1	AVMSJ5	Ig heavy chain V r
106	27	84.4	119	1	AVMST6	Ig heavy chain V r
107	27	84.4	119	1	AVMSX4	Ig heavy chain V r
108	27	84.4	121	2	A30560	Ig heavy chain V r
109	27	84.4	136	2	S13791	Ig heavy chain V r
110	27	84.4	139	2	A25912	Ig heavy chain pre
111	27	84.4	159	2	S77185	hypothetical prote
112	27	84.4	173	2	D58893	NADH2 dehydrogenas
113	27	84.4	185	2	T12476	hypothetical prote
114	27	84.4	185	2	G90903	hypothetical prote
115	27	84.4	185	2	D85713	unknown protein en
116	27	84.4	189	2	T39849	anaphase promoting
117	27	84.4	254	1	S77113	hypothetical prote
118	27	84.4	254	2	S28362	coat protein - bee
119	27	84.4	255	2	T41451	very hypothetical
120	27	84.4	299	2	B83888	transcription regu
121	27	84.4	301	2	G83181	probable transcrip
122	27	84.4	316	2	AH3552	transcription regu
123	27	84.4	317	2	D83429	conserved hypothet
124	27	84.4	363	2	I40234	carboxymethylcellu
125	27	84.4	366	2	C70907	hypothetical prote
126	27	84.4	378	2	T26684	hypothetical prote
127	27	84.4	386	2	T26563	hypothetical prote
128	27	84.4	414	2	F70538	hypothetical prote
129	27	84.4	419	2	T04530	hypothetical prote
130	27	84.4	419	2	D85334	hypothetical prote
131	27	84.4	431	1	A59201	acid phosphatase (
132	27	84.4	436	2	T00908	hypothetical prote
133	27	84.4	444	2	S09681	citrate transport
134	27	84.4	446	2	F90332	hypothetical prote
135	27	84.4	465	2	D86166	protein F21B7.12 [
136	27	84.4	469	2	C86170	hypothetical prote
137	27	84.4	470	2	S50083	photolyase - short
138	27	84.4	470	2	F83022	probable amino aci
139	27	84.4	493	2	T48630	high affinity nitr
140	27	84.4	507	2	JC5054	high affinity nitr
141	27	84.4	509	2	JC5055	high affinity nitr
142	27	84.4	510	2	S55204	hypothetical prote
143	27	84.4	512	2	G70662	probable plcB prot
144	27	84.4	517	2	T17975	bcsA protein homol
145	27	84.4	522	2	F86215	protein T6D22.18 [
146	27	84.4	526	2	S43561	YCR37C homolog K08
147	27	84.4	530	2	T16972	probable high affi
148	27	84.4	530	2	T51836	high affinity nitr
149	27	84.4	530	2	T06237	probable high affi
150	27	84.4	533	2	S52046	deoxyribodipyrimid
151	27	84.4	533	2	T01864	hypothetical prote
152	27	84.4	534	2	G88575	protein K08E5.2 [i
153	27	84.4	546	2	A69166	5-methylcytosine-s
154	27	84.4	547	2	S53920	SNG1 protein - yea
155	27	84.4	556	2	A45098	photolyase - goldf
156	27	84.4	559	2	B88474	protein C05D10.3 [
157	27	84.4	640	2	S52047	deoxyribodipyrimid
158	27	84.4	696	2	H90798	Iha adhesin [impor
159	27	84.4	696	2	G85607	probable receptor
160	27	84.4	735	2	AD0341	probable membrane
161	27	84.4	771	2	AF2381	hypothetical prote
162	27	84.4	809	2	F81312	leucine-tRNA ligas
163	27	84.4	818	2	F96586	hypothetical prote
164	27	84.4	832	2	E84543	probable beta-gala
165	27	84.4	1036	2	T05687	beta-galactosidase
166	27	84.4	1043	2	F97302	hypothetical prote
167	27	84.4	1331	1	XORTDH	xanthine dehydroge
168	27	84.4	1335	1	XOMSDH	xanthine dehydroge
169	27	84.4	1433	2	T30261	chitinase (EC 3.2.
170	27	84.4	1581	1	VGWJBV	peplomer glycoprot
171	27	84.4	2108	2	S28417	CDC39 protein - ye
172	27	84.4	2609	2	T40399	probable transport
173	27	84.4	3587	2	I40486	surfactin syntheta
174	27	84.4	4540	2	T30838	cytoplasmic dynein
175	26	81.2	68	2	AC3561	hypothetical prote
176	26	81.2	76	2	T14724	hypothetical prote
177	26	81.2	95	2	C89983	hypothetical prote
178	26	81.2	99	2	B82720	hypothetical prote
179	26	81.2	141	2	F75252	hypothetical prote
180	26	81.2	156	2	A90310	hypothetical prote
181	26	81.2	157	2	AE2434	hypothetical prote
182	26	81.2	162	1	LNRC1	lectin BRA3-1 prec
183	26	81.2	162	1	LNRC3	lectin BRA3-2 prec
184	26	81.2	199	2	T37855	probable transcrip
185	26	81.2	218	2	H71015	hypothetical prote
186	26	81.2	238	2	F72533	hypothetical prote
187	26	81.2	256	1	TRFF	trypsin-like prote
188	26	81.2	258	2	AG2542	hypothetical prote
189	26	81.2	274	2	T30350	probable protein k
190	26	81.2	291	2	S74948	hypothetical prote
191	26	81.2	303	2	D96018	conserved hypothet
192	26	81.2	305	2	AF3390	2-dehydro-3-deoxyg
193	26	81.2	305	2	C87356	conserved hypothet
194	26	81.2	308	2	AI2601	conserved hypothet
195	26	81.2	312	2	T25510	hypothetical prote
196	26	81.2	321	2	D81179	spermidine/putresc
197	26	81.2	321	2	H81926	probable polyamine
198	26	81.2	323	2	T19681	hypothetical prote
199	26	81.2	328	2	A97384	hypothetical prote
200	26	81.2	330	2	B37756	traU protein - Esc
201	26	81.2	337	2	T04035	hypothetical prote
202	26	81.2	340	1	QQBES6	UL20 protein precu
203	26	81.2	347	2	T20618	hypothetical prote
204	26	81.2	353	2	T01978	hypothetical prote
205	26	81.2	376	2	B84463	hypothetical prote
206	26	81.2	391	2	PC4117	replication protei
207	26	81.2	399	2	AD3512	hypothetical prote
208	26	81.2	400	2	F86887	hypothetical prote
209	26	81.2	410	2	E96729	unknown protein F5
210	26	81.2	414	2	B71345	probable carhohydr
211	26	81.2	415	2	T02377	hypothetical prote
212	26	81.2	419	1	JC1211	beta-ketoacyl synt
213	26	81.2	422	2	H96595	unknown protein, 9
214	26	81.2	424	2	E86367	protein F26F24.22
215	26	81.2	425	2	E71276	hypothetical prote
216	26	81.2	438	2	D84331	hypothetical prote
217	26	81.2	438	2	T35789	probable secreted
218	26	81.2	452	2	A75213	tldd protein PAB01
219	26	81.2	474	2	D84631	probable serine ca
220	26	81.2	484	2	T36427	probable rhamnose
221	26	81.2	504	1	G71248	tldD homolog PH024
222	26	81.2	505	2	T18933	hypothetical prote
223	26	81.2	514	2	B72752	hypothetical prote
224	26	81.2	530	2	T18932	hypothetical prote
225	26	81.2	539	2	A83903	ABC transporter (A
226	26	81.2	543	2	T27190	hypothetical prote
227	26	81.2	549	2	AH1019	Sodium,solute symp
228	26	81.2	549	2	A98260	probable transport
229	26	81.2	549	2	E86100	probable transport
230	26	81.2	549	2	B65215	hypothetical 59.2
231	26	81.2	551	2	F83241	probable sodium/so
232	26	81.2	551	2	AE0031	probable transmemb
233	26	81.2	552	2	T27191	hypothetical prote
234	26	81.2	567	2	D70769	hypothetical prote
235	26	81.2	570	2	AC2356	hypothetical prote
236	26	81.2	589	2	S42385	hypothetical prote
237	26	81.2	616	2	T34722	hypothetical prote
238	26	81.2	704	2	B84685	hypothetical prote
239	26	81.2	716	2	E82016	probable integral
240	26	81.2	716	2	H81242	conserved hypothet
241	26	81.2	717	2	H84057	pullulanase amyX [
242	26	81.2	764	2	JC8016	acylaminoacyl-pept
243	26	81.2	810	2	B84185	cytochrome-like pr
244	26	81.2	817	2	A96640	protein T1F9.2 [im
245	26	81.2	821	2	T19705	hypothetical prote
246	26	81.2	823	2	S44873	ZC21.2 protein - C
247	26	81.2	826	1	T02753	S-receptor kinase
248	26	81.2	839	2	S54174	DNA topoisomerase

249	26	81.2	842	2	T23715	hypothetical prote
250	26	81.2	848	1	T02053	S-receptor kinase
251	26	81.2	1005	2	S33525	guanylate cyclase
252	26	81.2	1070	2	G84982	exodeoxyribonuclea
253	26	81.2	1073	1	OYHUHX	heat-stable entero
254	26	81.2	1075	1	OYRTHX	heat-stable entero
255	26	81.2	1080	2	A35088	phycobilisome link
256	26	81.2	1110	2	I59370	guanylate cyclase
257	26	81.2	1160	2	T23713	hypothetical prote
258	26	81.2	1187	2	T20544	hypothetical prote
259	26	81.2	1188	2	T38467	probable nuclear p
260	26	81.2	1223	2	S62011	PHO85 protein - ye
261	26	81.2	1286	2	T23714	hypothetical prote
262	26	81.2	1451	2	B86286	F9L1.15 protein -
263	26	81.2	1469	2	H96622	probable ABC trans
264	26	81.2	1501	2	S50992	SNQ2 protein - yea
265	26	81.2	1657	2	T15838	hypothetical prote
266	26	81.2	1679	2	T15968	hypothetical prote
267	26	81.2	4450	2	JX0340	gramicidin S synth
268	26	81.2	4452	1	YGBSG2	gramicidin S synth
269	25	78.1	40	2	F84316	hypothetical prote
270	25	78.1	69	2	AB1333	hypothetical prote
271	25	78.1	69	2	AB1704	hypothetical prote
272	25	78.1	73	2	D82519	hypothetical prote
273	25	78.1	83	2	E83178	30S ribosomal prot
274	25	78.1	87	2	AG1230	hypothetical prote
275	25	78.1	89	2	D84360	hypothetical prote
276	25	78.1	96	2	A64606	hypothetical prote
277	25	78.1	100	1	F70309	protein export mem
278	25	78.1	101	2	H37262	Ig heavy chain V r
279	25	78.1	102	2	PH1272	Ig heavy chain V r
280	25	78.1	102	2	PH1232	Ig heavy chain V r
281	25	78.1	103	2	PH0986	Ig heavy chain V r
282	25	78.1	106	2	S26315	Ig heavy chain V r
283	25	78.1	108	2	S26316	Ig heavy chain V r
284	25	78.1	110	2	S26317	Ig heavy chain V r
285	25	78.1	110	2	A65090	hypothetical prote
286	25	78.1	111	2	S64145	hypothetical prote
287	25	78.1	117	2	G45722	anti-glycoprotein
288	25	78.1	118	2	C30560	Ig heavy chain V r
289	25	78.1	120	2	PD0008	Ig heavy chain V r
290	25	78.1	123	2	PH1423	Ig heavy chain V r
291	25	78.1	125	2	PH1410	Ig heavy chain V r
292	25	78.1	126	2	E71185	hypothetical prote
293	25	78.1	134	2	PH1422	Ig heavy chain V r
294	25	78.1	137	2	F29380	Ig heavy chain pre
295	25	78.1	143	2	AF2817	50S Ribosomal Prot
296	25	78.1	143	2	G97595	l11 (AF176664) [im
297	25	78.1	145	2	T06616	hypothetical prote
298	25	78.1	147	2	F83583	probable acetyltra
299	25	78.1	155	2	H64470	hypothetical prote
300	25	78.1	156	2	AH2229	hypothetical prote
301	25	78.1	160	2	F75488	hypothetical prote
302	25	78.1	161	2	S49488	collagen alpha 3(I
303	25	78.1	161	2	A25633	lincomycin resista
304	25	78.1	167	2	B24988	NADH2 dehydrogenas
305	25	78.1	167	2	D82561	probable signal pe
306	25	78.1	169	2	AC2168	two-component syst
307	25	78.1	170	2	B96945	probable acetyltra
308	25	78.1	174	2	G83712	hypothetical prote
309	25	78.1	174	2	G90432	conserved hypothet
310	25	78.1	180	2	T39395	hypothetical oligo
311	25	78.1	185	2	A69937	hypothetical prote
312	25	78.1	190	2	A45601	22K antigen - fluk
313	25	78.1	190	2	A54518	22.6k tegument ant
314	25	78.1	191	2	S43178	gene sj22 protein
315	25	78.1	199	2	T50953	hypothetical prote
316	25	78.1	204	2	B82166	conserved hypothet
317	25	78.1	212	2	AB2522	glutathione S-tran
318	25	78.1	216	2	A72291	hypothetical prote
319	25	78.1	220	2	C87601	glutathione S-tran
320	25	78.1	220	2	B49736	collagen alpha 3(I
321	25	78.1	223	2	G97210	hypothetical prote
322	25	78.1	226	2	T29404	hypothetical prote
323	25	78.1	236	2	T29304	hypothetical prote
324	25	78.1	238	1	JH0367	ribonuclease (EC 3
325	25	78.1	241	2	T26488	hypothetical prote
326	25	78.1	246	2	I48302	collagen alpha 3(I
327	25	78.1	253	2	I48304	collagen alpha 5(I
328	25	78.1	254	2	AG0334	VacJ lipoprotein [
329	25	78.1	254	2	E83619	probable transport
330	25	78.1	258	2	B61228	collagen alpha 1(I
331	25	78.1	258	2	D70758	hypothetical prote
332	25	78.1	261	2	S07752	NADH2 dehydrogenas
333	25	78.1	261	2	A34476	collagen alpha 2(I
334	25	78.1	266	2	AB2473	probable 3',5'-cyc
335	25	78.1	269	2	S75243	hypothetical prote
336	25	78.1	272	2	S76524	hypothetical prote
337	25	78.1	274	2	T20248	hypothetical prote
338	25	78.1	276	2	B71907	hypothetical prote
339	25	78.1	278	2	AB3620	high-affinity iron
340	25	78.1	281	2	E84637	hypothetical prote
341	25	78.1	281	2	F96736	unknown protein F2
342	25	78.1	291	2	B90444	hypothetical prote
343	25	78.1	295	2	F69976	conserved hypothet
344	25	78.1	297	2	S74335	carbon dioxide con
345	25	78.1	299	2	AB3191	hypothetical prote
346	25	78.1	301	2	H97505	probable nikC prot
347	25	78.1	301	2	AD2724	ABC transporter, m
348	25	78.1	302	2	T39010	hypothetical prote
349	25	78.1	312	2	I48303	collagen alpha 4(I
350	25	78.1	314	2	AC2690	conserved hypothet
351	25	78.1	328	1	C70039	two-component sens
352	25	78.1	332	2	T19649	hypothetical prote
353	25	78.1	333	2	T07009	omega-6 fatty acid
354	25	78.1	335	2	T03230	membrane protein,
355	25	78.1	338	2	T49182	probable chloropla
356	25	78.1	341	2	G97471	hypothetical prote
357	25	78.1	342	2	E90772	periplasmic protei
358	25	78.1	342	2	T16806	hypothetical prote
359	25	78.1	342	2	A85635	part of regulation
360	25	78.1	342	2	H64840	torT protein precu
361	25	78.1	344	2	H87710	hypothetical prote
362	25	78.1	344	2	S14409	membrane protein,
363	25	78.1	346	1	JH0387	alkanal monooxygen
364	25	78.1	346	2	AE0959	Solute binding rec
365	25	78.1	346	2	G90045	hypothetical prote
366	25	78.1	347	2	T02280	hypothetical prote
367	25	78.1	349	2	C82427	periplasmic protei
368	25	78.1	349	2	E82349	probable lipopolys
369	25	78.1	358	2	T45934	hypothetical prote
370	25	78.1	359	1	LQBP37	DNA ligase (ATP) (
371	25	78.1	365	2	T20958	hypothetical prote
372	25	78.1	368	2	G71961	hypothetical prote
373	25	78.1	368	2	H64546	conserved hypothet
374	25	78.1	372	2	T42426	conserved hypothet
375	25	78.1	374	2	B87272	purine nucleoside
376	25	78.1	377	2	AE0715	probable membrane
377	25	78.1	380	2	T11845	ubiquinol-cytochro
378	25	78.1	384	2	G84482	hypothetical prote
379	25	78.1	384	2	T49128	hypothetical prote
380	25	78.1	385	2	S39683	ywbM protein - Bac
381	25	78.1	388	2	T49253	purple acid phosph
382	25	78.1	389	2	S36654	surface antigen -
383	25	78.1	389	2	T19883	hypothetical prote
384	25	78.1	393	2	H64233	hypothetical prote
385	25	78.1	394	1	WHPSBF	4-hydroxybenzoate
386	25	78.1	394	2	S75004	hypothetical prote
387	25	78.1	400	2	D89810	conserved hypothet
388	25	78.1	405	2	C90194	hypothetical prote
389	25	78.1	405	2	T19593	hypothetical prote
390	25	78.1	409	2	F90825	probable integrase
391	25	78.1	410	2	AH3376	glycosyltransferas
392	25	78.1	411	2	G95241	MATE efflux family
393	25	78.1	414	2	T32995	hypothetical prote
394	25	78.1	416	2	A85684	probable integrase

395	25	78.1	416	2	S75321	serine/threonine-s
396	25	78.1	416	2	F89779	hypothetical prote
397	25	78.1	417	2	D82172	serine transporter
398	25	78.1	422	2	B24815	calpain (EC 3.4.22
399	25	78.1	426	2	B98106	hypothetical prote
400	25	78.1	436	2	S41782	ABD1 protein - yea
401	25	78.1	437	2	T16477	hypothetical prote
402	25	78.1	438	2	B96759	protein serine car
403	25	78.1	441	2	F84560	purple acid phosph
404	25	78.1	447	2	H86534	hypothetical prote
405	25	78.1	447	2	H72089	hypothetical prote
406	25	78.1	449	2	T34619	NADH2 dehydrogenas
407	25	78.1	450	2	T39433	glucoamylase precu
408	25	78.1	451	2	T16481	hypothetical prote
409	25	78.1	452	2	H88337	protein F15A4.1 [i
410	25	78.1	455	2	T37517	hypothetical prote
411	25	78.1	456	2	AF1305	conserved hypothet
412	25	78.1	456	2	AF1677	conserved hypothet
413	25	78.1	458	2	D89791	hypothetical prote
414	25	78.1	461	1	HWHUFA	alpha-L-fucosidase
415	25	78.1	463	2	B81580	hypothetical prote
416	25	78.1	464	1	S37616	transcription fact
417	25	78.1	466	1	F96605	acid phosphatase (
418	25	78.1	467	2	AG1059	probable membrane
419	25	78.1	468	2	AF2163	hypothetical prote
420	25	78.1	471	2	A39024	collagen alpha 3(I
421	25	78.1	472	2	AD1889	adenylate cyclase
422	25	78.1	473	2	E82419	methyl-accepting c
423	25	78.1	474	2	S75032	hypothetical prote
424	25	78.1	475	2	T36137	probable amino aci
425	25	78.1	478	4	T41193	probable capsid pr
426	25	78.1	480	2	T08818	probable UDPglucos
427	25	78.1	480	2	T51527	UDP-glucose dehydr
428	25	78.1	480	2	E88656	protein F56D6.2 [i
429	25	78.1	481	2	G86392	T1K7.6 protein - A
430	25	78.1	483	2	AD3425	xylulokinase (EC 2
431	25	78.1	486	2	G84961	cardiolipin synthe
432	25	78.1	489	2	AF2970	conserved hypothet
433	25	78.1	489	2	D98312	hypothetical prote
434	25	78.1	492	2	AB0384	Beta-lactamase ind
435	25	78.1	495	1	Q1AD52	early E1B 55K prot
436	25	78.1	496	1	Q1AD55	early E1B 55K prot
437	25	78.1	497	2	AD3514	D-serine/D-alanine
438	25	78.1	509	2	T29303	hypothetical prote
439	25	78.1	509	2	T37583	hypothetical prote
440	25	78.1	512	1	G69170	2-oxoacid-ferredox
441	25	78.1	512	2	S28267	pherophorin I prec
442	25	78.1	513	1	A35742	aqualysin (EC 3.4.
443	25	78.1	520	2	T20226	hypothetical prote
444	25	78.1	527	2	T04329	importin alpha - t
445	25	78.1	532	2	T33842	hypothetical prote
446	25	78.1	532	2	T52102	probable nuclear t
447	25	78.1	532	2	T52268	importin alpha [va
448	25	78.1	534	1	A48529	ubiquinol-cytochro
449	25	78.1	535	2	T52098	probable nuclear t
450	25	78.1	535	2	C70769	hypothetical prote
451	25	78.1	535	2	E87656	hypothetical prote
452	25	78.1	540	2	T34187	hypothetical prote
453	25	78.1	547	2	E91135	probable alkaline
454	25	78.1	547	2	H85980	probable alkaline
455	25	78.1	547	2	H65107	hypothetical 61.6
456	25	78.1	553	2	B83714	iron (III) transpo
457	25	78.1	554	2	D72760	hypothetical prote
458	25	78.1	554	2	JU0188	membrane protein 4
459	25	78.1	556	2	H82301	peptide ABC transp
460	25	78.1	572	2	S68119	laccase (EC 1.10.3
461	25	78.1	576	2	S68117	laccase (EC 1.10.3
462	25	78.1	583	2	C90327	n-methylhydantoina
463	25	78.1	585	2	S74477	hypothetical prote
464	25	78.1	588	2	A84108	N-acetylmuramoyl-L
465	25	78.1	597	2	E85090	probable transposo
466	25	78.1	613	2	A95292	hypothetical prote
467	25	78.1	621	2	S72493	laccase (EC 1.10.3
468	25	78.1	629	2	T37255	acetylcholinestera
469	25	78.1	633	2	F88478	protein F47D12.5 [
470	25	78.1	641	2	S63645	NADH2 dehydrogenas
471	25	78.1	651	2	C69374	conserved hypothet
472	25	78.1	654	2	H89871	hypothetical prote
473	25	78.1	654	2	T50198	probable transcrip
474	25	78.1	669	2	E84852	hypothetical prote
475	25	78.1	670	2	T06742	hypothetical prote
476	25	78.1	675	1	FYFFB	brown protein - fr
477	25	78.1	691	2	AD2766	conserved hypothet
478	25	78.1	691	2	H97546	hypothetical 81.9K
479	25	78.1	700	1	CIHUH2	calpain (EC 3.4.22
480	25	78.1	700	2	S38361	calpain (EC 3.4.22
481	25	78.1	706	2	A81848	probable TonB-depe
482	25	78.1	713	2	A81317	probable integral
483	25	78.1	736	2	S69074	hypothetical prote
484	25	78.1	742	2	C83061	probable TonB-depe
485	25	78.1	745	2	I57665	Sertoli cell leuci
486	25	78.1	754	2	A55267	collagen alpha 5(I
487	25	78.1	760	2	T34414	hypothetical prote
488	25	78.1	770	2	C87316	alpha-N-acetylgluc
489	25	78.1	775	2	A61228	collagen alpha 2(I
490	25	78.1	786	2	G88065	protein T16A1.2 [i
491	25	78.1	789	2	G90587	lipoprotein [impor
492	25	78.1	790	2	D83064	hypothetical prote
493	25	78.1	800	1	S31575	interleukin-4 rece
494	25	78.1	804	2	D69650	leucine-tRNA ligas
495	25	78.1	820	2	G75251	cytochrome-c oxida
496	25	78.1	837	2	H82970	hypothetical prote
497	25	78.1	838	2	T05410	hypothetical prote
498	25	78.1	843	2	T41237	conserved hypothet
499	25	78.1	844	2	AD2339	hypothetical prote
500	25	78.1	856	2	AD0042	enhancing factor (
501	25	78.1	859	2	A32713	reverse transcript
502	25	78.1	888	2	B87270	TonB-dependent rec
503	25	78.1	900	2	T41607	probable vacuolar
504	25	78.1	905	2	D86380	protein F5A9.14 [i
505	25	78.1	925	2	B86380	protein F5A9.18 [i
506	25	78.1	936	2	I40711	sapB protein - Cam
507	25	78.1	946	2	T31488	hypothetical prote
508	25	78.1	949	2	G86380	protein F5A9.8 [im
509	25	78.1	1010	2	F75134	hypothetical prote
510	25	78.1	1012	2	D86381	hypothetical prote
511	25	78.1	1012	2	T13603	probable N-methyl-
512	25	78.1	1020	2	A86381	hypothetical prote
513	25	78.1	1025	2	T21319	hypothetical prote
514	25	78.1	1047	1	OYHUBR	natriuretic peptid
515	25	78.1	1047	1	OYRTBR	atrial natriuretic
516	25	78.1	1047	2	I45882	guanylate cyclase
517	25	78.1	1050	2	S45636	natriuretic-peptid
518	25	78.1	1056	2	B82557	hypothetical prote
519	25	78.1	1057	1	OYRTR	atrial natriuretic
520	25	78.1	1057	2	I55319	guanylyl cyclase A
521	25	78.1	1057	2	I57963	natriuretic peptid
522	25	78.1	1058	2	B95292	probable adenylate
523	25	78.1	1061	1	OYHUAR	natriuretic peptid
524	25	78.1	1068	2	T42382	guanylate cyclase
525	25	78.1	1081	2	B81303	probable membrane
526	25	78.1	1093	2	T18672	hypothetical prote
527	25	78.1	1095	2	T41171	importin beta subu
528	25	78.1	1108	2	A55915	guanylate cyclase
529	25	78.1	1110	1	S55279	guanylate cyclase
530	25	78.1	1143	2	T28129	hypothetical prote
531	25	78.1	1150	2	S58775	myp1 protein - smu
532	25	78.1	1161	2	T18642	hypothetical prote
533	25	78.1	1170	2	T27564	hypothetical prote
534	25	78.1	1199	2	C71500	probable swi/snf h
535	25	78.1	1246	2	T00826	hypothetical prote
536	25	78.1	1280	2	T29021	hypothetical prote
537	25	78.1	1297	2	T30274	proteoliaisin - se
538	25	78.1	1447	2	T15200	hypothetical prote
539	25	78.1	1466	2	T30566	ATP-binding casset
540	25	78.1	1526	2	A96528	protein F27J15.14

541	25	78.1	1669	1	CGHU4B	collagen alpha 1(I
542	25	78.1	1669	1	CGMS4B	collagen alpha 1(I
543	25	78.1	1670	1	CGHU3B	collagen alpha 3(I
544	25	78.1	1691	1	CGHU6B	collagen alpha 6(I
545	25	78.1	1691	1	S22917	collagen alpha 5(I
546	25	78.1	1707	2	A33526	collagen alpha 2(I
547	25	78.1	1707	2	T18951	hypothetical prote
548	25	78.1	1712	1	CGHU2B	collagen alpha 2(I
549	25	78.1	1752	2	A45407	collagen alpha 3(I
550	25	78.1	1753	2	T00350	hypothetical prote
551	25	78.1	1758	2	T29350	hypothetical prote
552	25	78.1	1759	2	T29351	collagen alpha 2(I
553	25	78.1	1763	2	S16366	collagen alpha 2(I
554	25	78.1	1768	2	E85062	hypothetical prote
555	25	78.1	1816	2	A84845	probable ABC trans
556	24	75.0	35	2	S46472	Ig heavy chain V r
557	24	75.0	36	2	D31485	Ig heavy chain V r
558	24	75.0	48	2	A61065	sucrase-isomaltase
559	24	75.0	56	2	E49038	Ig lambda chain V
560	24	75.0	58	2	D49038	Ig lambda chain V
561	24	75.0	59	2	PT0204	protein kinase (EC
562	24	75.0	66	2	S36384	Ig heavy chain V r
563	24	75.0	67	2	AB2297	hypothetical prote
564	24	75.0	69	2	D25150	Ig heavy chain V r
565	24	75.0	73	2	JS0514	hypothetical 7.5K
566	24	75.0	73	2	A53237	l(3)S12 protein -
567	24	75.0	75	1	QQVUMB	hypothetical 9.3K
568	24	75.0	76	2	D82445	hypothetical prote
569	24	75.0	76	2	PH1153	Ig heavy chain V r
570	24	75.0	80	2	F28833	Ig kappa chain V r
571	24	75.0	84	2	T36258	hypothetical prote
572	24	75.0	86	2	A25150	Ig heavy chain V r
573	24	75.0	86	2	T42185	conserved hypothet
574	24	75.0	87	2	PH1162	Ig heavy chain V r
575	24	75.0	88	2	PH1161	Ig heavy chain V r
576	24	75.0	90	2	PH1152	Ig heavy chain V r
577	24	75.0	93	2	F90993	hypothetical prote
578	24	75.0	93	2	A85839	hypothetical prote
579	24	75.0	93	2	G64978	hypothetical 10.1
580	24	75.0	94	2	S42185	Ig gamma chain V r
581	24	75.0	94	2	PH1142	Ig heavy chain V r
582	24	75.0	94	2	JL0078	Ig heavy chain V r
583	24	75.0	96	2	S17616	Ig heavy chain V r
584	24	75.0	96	2	H89874	hypothetical prote
585	24	75.0	97	2	PH1137	Ig heavy chain V r
586	24	75.0	98	2	B48223	Ig heavy chain V r
587	24	75.0	98	2	PL0121	Ig heavy chain V-I
588	24	75.0	98	2	S29545	Ig heavy chain V r
589	24	75.0	98	2	PH0877	Ig heavy chain V r
590	24	75.0	98	2	PH1429	Ig heavy chain V r
591	24	75.0	98	2	S26896	Ig heavy chain V r
592	24	75.0	98	2	PH1164	Ig heavy chain V r
593	24	75.0	98	2	PH1141	Ig heavy chain V r
594	24	75.0	98	2	PH1138	Ig heavy chain V r
595	24	75.0	98	2	PH1154	Ig heavy chain V r
596	24	75.0	98	2	PH1118	Ig heavy chain V r
597	24	75.0	98	2	PH1139	Ig heavy chain V r
598	24	75.0	98	2	PH1150	Ig heavy chain V r
599	24	75.0	98	2	PH1129	Ig heavy chain V r
600	24	75.0	98	2	PH1156	Ig heavy chain V r
601	24	75.0	98	2	PH1125	Ig heavy chain V r
602	24	75.0	98	2	PH1134	Ig heavy chain V r
603	24	75.0	98	2	PH1105	Ig heavy chain V r
604	24	75.0	98	2	PH1126	Ig heavy chain V r
605	24	75.0	98	2	PH1128	Ig heavy chain V r
606	24	75.0	98	2	PH1108	Ig heavy chain V r
607	24	75.0	98	2	PH1119	Ig heavy chain V r
608	24	75.0	98	2	PH1124	Ig heavy chain V r
609	24	75.0	98	2	PH1149	Ig heavy chain V r
610	24	75.0	98	2	PH1157	Ig heavy chain V r
611	24	75.0	98	2	PH1114	Ig heavy chain V r
612	24	75.0	98	2	I28833	Ig kappa chain V r
613	24	75.0	98	2	PH1131	Ig heavy chain V r
614	24	75.0	98	2	PH1122	Ig heavy chain V r
615	24	75.0	100	2	A38685	apolipoprotein C-I
616	24	75.0	101	2	S12431	Ig heavy chain V r
617	24	75.0	102	2	PH1260	Ig heavy chain V r
618	24	75.0	102	2	PH1263	Ig heavy chain V r
619	24	75.0	102	2	S25025	Ig heavy chain - m
620	24	75.0	104	2	H83876	hypothetical prote
621	24	75.0	104	2	C90958	probable plasmid p
622	24	75.0	104	2	D85806	probable plasmid p
623	24	75.0	105	2	E84331	hypothetical prote
624	24	75.0	105	2	A97519	hypothetical prote
625	24	75.0	106	2	S24521	Ig heavy chain V r
626	24	75.0	106	2	S25036	Ig heavy chain V r
627	24	75.0	107	2	PH0987	Ig heavy chain V r
628	24	75.0	107	2	G90515	hypothetical prote
629	24	75.0	108	2	AG0076	probable exported
630	24	75.0	108	2	PH0985	Ig heavy chain V r
631	24	75.0	109	2	S25038	Ig heavy chain V r
632	24	75.0	110	2	S25028	Ig heavy chain V r
633	24	75.0	111	1	MHMS76	Ig heavy chain V-I
634	24	75.0	111	2	S25024	Ig heavy chain V r
635	24	75.0	111	2	S25032	Ig heavy chain V r
636	24	75.0	111	2	S25047	Ig heavy chain V r
637	24	75.0	111	2	S25055	Ig heavy chain V r
638	24	75.0	111	2	S25045	Ig heavy chain V r
639	24	75.0	111	2	S25054	Ig heavy chain V r
640	24	75.0	111	2	S25048	Ig heavy chain V r
641	24	75.0	111	2	S25052	Ig heavy chain V r
642	24	75.0	111	2	S25040	Ig heavy chain V r
643	24	75.0	111	2	S25051	Ig heavy chain V r
644	24	75.0	112	2	S25042	Ig heavy chain V r
645	24	75.0	113	1	AVMS09	Ig heavy chain V-I
646	24	75.0	113	1	AVMS57	Ig heavy chain V-I
647	24	75.0	113	1	AVMS61	Ig heavy chain V-I
648	24	75.0	113	1	AVMSAB	Ig heavy chain V-I
649	24	75.0	113	1	AVMSB7	Ig heavy chain V-I
650	24	75.0	113	1	HVMSAM	Ig heavy chain V r
651	24	75.0	113	2	S25044	Ig heavy chain V r
652	24	75.0	113	2	S25041	Ig heavy chain V r
653	24	75.0	113	2	T05282	ribosomal protein
654	24	75.0	113	2	S16254	hypothetical prote
655	24	75.0	113	2	I38216	protein-serine/thr
656	24	75.0	114	2	PT0181	Ig heavy chain V r
657	24	75.0	115	1	AVMS06	Ig heavy chain V-I
658	24	75.0	115	1	AVMS82	Ig heavy chain V-I
659	24	75.0	115	2	PH1560	Ig heavy chain V r
660	24	75.0	115	2	S09382	Ig heavy chain - c
661	24	75.0	115	2	A25803	Ig heavy chain V r
662	24	75.0	115	2	C27563	Ig heavy chain V r
663	24	75.0	116	2	I84704	gene VH104B protei
664	24	75.0	116	2	H29380	Ig heavy chain pre
665	24	75.0	116	2	S26309	Ig heavy chain V r
666	24	75.0	116	2	S53751	antibody Fab Jel 1
667	24	75.0	117	1	HVMS02	Ig heavy chain pre
668	24	75.0	117	1	HVMS23	Ig heavy chain pre
669	24	75.0	117	1	HVMS3	Ig heavy chain pre
670	24	75.0	117	1	HVMS45	Ig heavy chain pre
671	24	75.0	117	1	HVMS61	Ig heavy chain pre
672	24	75.0	117	1	MHMSB4	Ig heavy chain pre
673	24	75.0	117	2	S19669	Ig heavy chain V r
674	24	75.0	117	2	JC2269	PL7-6 antibody hea
675	24	75.0	117	2	S55541	Ig heavy chain V r
676	24	75.0	118	2	A31485	Ig heavy chain V r
677	24	75.0	118	2	S74769	hypothetical prote
678	24	75.0	118	2	H97853	hypothetical prote
679	24	75.0	118	2	H71640	hypothetical prote
680	24	75.0	119	2	S36257	Ig heavy chain V r
681	24	75.0	119	2	PL0086	Ig heavy chain V r
682	24	75.0	119	2	T18114	hypothetical prote
683	24	75.0	120	1	MHMS15	Ig heavy chain V r
684	24	75.0	120	2	S25175	Ig heavy chain V r
685	24	75.0	120	2	S41394	Ig heavy chain V r
686	24	75.0	120	2	B22769	Ig heavy chain V r

687	24	75.0	122	2	PH1426	Ig heavy chain V r
688	24	75.0	122	2	S06825	Ig heavy chain V r
689	24	75.0	122	2	A27635	Ig heavy chain pre
690	24	75.0	123	2	PH1413	Ig heavy chain V r
691	24	75.0	126	2	S31930	Ig gamma chain pre
692	24	75.0	127	2	PH1409	Ig heavy chain V r
693	24	75.0	127	2	T31159	DNA primase homolo
694	24	75.0	128	2	S57955	thrombospondin 2 -
695	24	75.0	131	2	A27472	Ig heavy chain pre
696	24	75.0	133	2	B70027	hypothetical prote
697	24	75.0	134	1	ERAD28	early E3B 14.5K pr
698	24	75.0	134	1	ERAD78	early E3B 14.9K pr
699	24	75.0	134	1	WMVZK5	K5 protein - vacci
700	24	75.0	134	2	B46178	probable transcrip
701	24	75.0	136	2	JL0077	Ig heavy chain pre
702	24	75.0	137	2	PH1562	Ig heavy chain V r
703	24	75.0	137	2	B34903	Ig heavy chain pre
704	24	75.0	137	2	A34903	Ig heavy chain pre
705	24	75.0	137	2	D34903	Ig heavy chain pre
706	24	75.0	137	2	E34903	Ig heavy chain pre
707	24	75.0	137	2	F34903	Ig heavy chain pre
708	24	75.0	137	2	E81187	conserved hypothet
709	24	75.0	137	2	D81914	probable membrane
710	24	75.0	138	2	PH1564	Ig heavy chain V r
711	24	75.0	138	2	PH1565	Ig heavy chain V r
712	24	75.0	139	1	MHMS18	Ig heavy chain pre
713	24	75.0	141	2	S31685	Ig heavy chain V r
714	24	75.0	141	2	JL0076	Ig heavy chain pre
715	24	75.0	142	2	S36307	T-cell receptor de
716	24	75.0	143	2	S76665	hypothetical prote
717	24	75.0	144	2	PH1563	Ig heavy chain V r
718	24	75.0	145	2	C84112	hypothetical prote
719	24	75.0	145	2	E71096	hypothetical prote
720	24	75.0	146	2	S26197	alpha-amylase/tryp
721	24	75.0	147	2	PH1561	Ig heavy chain V r
722	24	75.0	149	2	AC0375	probable membrane
723	24	75.0	149	2	S73156	hypothetical prote
724	24	75.0	152	2	C83751	hypothetical prote
725	24	75.0	153	2	T22005	hypothetical prote
726	24	75.0	154	2	H64562	hypothetical prote
727	24	75.0	156	2	S67248	hypothetical prote
728	24	75.0	156	2	AC3424	transcription elon
729	24	75.0	160	2	D87111	30S ribosomal prot
730	24	75.0	162	1	B41659	benzoate 1,2-dioxy
731	24	75.0	162	2	H70927	probable rpsP prot
732	24	75.0	164	2	D83084	rod shape-determin
733	24	75.0	164	2	A69865	conserved hypothet
734	24	75.0	167	2	T41990	hypothetical prote
735	24	75.0	167	2	AD2430	hypothetical prote
736	24	75.0	169	2	T33949	hypothetical prote
737	24	75.0	171	2	AD0017	transcription elon
738	24	75.0	175	2	S57903	probable amino aci
739	24	75.0	176	2	F84583	pathogenesis-relat
740	24	75.0	177	2	C96774	AtHVA22a, 65476-64
741	24	75.0	179	2	T15578	hypothetical prote
742	24	75.0	180	2	S54502	Ypt-interacting pr
743	24	75.0	181	2	D65179	hypothetical 20.8
744	24	75.0	181	2	F75561	hypothetical prote
745	24	75.0	182	2	A98216	hypothetical prote
746	24	75.0	182	2	AE2355	hypothetical prote
747	24	75.0	184	2	H96718	AtHVA22c, 50565-49
748	24	75.0	185	2	A39658	polyposis coli reg
749	24	75.0	185	2	JC4667	TB2/DP1 protein ho
750	24	75.0	189	2	A83151	probable pseudouri
751	24	75.0	190	2	G97323	probable tesA-like
752	24	75.0	193	2	D75332	hypothetical prote
753	24	75.0	193	2	AD1949	hypothetical prote
754	24	75.0	194	2	T15549	hypothetical prote
755	24	75.0	194	2	A75515	conserved hypothet
756	24	75.0	194	2	AC0370	hypothetical prote
757	24	75.0	194	2	A82198	hypothetical prote
758	24	75.0	195	2	G75488	hypothetical prote
759	24	75.0	198	2	B83267	probable glutathio
760	24	75.0	199	2	AB2171	hypothetical prote
761	24	75.0	201	2	AE2855	ATP-dependent Clp
762	24	75.0	201	2	AD1191	conserved hypothet
763	24	75.0	201	2	AD1549	conserved hypothet
764	24	75.0	204	2	AH1874	hypothetical prote
765	24	75.0	204	2	AB0299	probable LuxR-fami
766	24	75.0	205	2	I64155	hypothetical prote
767	24	75.0	205	2	G70304	hypothetical prote
768	24	75.0	206	2	E71308	conserved hypothet
769	24	75.0	207	2	F70135	flagellar protein
770	24	75.0	209	1	OBUTMB	cytochrome-c oxida
771	24	75.0	213	2	T30116	hypothetical prote
772	24	75.0	214	2	AG3525	hydrolase family p
773	24	75.0	214	2	T20683	hypothetical prote
774	24	75.0	216	2	D72587	phosphoesterase-re
775	24	75.0	217	2	T48949	hypothetical prote
776	24	75.0	218	2	T27954	hypothetical prote
777	24	75.0	218	2	T46596	hypothetical prote
778	24	75.0	220	2	B82136	septum site-determ
779	24	75.0	221	1	QQECW7	yecA protein - Esc
780	24	75.0	221	2	H90955	hypothetical prote
781	24	75.0	221	2	E85804	hypothetical prote
782	24	75.0	221	2	T18505	hypothetical prote
783	24	75.0	225	2	D82957	probable permease
784	24	75.0	228	2	AF0253	cell division inhi
785	24	75.0	228	2	E83216	conserved hypothet
786	24	75.0	229	1	S54799	nitrile hydratase
787	24	75.0	229	1	S19713	nitrile hydratase
788	24	75.0	229	2	AC0002	probable GntR-faml
789	24	75.0	230	2	B86062	hypothetical prote
790	24	75.0	231	1	CEECIC	cell division inhi
791	24	75.0	231	2	F90837	septum-site determ
792	24	75.0	231	2	G85695	septum-site determ
793	24	75.0	233	2	B95218	hypothetical prote
794	24	75.0	233	2	A98082	UDPglucose 4-epime
795	24	75.0	234	2	AG0951	hypothetical 20.8
796	24	75.0	235	2	AG0724	septum site determ
797	24	75.0	236	2	E86635	hypothetical prote
798	24	75.0	237	2	C84968	cell division inhi
799	24	75.0	239	2	AF3513	channel protein vi
800	24	75.0	239	2	F84887	probable cis-Golgi
801	24	75.0	239	2	T22987	hypothetical prote
802	24	75.0	240	2	I64156	probable pseudouri
803	24	75.0	240	2	H70091	hypothetical prote
804	24	75.0	242	2	A97504	yci protein [impor
805	24	75.0	242	2	AD2722	conserved hypothet
806	24	75.0	242	2	JC7933	spermatogenic cell
807	24	75.0	243	2	T30500	hypothetical prote
808	24	75.0	245	2	E86450	F5D14.29 protein -
809	24	75.0	246	2	AB1345	hypothetical prote
810	24	75.0	246	2	AE1715	hypothetical prote
811	24	75.0	246	2	S74408	lipopeptide antibi
812	24	75.0	247	2	F87704	heme exporter prot
813	24	75.0	247	2	B90733	probable major tai
814	24	75.0	249	2	D85583	probable tail comp
815	24	75.0	250	2	E82477	oxidoreductase, sh
816	24	75.0	252	2	A48904	aminoglycoside ade
817	24	75.0	252	2	T46336	hypothetical prote
818	24	75.0	252	2	T48422	hypothetical prote
819	24	75.0	253	1	A40582	type IV prepilin p
820	24	75.0	253	2	D82273	leader peptidase T
821	24	75.0	253	2	A64456	hypothetical prote
822	24	75.0	255	2	S41690	cytochrome-c oxida
823	24	75.0	255	2	AG1184	hypothetical prote
824	24	75.0	257	2	S76537	hypothetical prote
825	24	75.0	257	2	T23332	hypothetical prote
826	24	75.0	258	2	AF2287	group 3 sigma 37-t
827	24	75.0	259	2	T50657	beta-expansin [imp
828	24	75.0	260	2	S65174	vanadate resistanc
829	24	75.0	261	2	T41508	hypothetical prote
830	24	75.0	261	2	T09075	hypothetical prote
831	24	75.0	262	2	A53452	phenylalanine hydr
832	24	75.0	262	2	F83535	phenylalanine-4-hy

833	24	75.0	264	2	S73437	glycerol uptake fa
834	24	75.0	265	1	F69296	p-nitrophenyl phos
835	24	75.0	265	2	F84071	hypothetical prote
836	24	75.0	266	2	S40988	hypothetical prote
837	24	75.0	268	2	B97632	ATP-dependent clp
838	24	75.0	269	2	T45007	probable ABC-trans
839	24	75.0	271	2	H84592	beta-expansin [imp
840	24	75.0	271	2	F82261	hypothetical prote
841	24	75.0	273	2	G97406	probable sugar tra
842	24	75.0	273	2	AH2624	ABC transporter, m
843	24	75.0	273	2	A71925	hypothetical prote
844	24	75.0	273	2	C64589	hypothetical prote
845	24	75.0	273	2	A72378	conserved hypothet
846	24	75.0	273	2	H75393	conserved hypothet
847	24	75.0	275	2	C81843	carboxylesterase (
848	24	75.0	275	2	G81097	esterase, probable
849	24	75.0	275	2	A64145	hypothetical prote
850	24	75.0	275	2	C84284	hypothetical prote
851	24	75.0	276	2	S75249	esterase sll0992 -
852	24	75.0	277	2	B90680	probable esterase
853	24	75.0	277	2	F85530	carboxylesterase (
854	24	75.0	277	2	C64763	yaiM protein - Esc
855	24	75.0	277	2	E82739	hypothetical prote
856	24	75.0	278	2	A64984	hypothetical 31.3
857	24	75.0	278	2	F91009	probable esterase
858	24	75.0	278	2	H85853	probable esterase
859	24	75.0	278	2	S27149	gene 30.2 protein
860	24	75.0	280	2	AI0182	carboxylesterase (
861	24	75.0	280	2	T26582	hypothetical prote
862	24	75.0	281	2	C82102	conserved hypothet
863	24	75.0	281	2	S55646	hypothetical prote
864	24	75.0	283	2	A83191	probable esterase
865	24	75.0	284	2	T00809	probable esterase
866	24	75.0	284	2	B85042	probable chloropla
867	24	75.0	284	2	F71015	hypothetical prote
868	24	75.0	285	2	AB0782	probable esterase
869	24	75.0	285	2	AD0613	probable formate t
870	24	75.0	285	2	A32305	probable formate t
871	24	75.0	285	2	C90752	probable formate t
872	24	75.0	285	2	A85616	probable formate t
873	24	75.0	285	2	AB0169	probable formate t
874	24	75.0	287	4	PC4402	pelB leader/Ig hea
875	24	75.0	288	2	A84650	hypothetical prote
876	24	75.0	290	2	A82236	pseudouridine synt
877	24	75.0	291	2	B72284	oligopeptide ABC t
878	24	75.0	292	2	S76003	hypothetical prote
879	24	75.0	294	2	AC1905	ABC transporter su
880	24	75.0	297	2	AE0400	probable membrane
881	24	75.0	298	2	G89898	hypothetical prote
882	24	75.0	298	2	AB3190	hypothetical prote
883	24	75.0	298	2	AE1752	hypothetical prote
884	24	75.0	298	2	AH1728	AbiD phage protein
885	24	75.0	299	2	E96012	probable sugar upt
886	24	75.0	299	2	T20953	hypothetical prote
887	24	75.0	300	2	T46751	inner membrane pro
888	24	75.0	300	2	T16255	hypothetical prote
889	24	75.0	300	2	A84399	hypothetical prote
890	24	75.0	304	2	H96496	TNP2-like transpos
891	24	75.0	305	2	E97346	oligopeptide ABC t
892	24	75.0	305	2	A96035	probable sugar upt
893	24	75.0	305	2	AC2730	conserved hypothet
894	24	75.0	305	2	D97511	probable integral
895	24	75.0	308	2	B97347	oligopeptide ABC t
896	24	75.0	310	2	C47045	ferrochelatase (EC
897	24	75.0	310	2	H82138	probable phosphati
898	24	75.0	311	2	A56235	transcription acti
899	24	75.0	312	2	T35940	probable transport
900	24	75.0	312	2	AG2884	hypothetical prote
901	24	75.0	312	2	D97660	hypothetical prote
902	24	75.0	312	2	D86488	bacterial IS-eleme
903	24	75.0	312	2	AG1789	secreted protein w
904	24	75.0	312	2	AH1413	secreted protein w
905	24	75.0	313	2	S44895	ZK1236.5 protein -
906	24	75.0	314	1	A46489	pan-epithelial gly
907	24	75.0	314	2	B48149	epithelial glycopr
908	24	75.0	315	2	H86836	carbamate kinase (
909	24	75.0	315	2	A86710	transposase of IS9
910	24	75.0	315	2	G86712	transposase of IS9
911	24	75.0	315	2	D86741	transposase of IS9
912	24	75.0	315	2	G86787	transposase of IS9
913	24	75.0	315	2	G86794	transposase of IS9
914	24	75.0	315	2	C86814	transposase of IS9
915	24	75.0	315	2	B86837	transposase of IS9
916	24	75.0	315	2	E86860	transposase of IS9
917	24	75.0	315	2	D86863	transposase of IS9
918	24	75.0	315	2	C86866	transposase of IS9
919	24	75.0	315	2	A86867	transposase of IS9
920	24	75.0	315	2	F86882	transposase of IS9
921	24	75.0	315	2	G86891	transposase of IS9
922	24	75.0	315	2	G86897	transposase of IS9
923	24	75.0	316	2	H97664	hypothetical prote
924	24	75.0	316	2	AC2889	hypothetical prote
925	24	75.0	320	2	S77147	hydroxymethylbilan
926	24	75.0	321	2	T47280	transposase-like p
927	24	75.0	322	2	T40393	thioredoxin-disulf
928	24	75.0	322	2	T16633	hypothetical prote
929	24	75.0	323	2	I49529	transcription fact
930	24	75.0	324	2	E84505	hypothetical prote
931	24	75.0	324	2	B96738	probable ABC trans
932	24	75.0	325	2	H69732	PBSX prophage ORF
933	24	75.0	325	2	AI0904	probable membrane
934	24	75.0	325	2	C91138	hypothetical prote
935	24	75.0	325	2	F85983	hypothetical prote
936	24	75.0	325	2	F65110	hypothetical 34.7
937	24	75.0	326	2	D69948	phage-related prot
938	24	75.0	327	2	D75263	hypothetical prote
939	24	75.0	329	2	T31848	hypothetical prote
940	24	75.0	329	2	S52563	hypothetical prote
941	24	75.0	329	2	AG0206	probable membrane
942	24	75.0	331	2	T23504	hypothetical prote
943	24	75.0	332	2	E71105	hypothetical prote
944	24	75.0	333	1	C69812	ferrichrome ABC tr
945	24	75.0	333	2	G75055	hypothetical prote
946	24	75.0	333	2	AB2495	hypothetical prote
947	24	75.0	334	1	B49888	thioredoxin-disulf
948	24	75.0	334	2	AH2585	hypothetical prote
949	24	75.0	334	2	G97367	probable dehydroge
950	24	75.0	334	2	T36052	probable cytochrom
951	24	75.0	335	2	G90276	catechol 2,3-dioxy
952	24	75.0	335	2	B98142	hypothetical prote
953	24	75.0	335	2	H96667	AP2-containing DNA
954	24	75.0	336	2	AH2040	porphobilinogen de
955	24	75.0	337	2	B97431	alpha-glucosides t
956	24	75.0	337	2	T18708	hypothetical prote
957	24	75.0	338	2	JC8010	single-stranded nu
958	24	75.0	338	2	T28779	hypothetical prote
959	24	75.0	339	2	E97261	hypothetical prote
960	24	75.0	340	2	B70781	hypothetical prote
961	24	75.0	341	2	T45350	hypothetical prote
962	24	75.0	343	2	T42129	probable acyltrans
963	24	75.0	343	2	T15253	hypothetical prote
964	24	75.0	344	2	F90500	glycolate oxidase
965	24	75.0	344	2	T18019	probable site-spec
966	24	75.0	345	2	E90817	hypothetical prote
967	24	75.0	345	2	C90974	hypothetical prote
968	24	75.0	345	2	A85677	unknown protein en
969	24	75.0	345	2	E85821	unknown protein en
970	24	75.0	346	2	D70558	probable cydB prot
971	24	75.0	346	2	T45748	hypothetical prote
972	24	75.0	346	2	T24803	hypothetical prote
973	24	75.0	347	2	F90904	hypothetical prote
974	24	75.0	347	2	G85712	unknown protein en
975	24	75.0	348	2	G69142	GDP-D-mannose dehy
976	24	75.0	348	2	E82896	hemin permease UU3
977	24	75.0	350	2	T15711	hypothetical prote
978	24	75.0	353	2	S43134	hypothetical prote

979	24	75.0	356	2	AI3145	GDP-mannose 4,6-de
980	24	75.0	358	2	T11165	ubiquinol-cytochro
981	24	75.0	358	2	H83554	hypothetical prote
982	24	75.0	359	2	F90055	conserved hypothet
983	24	75.0	360	2	AB3496	gluconate 2-dehydr
984	24	75.0	360	2	H71551	hypothetical prote
985	24	75.0	362	2	T27804	hypothetical prote
986	24	75.0	363	2	E96703	hypothetical prote
987	24	75.0	365	2	E81704	conserved hypothet
988	24	75.0	365	2	C64421	hypothetical prote
989	24	75.0	366	2	T11271	ubiquinol-cytochro
990	24	75.0	366	2	T04763	chitinase homolog
991	24	75.0	368	2	T29320	hypothetical prote
992	24	75.0	368	2	T15492	hypothetical prote
993	24	75.0	369	1	TVFVAF	transforming prote
994	24	75.0	370	2	I57555	c-Maf protein - mo
995	24	75.0	370	2	E82751	lipopolysaccharide
996	24	75.0	371	2	AF2396	two-component sens
997	24	75.0	372	1	A32375	L-selectin precurs
998	24	75.0	372	2	T52621	mitogen-activated
999	24	75.0	374	2	AH3102	hippurate hydrolas
1000	24	75.0	374	2	B98184	probable hydrolase

ALIGNMENTS

RESULT 1
S43573
C05B5.4 protein (clone C05B5) - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
C;Accession: S43573
R;Mortimore, B.
submitted to the EMBL Data Library, April 1994
A;Reference number: S43570
A;Accession: S43573
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-309 <MOR>
A;Cross-references: UNIPARC:UPI000017B6AC; EMBL:Z32679
C;Genetics:
A;Introns: 53/3; 178/3; 236/2; 263/2

Query Match 100.0%; Score 32; DB 2; Length 309;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 275 TYWMS 279

RESULT 2
B88571
protein C05B5.4 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B88571
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: B88571
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-315 <STO>
A;Cross-references: UNIPROT:P34292; UNIPARC:UPI000013B732; GB:chr_III; PIDN:CAA83591.1;
C;Genetics:
A;Gene: C05B5.4
A;Map position: 3

Query Match 100.0%; Score 32; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 281 TYWMS 285

RESULT 3
F83760
hypothetical protein BH0886 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: F83760
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and g
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83760
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-454 <STO>
A;Cross-references: UNIPROT:Q9KEG6; UNIPARC:UPI00000C3A11; GB:AP001510; GB:BA000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0886
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0709

Query Match 100.0%; Score 32; DB 2; Length 454;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 402 TYWMS 406

RESULT 4
T21588
hypothetical protein F31C3.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21588
R;Cottage, A.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z19446
A;Accession: T21588
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2025 <WIL>
A;Cross-references: UNIPROT:O62191; UNIPARC:UPI0000164007; EMBL:Z92784; PIDN:CAB07193.1;
A;Experimental source: clone F31C3
C;Genetics:
A;Gene: CESP:F31C3.3
A;Map position: 1
A;Introns: 395/2; 549/2; 768/1; 925/1; 1076/3; 1871/3; 1927/3; 2006/3

Query Match 100.0%; Score 32; DB 2; Length 2025;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 1172 TYWMS 1176

RESULT 5
S42183
Ig gamma chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1994 #sequence_revision 21-Jul-1995 #text_change 23-Jul-1999

C;Accession: S42183
R;Mo, J.A.; Bona, C.A.; Holmdahl, R.
Eur. J. Immunol. 23, 2503-2510, 1993
A;Title: Variable region gene selection of immunoglobulin G-expressing B cells with spec
A;Reference number: S42176; MUID:94009207; PMID:7691608
A;Accession: S42183
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-101 <MOJ>
A;Cross-references: UNIPARC:UPI0000116565; EMBL:Z25455; NID:g407824; PIDN:CAA80942.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

 Query Match 90.6%; Score 29; DB 2; Length 101;
 Best Local Similarity 80.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:
Db 31 TYWMN 35

RESULT 6
AE3516
hypothetical protein BMEII0055 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AE3516
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AE3516
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-116 <KUR>
A;Cross-references: UNIPROT:Q8YDW9; UNIPARC:UPI0000058326; GB:AE008918; PIDN:AAL53296.1;
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEII0055
A;Map position: II

 Query Match 90.6%; Score 29; DB 2; Length 116;
 Best Local Similarity 80.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 79 TYWLS 83

RESULT 7
S03289
Ig heavy chain precursor V region (VAR100) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999
C;Accession: S03289
R;Blankenstein, T.; Bonhomme, F.; Krawinkel, U.
Immunogenetics 26, 237-248, 1987
A;Title: Evolution of pseudogenes in the immunoglobulin V(H)-gene family of the mouse.
A;Reference number: S03289; MUID:88006305; PMID:2820872
A;Accession: S03289
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-117 <BLA>
A;Cross-references: UNIPARC:UPI000011678D; EMBL:X06866; NID:g52454; PIDN:CAA29991.1; PID
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

 Query Match 90.6%; Score 29; DB 2; Length 117;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:
Db 50 TYWMN 54

RESULT 8
S31509
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31509
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA autoa
A;Reference number: S31509
A;Accession: S31509
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-123 <CHA>
A;Cross-references: UNIPARC:UPI00001160FD; EMBL:X69864; NID:g33090; PIDN:CAA49498.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;23-106/Domain: immunoglobulin homology <IMM>

 Query Match 90.6%; Score 29; DB 2; Length 123;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:
Db 39 TYWMT 43

RESULT 9
G84812
hypothetical protein At2g39070 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: G84812
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84812
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-124 <STO>
A;Cross-references: UNIPROT:Q9ZV01; UNIPARC:UPI00000A1CE7; GB:AE002093; NID:g3928091; PII
C;Genetics:
A;Gene: At2g39070
A;Map position: 2

 Query Match 90.6%; Score 29; DB 2; Length 124;
 Best Local Similarity 80.0%; Pred. No. 1.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 16 TYWLS 20

RESULT 10
B47159
Ig heavy chain V region, anti-carcinoembryonic maId T84.66 antigen monoclonal anti-idiot
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996

```
C;Accession: B47159
R;Gaida, F.J.; Pieper, D.; Roder, U.W.; Shively, J.E.; Wagener, C.; Neumaier, M.
J. Biol. Chem. 268, 14138-14145, 1993
A;Title: Molecular characterization of a cloned idiotypic cascade containing a network a
A;Reference number: A47159; MUID:93300804; PMID:7686150
A;Accession: B47159
A;Status: preliminary
A;Molecule type: DNA; protein
A;Residues: 1-136 <GAI>
A;Cross-references: UNIPARC:UPI0000176C84
A;Experimental source: hybridoma 6G6.C4
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:134421, NCBIP:134422)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match             90.6%;  Score 29;  DB 2;  Length 136;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db         50 TYWMN 54


RESULT 11
A84069
hypothetical protein BH3353 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 12-Jul-2004
C;Accession: A84069
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A84069
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-158 <STO>
A;Cross-references: UNIPROT:Q9K7K8; UNIPARC:UPI000012E9D3; GB:AP001518; GB:BA000004; NID
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH3353
C;Superfamily: autoinducer-2 production protein LuxS

  Query Match             90.6%;  Score 29;  DB 2;  Length 158;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        142 TYWLS 146


RESULT 12
S74997
hypothetical protein slr1052 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74997
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74997
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-170 <KAN>
A;Cross-references: UNIPROT:P73017; UNIPARC:UPI00000C0C73; EMBL:D90902; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

  Query Match             90.6%;  Score 29;  DB 2;  Length 170;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        166 TYWLS 170


RESULT 13
T19594
hypothetical protein C31A11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19594
R;McMurray, A.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19149
A;Accession: T19594
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-282 <WIL>
A;Cross-references: UNIPROT:O45281; UNIPARC:UPI000007B915; EMBL:Z83218; PIDN:CAB05686.1;
A;Experimental source: clone C31A11
C;Genetics:
A;Gene: CESP:C31A11.4
A;Map position: 5
A;Introns: 210/3
C;Superfamily: Caenorhabditis elegans hypothetical protein B0250.6

  Query Match             90.6%;  Score 29;  DB 2;  Length 282;
  Best Local Similarity   80.0%;  Pred. No. 2.8e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        169 TYWLS 173


RESULT 14
AG2812
conserved hypothetical protein Atu1921 [imported] - Agrobacterium tumefaciens (strain C58
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 12-Jul-2004
C;Accession: AG2812
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClella
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, B
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AG2812
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-290 <KUR>
A;Cross-references: UNIPROT:Q8UE42; UNIPARC:UPI0000164671; GB:AE008688; PIDN:AAL42917.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu1921
A;Map position: circular chromosome
C;Superfamily: membrane protein

  Query Match             90.6%;  Score 29;  DB 2;  Length 290;
  Best Local Similarity   80.0%;  Pred. No. 2.9e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db        167 TYWMA 171
```

RESULT 15
A97591
hypothetical protein AGR_C_3514 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 12-Jul-2004
C;Accession: A97591
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A97591
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-298 <KUR>
A;Cross-references: UNIPROT:Q8UE42; UNIPARC:UPI00000D1D0D; GB:AE007869; PIDN:AAK87682.1;
C;Genetics:
A;Gene: AGR_C_3514
A;Map position: circular chromosome
C;Superfamily: membrane protein

Query Match 90.6%; Score 29; DB 2; Length 298;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:
Db 175 TYWMA 179

RESULT 16
H84673
hypothetical protein At2g27520 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C;Accession: H84673
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84673
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <STO>
A;Cross-references: UNIPROT:Q9ZNQ3; UNIPARC:UPI00000A0ED9; GB:AE002093; NID:g3860278; PI
C;Genetics:
A;Gene: At2g27520
A;Map position: 2
C;Superfamily: hypothetical protein containing F-box domain

Query Match 90.6%; Score 29; DB 2; Length 347;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 189 TYWLS 193

RESULT 17
T48821
hypothetical protein 68B2.50 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 31-Dec-2004
C;Accession: T48821
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24541
A;Accession: T48821
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-386 <SCH>
A;Cross-references: UNIPROT:Q96UB7; UNIPARC:UPI0000179492; EMBL:AL353821; GSPDB:GN00112;
A;Experimental source: cosmid contig 68B2; strain 74
C;Genetics:
A;Gene: NCSP:68B2.50
A;Map position: 2
A;Introns: 207/1; 271/3

Query Match 90.6%; Score 29; DB 2; Length 386;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 114 TYWLS 118

RESULT 18
S41035
hypothetical protein R10E12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S41035
R;Smith, A.
submitted to the EMBL Data Library, January 1994
A;Reference number: S41034
A;Accession: S41035
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-395 <SMI>
A;Cross-references: UNIPROT:P34553; UNIPARC:UPI000013BB6D; EMBL:Z29561; NID:g450897; PID
C;Genetics:
A;Introns: 72/3; 124/3; 268/2

Query Match 90.6%; Score 29; DB 2; Length 395;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:
Db 281 TYWMT 285

RESULT 19
E87571
amine oxidase, flavin-containing [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: E87571
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolona
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: E87571
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-454 <STO>
A;Cross-references: UNIPROT:Q9A564; UNIPARC:UPI00000C779C; GB:AE005673; NID:g13424171; PI
C;Genetics:
A;Gene: CC2600
C;Superfamily: Neurospora crassa hypothetical protein B1D1.190

Query Match 90.6%; Score 29; DB 2; Length 454;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:
Db 338 TYWMN 342

RESULT 20
AF2819
amine oxidase, flavin-containing [imported] - Agrobacterium tumefaciens (strain C58, Dup
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2819
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF2819
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-457 <KUR>
A;Cross-references: UNIPROT:Q8UDY9; UNIPARC:UPI00000D1D34; GB:AE008688; PIDN:AAL42972.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu1977
A;Map position: circular chromosome
C;Superfamily: Neurospora crassa hypothetical protein B1D1.190

 Query Match 90.6%; Score 29; DB 2; Length 457;
 Best Local Similarity 80.0%; Pred. No. 4.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||| :
Db 335 TYWMN 339

RESULT 21
F97597
hypothetical protein AGR_C_3599 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97597
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97597
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-457 <KUR>
A;Cross-references: UNIPROT:Q8UDY9; UNIPARC:UPI00000D1D34; GB:AE007869; PIDN:AAK87735.1;
C;Genetics:
A;Gene: AGR_C_3599
A;Map position: circular chromosome
C;Superfamily: Neurospora crassa hypothetical protein B1D1.190

 Query Match 90.6%; Score 29; DB 2; Length 457;
 Best Local Similarity 80.0%; Pred. No. 4.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||| :
Db 335 TYWMN 339

RESULT 22
AD2395
two-component sensor histidine kinase alr4716 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AD2395
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anab
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2395
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-468 <KUR>
A;Cross-references: UNIPROT:Q8YN54; UNIPARC:UPI00000CEC16; GB:BA000019; PIDN:BAB76415.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr4716

 Query Match 90.6%; Score 29; DB 2; Length 468;
 Best Local Similarity 80.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 90 TYWLS 94

RESULT 23
E89790
6-phospho-beta-glucosidase [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: E89790
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; H
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89790
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-478 <KUR>
A;Cross-references: UNIPROT:Q99WV9; UNIPARC:UPI00000CAA7F; GB:BA000018; PID:g13700182; PI
A;Experimental source: strain N315
C;Genetics:
A;Gene: bglA
C;Superfamily: Agrobacterium beta-glucosidase

 Query Match 90.6%; Score 29; DB 2; Length 478;
 Best Local Similarity 80.0%; Pred. No. 4.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||| :
Db 169 TYWMT 173

RESULT 24
F64165
hypothetical protein HI1064 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: F64165
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: F64165
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-485 <TIGR>
A;Cross-references: UNIPROT:P71367; UNIPARC:UPI0000139F92; GB:U32786; GB:L42023; NID:g157
A;Note: best homolog was a hypothetical protein from Escherichia coli

C;Genetics:
A;Start codon: GTG

Query Match 90.6%; Score 29; DB 2; Length 485;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 300 TYWLS 304

RESULT 25
AB2335
hypothetical protein all4233 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AB2335
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AB2335
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-490 <KUR>
A;Cross-references: UNIPROT:Q8YPG1; UNIPARC:UPI00000CEA6D; GB:BA000019; PIDN:BAB75932.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all4233

Query Match 90.6%; Score 29; DB 2; Length 490;
Best Local Similarity 80.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 42 TYWLS 46

RESULT 26
B64469
hypothetical protein MJ1355 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: B64469
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: B64469
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-571 <BUL>
A;Cross-references: UNIPROT:Q58750; UNIPARC:UPI0000065003; GB:U67575; GB:L77117; NID:g15
C;Genetics:
A;Map position: FOR1304821-1306536
A;Start codon: GTG

Query Match 90.6%; Score 29; DB 2; Length 571;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:
Db 330 TYWMT 334

RESULT 27
T02829
conserved hypothetical protein L4171.1L [imported] - Leishmania major (strain Friedlin)
C;Species: Leishmania major
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: A81460; T02829
R;Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.; P
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-co
A;Reference number: A81455; MUID:99178987; PMID:10077609
A;Accession: A81460
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-587 <PYL>
A;Cross-references: UNIPROT:O00904; UNIPARC:UPI00000756B7; GB:AE001274; NID:g3264850; PII
A;Experimental source: strain MHOM/IL/81/Friedlin
C;Genetics:
A;Gene: L4171.1L
A;Map position: 1
C;Superfamily: Leishmania major hypothetical protein L4171.1L

Query Match 90.6%; Score 29; DB 2; Length 587;
Best Local Similarity 80.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 97 TYWLS 101

RESULT 28
T08934
hypothetical protein F27G19.20 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08934
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16519
A;Accession: T08934
A;Molecule type: DNA
A;Residues: 1-635 <BEV>
A;Cross-references: UNIPROT:Q9SZR9; UNIPARC:UPI00000A1E91; EMBL:AL078467; GSPDB:GN00062;
A;Experimental source: cultivar Columbia; BAC clone F27G19
C;Genetics:
A;Gene: ATSP:F27G19.20
A;Map position: 4
A;Introns: 38/3; 253/1; 304/1; 414/3
C;Superfamily: fruit fly white protein; ATP-binding cassette homology

Query Match 90.6%; Score 29; DB 2; Length 635;
Best Local Similarity 80.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:
Db 481 TYWMA 485

RESULT 29
T43201
MutS protein homolog - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43201
R;Winand, N.J.; Panzer, J.A.; Kolodner, R.D.
Genomics 53, 69-80, 1998
A;Title: Cloning and characterization of the human and Caenorhabditis elegans homologs of
A;Reference number: Z22333; MUID:99005534; PMID:9787078
A;Accession: T43201
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-933 <WIN>

```
A;Cross-references: UNIPROT:Q19272; UNIPARC:UPI000016B67D; EMBL:AF070070; NID:g3831700;
C;Genetics:
A;Gene: msh-5

  Query Match             90.6%;  Score 29;  DB 2;  Length 933;
  Best Local Similarity   80.0%;  Pred. No. 8.7e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db        738 TYWMN 742


RESULT 30
T15720
hypothetical protein C30G4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15720
R;Latreille, P.
submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid C30G4.
A;Reference number: Z18394
A;Accession: T15720
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1057 <LAT>
A;Cross-references: UNIPROT:Q18331; UNIPARC:UPI000007BC9F; EMBL:U49947; NID:g1208826; PI
C;Genetics:
A;Gene: CESP:C30G4.3
A;Introns: 42/3; 66/2; 113/3; 150/1; 202/1; 239/3; 292/1; 345/3; 381/1; 404/2; 448/3; 53
C;Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain homo

  Query Match             90.6%;  Score 29;  DB 2;  Length 1057;
  Best Local Similarity   80.0%;  Pred. No. 9.8e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db       1020 TYWMN 1024


RESULT 31
T30202
probable chitin synthase (EC 2.4.1.16) Chs3 - Rhizopus microsporus var. oligosporus
C;Species: Rhizopus microsporus var. oligosporus
A;Variety: var. oligosporus
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T30202
R;Motoyama, T.; Horiuchi, H.; Ohta, A.; Yamaguchi, I.; Takagi, M.
FEMS Microbiol. Lett. 169, 1-8, 1998
A;Title: Isolation of a class IV chitin synthase gene from a Zygomycetes fungus, Rhizopu
A;Reference number: Z20776; MUID:99068016; PMID:9851030
A;Accession: T30202
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1112 <MOT>
A;Cross-references: UNIPROT:O93787; UNIPARC:UPI000006A94A; EMBL:AB004547; NID:d1245413;
A;Experimental source: var. oligosporus
C;Genetics:
A;Introns: 136/1; 321/2; 770/3; 817/1; 911/3
A;Note: chs3
C;Function:
A;Description: catalyzes the alpha-1,4-glycosylation of chitin by UDP-N-acetyl-D-glucosa
A;Pathway: chitin biosynthesis
C;Superfamily: chitin synthase chs4
C;Keywords: chitin biosynthesis; glycosyltransferase; hexosyltransferase

  Query Match             90.6%;  Score 29;  DB 2;  Length 1112;
  Best Local Similarity   80.0%;  Pred. No. 1e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        358 TYWLS 362


RESULT 32
T20660
hypothetical protein F09E8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20660
R;Percy, C.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19307
A;Accession: T20660
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1139 <WIL>
A;Cross-references: UNIPARC:UPI000017B8CE; EMBL:Z73896; PIDN:CAA98059.1; GSPDB:GN00022; (
A;Experimental source: clone F09E8
C;Genetics:
A;Gene: CESP:F09E8.3
A;Map position: 4
A;Introns: 52/1; 105/1; 132/1; 198/1; 237/3; 274/2; 444/3; 471/3; 508/3; 533/3; 558/1; 61

  Query Match             90.6%;  Score 29;  DB 2;  Length 1139;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db        839 TYWMN 843


RESULT 33
T20904
hypothetical protein F14F4.3a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20904; T22218
R;Wallis, J.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z19344
A;Accession: T20904
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1400 <WIL>
A;Cross-references: UNIPROT:O62170; UNIPARC:UPI000002A21F; EMBL:AL021446; PIDN:CAB54226.1
A;Experimental source: clone F14F4
R;Percy, C.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19531
A;Accession: T22218
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1400 <WI2>
A;Cross-references: UNIPARC:UPI000002A21F; EMBL:Z83227; PIDN:CAB54251.1; GSPDB:GN00028; (
A;Experimental source: clone F45B8
C;Genetics:
A;Gene: CESP:F14F4.3a
A;Map position: X
A;Introns: 26/2; 61/2; 116/2; 140/2; 218/2; 306/3; 356/1; 478/1; 534/3; 642/3; 741/2; 785
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

  Query Match             90.6%;  Score 29;  DB 2;  Length 1400;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        771 TYWLS 775


RESULT 34
```

H89715
protein F14F4.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
C;Accession: H89715
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: H89715
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1404 <STO>
A;Cross-references: UNIPARC:UPI000017CB9D; GB:chr_X; PIDN:CAB05730.1; PID:g3877148; GSPD
C;Genetics:
A;Gene: F14F4.3
A;Map position: X

 Query Match 90.6%; Score 29; DB 2; Length 1404;
 Best Local Similarity 80.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 775 TYWLS 779

RESULT 35
T20903
hypothetical protein F14F4.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20903; T22217
R;Wallis, J.
submitted to the EMBL Data Library, January 1998
A;Reference number: Z19344
A;Accession: T20903
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1427 <WIL>
A;Cross-references: UNIPROT:O62170; UNIPARC:UPI00000866B9; EMBL:AL021446; PIDN:CAB54225.
A;Experimental source: clone F14F4
R;Percy, C.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19531
A;Accession: T22217
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1427 <WI2>
A;Cross-references: UNIPARC:UPI00000866B9; EMBL:Z83227; PIDN:CAB54250.1; GSPDB:GN00028;
A;Experimental source: clone F45B8
C;Genetics:
A;Gene: CESP:F14F4.3b
A;Map position: X
A;Introns: 26/2; 61/2; 116/2; 140/2; 218/2; 306/3; 356/1; 478/1; 534/3; 642/3; 669/3; 76
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology

 Query Match 90.6%; Score 29; DB 2; Length 1427;
 Best Local Similarity 80.0%; Pred. No. 1.3e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 798 TYWLS 802

RESULT 36
G81042
hypothetical protein NMB1781 [imported] - Neisseria meningitidis (strain MC58 serogroup
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: G81042; H81988
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: G81042
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-56 <TET>
A;Cross-references: UNIPROT:Q9JQR1; UNIPARC:UPI00000C4E75; GB:AE002528; GB:AE002098; NID
A;Experimental source: serogroup B, strain MC58
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: H81988
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-56 <PAR>
A;Cross-references: UNIPARC:UPI00000C4E75; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:C
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMB1781; NMA0685

 Query Match 87.5%; Score 28; DB 2; Length 56;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWM 4
||||
Db 32 TYWM 35

RESULT 37
PL0123
Ig heavy chain V-III region (TD-Vr) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C;Accession: PL0123; S26897
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin
A;Reference number: PL0116; MUID:88286083; PMID:2840480
A;Accession: PL0123
A;Molecule type: mRNA
A;Residues: 1-98 <BIR>
A;Cross-references: UNIPARC:UPI0000116413
A;Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL
A;Note: the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement fr
R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A;Reference number: S26885; MUID:93021117; PMID:1404388
A;Accession: S26897
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Cross-references: UNIPARC:UPI0000116413; EMBL:Z12354; NID:g32930; PIDN:CAA78224.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;31-35/Region: complementarity-determining 1
F;49-65/Region: complementarity-determining 2

 Query Match 87.5%; Score 28; DB 2; Length 98;
 Best Local Similarity 80.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5

```
              :||||
Db         31 SYWMS 35


RESULT 38
S26460
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26460
R;Kavaler, J.
submitted to the EMBL Data Library, April 1991
A;Reference number: S26459
A;Accession: S26460
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-101 <KAV>
A;Cross-references: UNIPARC:UPI0000115F60; EMBL:X59106; NID:g51707; PIDN:CAA41832.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             87.5%;  Score 28;  DB 2;  Length 101;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         13 SYWMS 17


RESULT 39
PH1655
Ig heavy chain V region (clone 2E8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1655
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylc
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1655
A;Molecule type: mRNA
A;Residues: 1-110 <HIL>
A;Cross-references: UNIPARC:UPI0000176BDC
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

  Query Match             87.5%;  Score 28;  DB 2;  Length 110;
  Best Local Similarity   80.0%;  Pred. No. 1.8e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         23 SYWMS 27


RESULT 40
S36280
Ig heavy chain V region (clone alpha-FOG1-A3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: S36280
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36280
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-114 <GRI>
A;Cross-references: UNIPROT:Q9ULB6; UNIPARC:UPI0000176D1E; EMBL:Z18822
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             87.5%;  Score 28;  DB 2;  Length 114;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         31 SYWMS 35


RESULT 41
S38714
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38714
R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A;Reference number: S38713
A;Accession: S38714
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <CIM>
A;Cross-references: UNIPARC:UPI000011753D; EMBL:X76014; NID:g416092; PIDN:CAA53601.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-99/Domain: immunoglobulin homology <IMM>

  Query Match             87.5%;  Score 28;  DB 2;  Length 115;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         30 SYWMS 34


RESULT 42
S17079
Ig heavy chain V-gene (clone HHG19) - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S60299; S17079
R;Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.
Immunol. Lett. 34, 57-62, 1992
A;Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 positive immu
A;Reference number: S60295; MUID:93122853; PMID:1282498
A;Accession: S60299
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <KU2>
A;Cross-references: UNIPARC:UPI0000115FF4; EMBL:X62128; NID:g38340; PIDN:CAA44059.1; PID:
A;Note: the authors did not translate the codons for residues 6, 52, 54, 68, 69, 71, 72,
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match             87.5%;  Score 28;  DB 2;  Length 117;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         50 SYWMS 54


RESULT 43
S78486
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Ig heavy chain V region (clone FL13-28) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: S78486; S31115
R;Raaphorst, F.M.
submitted to the EMBL Data Library, October 1991
A;Reference number: S78486
A;Accession: S78486
A;Molecule type: mRNA
A;Residues: 1-117 <RAA>
A;Cross-references: UNIPROT:Q9UL90; UNIPARC:UPI000017699A; EMBL:X62965
A;Experimental source: clone FL13-28
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complem
A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31115
A;Molecule type: mRNA
A;Residues: 1-4,'L',6-32,'G',34-52,'E',54-73,'K',75-97 <RAW>
A;Cross-references: UNIPARC:UPI000017699B; EMBL:X62965
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             87.5%;  Score 28;  DB 2;  Length 117;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         31 SYWMS 35


RESULT 44
S00700
Ig heavy chain V region - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
C;Accession: S00700
R;Yamawaki-Kataoka, Y.; Honjo, T.
Nucleic Acids Res. 15, 5888, 1987
A;Title: Nucleotide sequences of variable region segments of the immunoglobulin heavy ch
A;Reference number: S00700; MUID:87289054; PMID:3112743
A;Accession: S00700
A;Molecule type: DNA
A;Residues: 1-118 <YAM>
A;Cross-references: UNIPARC:UPI00001162E9; EMBL:Y00380; NID:g64810; PIDN:CAA68452.1; PID
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Introns: 15/3
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

  Query Match             87.5%;  Score 28;  DB 2;  Length 118;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         50 SYWMS 54


RESULT 45
S31675
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31675
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31675
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-122 <CUI>
A;Cross-references: UNIPARC:UPI000011645C; EMBL:Z14175; NID:g31015; PIDN:CAA78544.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;21-104/Domain: immunoglobulin homology <IMM>

  Query Match             87.5%;  Score 28;  DB 2;  Length 122;
  Best Local Similarity   80.0%;  Pred. No. 2e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         37 SYWMS 41


RESULT 46
A33989
Ig heavy chain V-1-D-J region - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 16-Aug-1996
C;Accession: A33989
R;Hsu, E.; Schwager, J.; Alt, F.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 8010-8014, 1989
A;Title: Evolution of immunoglobulin genes: V-H families in the amphibian Xenopus.
A;Reference number: A33989; MUID:90046727; PMID:2510156
A;Accession: A33989
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-122 <HSU>
A;Cross-references: UNIPARC:UPI0000176C47
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>

  Query Match             87.5%;  Score 28;  DB 2;  Length 122;
  Best Local Similarity   80.0%;  Pred. No. 2e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         31 SYWMS 35


RESULT 47
PH1412
Ig heavy chain V region (clone P1-55) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: PH1412
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of sh
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1412
A;Molecule type: mRNA
A;Residues: 1-126 <VAN>
A;Cross-references: UNIPARC:UPI0000176A33
A;Experimental source: PBMC
A;Note: the authors translated the codon CTG for residue 117 as Met
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             87.5%;  Score 28;  DB 2;  Length 126;
  Best Local Similarity   80.0%;  Pred. No. 2e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
```

```
Db         31 TYWIS 35


RESULT 48
S31587
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31587
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S31585
A;Accession: S31587
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-136 <CUI>
A;Cross-references: UNIPARC:UPI0000116468; EMBL:Z14189; NID:g31005; PIDN:CAA78558.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-114/Domain: immunoglobulin homology <IMM>

  Query Match             87.5%;  Score 28;  DB 2;  Length 136;
  Best Local Similarity   80.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         47 SYWMS 51


RESULT 49
S78054
Ig heavy chain precursor V-D-J region (clone mAB 60VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C;Accession: S78054; S23719
R;Harindranath, N.
submitted to the EMBL Data Library, August 1990
A;Reference number: S78051
A;Accession: S78054
A;Molecule type: mRNA
A;Residues: 1-137 <HAR>
A;Cross-references: UNIPARC:UPI0000115E85; EMBL:X54435; NID:g37812; PIDN:CAA38304.1; PID
R;Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A;Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A;Reference number: S23716; MUID:92031262; PMID:1718404
A;Accession: S23719
A;Molecule type: mRNA
A;Residues: 20-116 <HAW>
A;Cross-references: UNIPARC:UPI00001769D7; EMBL:X54435
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-137/Product: Ig heavy chain (fragment) #status predicted <MAT>
F;34-116/Domain: immunoglobulin homology <IMM>

  Query Match             87.5%;  Score 28;  DB 2;  Length 137;
  Best Local Similarity   100.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWM 4
              ||||
Db         50 TYWM 53


RESULT 50
I37781
Ig variable region (VDJ) (clone T21-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C;Accession: I37781; S25475
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by hu
A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: I37781
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <RES>
A;Cross-references: UNIPARC:UPI00001160E4; EMBL:X67908; NID:g33580; PIDN:CAA48106.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;35-118/Domain: immunoglobulin homology <IMM>

  Query Match             87.5%;  Score 28;  DB 2;  Length 139;
  Best Local Similarity   80.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         51 SYWMS 55


Search completed: March 23, 2006, 02:04:44
Job time : 17.9178 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:40:40 ; Search time 43.0137 Seconds
(without alignments)
82.012 Million cell updates/sec

Title: US-10-755-382-23
Perfect score: 32
Sequence: 1 TYWMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	168	1	LSPA_VIBVU	Q8des8 vibrio vuln
2	32	100.0	168	1	LSPA_VIBVY	Q7mnm7 vibrio vuln
3	32	100.0	169	1	LSPA_VIBPA	Q87s89 vibrio para
4	32	100.0	178	2	Q8WB24_9NEOP	Q8wb24 ostrinia fu
5	32	100.0	178	2	Q8WBV3_OSTNU	Q8wbv3 ostrinia nu
6	32	100.0	236	2	Q9XHV8_ORYSA	Q9xhv8 oryza sativ
7	32	100.0	236	2	Q688U1_ORYSA	Q688u1 oryza sativ
8	32	100.0	256	2	Q70EF4_9RHIZ	Q70ef4 methylocyst
9	32	100.0	256	2	Q9KX37_9RHIZ	Q9kx37 methylocyst
10	32	100.0	315	1	YKO4_CAEEL	P34292 caenorhabdi
11	32	100.0	322	2	Q61J61_CAEBR	Q61j61 caenorhabdi
12	32	100.0	357	2	Q8ED62_SHEON	Q8ed62 shewanella
13	32	100.0	454	2	Q9KEG6_BACHD	Q9keg6 bacillus ha
14	32	100.0	484	2	Q7N2H2_PHOLL	Q7n2h2 photorhabdu
15	32	100.0	516	2	Q8MS57_DROME	Q8ms57 drosophila
16	32	100.0	623	2	Q8SXX6_DROME	Q8sxx6 drosophila
17	32	100.0	623	2	Q9VTL3_DROME	Q9vtl3 drosophila
18	32	100.0	1238	2	Q4S5S6_TETNG	Q4s5s6 tetraodon n
19	32	100.0	1497	2	Q60V14_CAEBR	Q60v14 caenorhabdi
20	32	100.0	2021	2	O62191_CAEEL	O62191 caenorhabdi
21	29	90.6	30	2	Q8VVS0_STAAU	Q8vvs0 staphylococ
22	29	90.6	30	2	Q79ZU4_STAAW	Q79zu4 staphylococ
23	29	90.6	30	2	Q6GIX8_STAAR	Q6gix8 staphylococ
24	29	90.6	55	2	Q9AC83_STAAN	Q9ac83 staphylococ
25	29	90.6	83	1	RS16_PSEPK	Q88mv6 pseudomonas
26	29	90.6	102	2	Q57A45_BRUAB	Q57a45 brucella ab
27	29	90.6	116	2	Q8FXM7_BRUSU	Q8fxm7 brucella su
28	29	90.6	116	2	Q8YDW9_BRUME	Q8ydw9 brucella me
29	29	90.6	123	2	Q5N0Q1_SYNP6	Q5n0q1 synechococc
30	29	90.6	124	2	Q9ZV01_ARATH	Q9zv01 arabidopsis
31	29	90.6	145	2	Q8WSW6_DUGTI	Q8wsw6 dugesia tig
32	29	90.6	158	1	LUXS_BACHD	Q9k7k8 bacillus ha
33	29	90.6	159	2	Q88MJ3_PSEPK	Q88mj3 pseudomonas
34	29	90.6	170	2	P73017_SYNY3	P73017 synechocyst
35	29	90.6	173	2	Q8QQT8_PRRSV	Q8qqt8 porcine rep
36	29	90.6	182	2	Q950U9_HYACU	Q950u9 hyaloraphid
37	29	90.6	195	2	Q7V8H5_PROMM	Q7v8h5 prochloroco
38	29	90.6	201	2	Q6TF35_PRRSV	Q6tf35 porcine rep
39	29	90.6	201	2	Q8JJF4_PRRSV	Q8jjf4 porcine rep
40	29	90.6	228	2	Q5WG47_BACSK	Q5wg47 bacillus cl
41	29	90.6	231	2	Q8XXM7_RALSO	Q8xxm7 ralstonia s
42	29	90.6	233	2	Q5F6W3_NEIG1	Q5f6w3 neisseria g
43	29	90.6	239	2	Q62IL2_BURMA	Q62il2 burkholderi
44	29	90.6	239	2	Q63VQ6_BURPS	Q63vq6 burkholderi
45	29	90.6	245	2	Q7SC34_NEUCR	Q7sc34 neurospora
46	29	90.6	249	2	Q96UB7_NEUCR	Q96ub7 neurospora
47	29	90.6	252	2	Q525H6_MAGGR	Q525h6 magnaporthe
48	29	90.6	252	2	Q7QC09_ANOGA	Q7qc09 anopheles g
49	29	90.6	252	2	Q4LZS7_9BURK	Q4lzs7 burkholderi
50	29	90.6	253	2	Q9XDB7_METCA	Q9xdb7 methylococc
51	29	90.6	253	2	Q60C16_METCA	Q60c16 methylococc
52	29	90.6	256	2	Q9KX51_METTR	Q9kx51 methylosinu
53	29	90.6	258	2	Q680M5_ARATH	Q680m5 arabidopsis
54	29	90.6	258	2	Q6MZ18_9RHIZ	Q6mz18 methylocyst
55	29	90.6	258	2	Q81GY9_BACCR	Q81gy9 bacillus ce
56	29	90.6	260	2	P97047_METCA	P97047 methylococc
57	29	90.6	260	2	Q603F1_METCA	Q603f1 methylococc
58	29	90.6	262	2	Q8WTP2_DUGTI	Q8wtp2 dugesia tig
59	29	90.6	263	2	Q24696_DUGTI	Q24696 dugesia tig
60	29	90.6	263	2	Q8WTP3_DUGTI	Q8wtp3 dugesia tig
61	29	90.6	267	2	Q4FWK5_LEIMA	Q4fwk5 leishmania
62	29	90.6	282	2	O45281_CAEEL	O45281 caenorhabdi
63	29	90.6	289	2	O05111_METCA	O05111 methylococc
64	29	90.6	290	2	Q58G06_ARATH	Q58g06 arabidopsis
65	29	90.6	290	2	Q8UE42_AGRT5	Q8ue42 agrobacteri
66	29	90.6	291	2	Q873G8_NEUCR	Q873g8 neurospora
67	29	90.6	298	2	Q61G39_CAEBR	Q61g39 caenorhabdi
68	29	90.6	298	2	Q7CY85_AGRT5	Q7cy85 agrobacteri
69	29	90.6	309	2	Q4I4C6_GIBZE	Q4i4c6 gibberella
70	29	90.6	313	2	Q5QYS1_IDILO	Q5qys1 idiomarina
71	29	90.6	324	2	Q5BG50_EMENI	Q5bg50 aspergillus
72	29	90.6	328	2	Q5FK11_LACAC	Q5fk11 lactobacill
73	29	90.6	334	2	Q5P400_AZOSE	Q5p400 azoarcus sp
74	29	90.6	335	2	Q88K20_PSEPK	Q88k20 pseudomonas
75	29	90.6	337	2	Q55IF4_CRYNE	Q55if4 cryptococcu
76	29	90.6	337	2	Q5K7Z3_CRYNE	Q5k7z3 cryptococcu
77	29	90.6	343	1	Y1117_LACJO	Q74jj0 lactobacill
78	29	90.6	347	2	Q9ZNQ3_ARATH	Q9znq3 arabidopsis
79	29	90.6	351	2	Q67YQ9_ARATH	Q67yq9 arabidopsis
80	29	90.6	351	2	Q8VZB1_ARATH	Q8vzb1 arabidopsis
81	29	90.6	381	2	Q8WSW7_DUGTI	Q8wsw7 dugesia tig
82	29	90.6	381	2	Q8WSW8_DUGTI	Q8wsw8 dugesia tig
83	29	90.6	390	2	Q61J58_CAEBR	Q61j58 caenorhabdi
84	29	90.6	395	1	YNK2_CAEEL	P34553 caenorhabdi
85	29	90.6	395	2	Q6MMP9_BDEBA	Q6mmp9 bdellovibri
86	29	90.6	414	2	Q74AM5_GEOSL	Q74am5 geobacter s
87	29	90.6	419	2	Q6FBT7_ACIAD	Q6fbt7 acinetobact
88	29	90.6	436	2	Q6A642_PROAC	Q6a642 propionibac
89	29	90.6	437	2	Q6N6P3_RHOPA	Q6n6p3 rhodopseudo
90	29	90.6	440	2	Q623B2_CAEBR	Q623b2 caenorhabdi
91	29	90.6	441	2	Q7PNP0_ANOGA	Q7pnp0 anopheles g
92	29	90.6	447	2	Q5LTD2_SILPO	Q5ltd2 silicibacte
93	29	90.6	449	2	Q5H9J6_HUMAN	Q5h9j6 homo sapien
94	29	90.6	450	2	Q51ST3_MAGGR	Q51st3 magnaporthe
95	29	90.6	454	2	Q9A564_CAUCR	Q9a564 caulobacter
96	29	90.6	457	2	Q8UDY9_AGRT5	Q8udy9 agrobacteri
97	29	90.6	462	2	Q6PP77_HUMAN	Q6pp77 homo sapien
98	29	90.6	463	2	Q9FC72_STRCO	Q9fc72 streptomyce
99	29	90.6	468	2	Q8YN54_ANASP	Q8yn54 anabaena sp
100	29	90.6	478	2	Q88ZA9_LACPL	Q88za9 lactobacill
101	29	90.6	478	2	Q6GCK6_STAAS	Q6gck6 staphylococ
102	29	90.6	478	2	Q6GK45_STAAR	Q6gk45 staphylococ
103	29	90.6	478	2	Q5HJB0_STAAC	Q5hjb0 staphylococ
104	29	90.6	478	2	Q7A7T9_STAAN	Q7a7t9 staphylococ

105	29	90.6	478	2	Q8NYG9_STAAW	Q8nyg9	staphylococ
106	29	90.6	478	2	Q99WV9_STAAM	Q99wv9	staphylococ
107	29	90.6	485	1	Y1064_HAEIN	P71367	haemophilus
108	29	90.6	490	2	Q8YPG1_ANASP	Q8ypg1	anabaena sp
109	29	90.6	497	2	Q8H6D6_ORYSA	Q8h6d6	oryza sativ
110	29	90.6	508	2	Q695T4_9ADEN	Q695t4	simian aden
111	29	90.6	527	2	Q87G39_VIBPA	Q87g39	vibrio para
112	29	90.6	535	2	Q4QLM3_HAEI8	Q4qlm3	haemophilus
113	29	90.6	538	2	Q7W9P3_BORPA	Q7w9p3	bordetella
114	29	90.6	538	2	Q7WH14_BORBR	Q7wh14	bordetella
115	29	90.6	556	2	Q7N5F9_PHOLL	Q7n5f9	photorhabdu
116	29	90.6	558	2	Q7VWD3_BORPE	Q7vwd3	bordetella
117	29	90.6	570	2	Q4P564_USTMA	Q4p564	ustilago ma
118	29	90.6	571	1	Y1355_METJA	Q58750	methanococc
119	29	90.6	587	2	O00904_LEIMA	O00904	leishmania
120	29	90.6	588	2	Q4NZG9_9DELT	Q4nzg9	anaeromyxob
121	29	90.6	618	2	Q51LS2_MAGGR	Q51ls2	magnaporthe
122	29	90.6	635	2	Q9SZR9_ARATH	Q9szr9	arabidopsis
123	29	90.6	657	2	Q9FL52_ARATH	Q9fl52	arabidopsis
124	29	90.6	664	2	Q4P9Z4_USTMA	Q4p9z4	ustilago ma
125	29	90.6	680	2	Q55YS8_CRYNE	Q55ys8	cryptococcu
126	29	90.6	680	2	Q5KN48_CRYNE	Q5kn48	cryptococcu
127	29	90.6	753	2	Q93107_ACACA	Q93107	acanthamoeb
128	29	90.6	769	2	Q5L981_BACFN	Q51981	bacteroides
129	29	90.6	769	2	Q64PE2_BACFR	Q64pe2	bacteroides
130	29	90.6	790	2	Q6MJQ8_BDEBA	Q6mjq8	bdellovibri
131	29	90.6	796	2	Q6FLH0_CANGA	Q6flh0	candida gla
132	29	90.6	895	2	Q4LGZ5_9BURK	Q4lgz5	burkholderi
133	29	90.6	1015	2	Q7S2T3_NEUCR	Q7s2t3	neurospora
134	29	90.6	1057	2	Q18331_CAEEL	Q18331	caenorhabdi
135	29	90.6	1066	2	Q614J7_CAEBR	Q614j7	caenorhabdi
136	29	90.6	1105	2	Q7PM11_ANOGA	Q7pml1	anopheles g
137	29	90.6	1112	2	O93787_RHIOL	O93787	rhizopus ol
138	29	90.6	1116	2	Q8A2N4_BACTN	Q8a2n4	bacteroides
139	29	90.6	1219	2	Q4I760_GIBZE	Q4i760	gibberella
140	29	90.6	1221	2	Q52E44_MAGGR	Q52e44	magnaporthe
141	29	90.6	1270	2	Q8D679_VIBVU	Q8d679	vibrio vuln
142	29	90.6	1279	2	Q7RYN3_NEUCR	Q7ryn3	neurospora
143	29	90.6	1369	1	MSH5_CAEEL	Q19272	caenorhabdi
144	29	90.6	1400	2	Q7JKH2_CAEEL	Q7jkh2	caenorhabdi
145	29	90.6	1419	2	Q56EE3_9CAUD	Q56ee3	aeromonas p
146	29	90.6	1420	2	Q6U981_9CAUD	Q6u981	bacteriopha
147	29	90.6	1424	2	Q61P83_CAEBR	Q61p83	caenorhabdi
148	29	90.6	1427	2	O62170_CAEEL	O62170	caenorhabdi
149	29	90.6	1464	2	Q6PCK2_XENLA	Q6pck2	xenopus lae
150	29	90.6	1526	2	Q9VVK6_DROME	Q9vvk6	drosophila
151	29	90.6	1600	2	Q4WRB4_ASPFU	Q4wrb4	aspergillus
152	29	90.6	1625	2	Q9V912_DROME	Q9v912	drosophila
153	29	90.6	1665	2	Q8MLK5_DROME	Q8mlk5	drosophila
154	29	90.6	1677	2	Q6XBG1_MOUSE	Q6xbg1	mus musculu
155	29	90.6	1764	2	Q8MUA3_STRPU	Q8mua3	strongyloce
156	29	90.6	1802	2	Q17163_BRUMA	Q17163	brugia mala
157	28	87.5	49	2	Q6PK47_HUMAN	Q6pk47	homo sapien
158	28	87.5	49	2	Q8JJW5_9CLOS	Q8jjw5	sweet potat
159	28	87.5	56	2	Q9JQR1_NEIMA	Q9jqr1	neisseria m
160	28	87.5	56	2	Q7DD82_NEIMB	Q7dd82	neisseria m
161	28	87.5	60	2	Q88YV5_LACPL	Q88yv5	lactobacill
162	28	87.5	74	2	Q5BTE5_SCHJA	Q5bte5	schistosoma
163	28	87.5	95	2	Q9ULB6_HUMAN	Q9ulb6	homo sapien
164	28	87.5	104	2	Q5FBY4_HUMAN	Q5fby4	homo sapien
165	28	87.5	104	2	Q9J510_FOWPV	Q9j510	fowlpox vir
166	28	87.5	104	2	Q70GT7_FOWPV	Q70gt7	fowlpox vir
167	28	87.5	121	2	Q8SCP1_9CAUD	Q8scp1	pseudomonas
168	28	87.5	134	2	Q4SG49_TETNG	Q4sg49	tetraodon n
169	28	87.5	135	2	Q5FVX5_XENTR	Q5fvx5	xenopus tro
170	28	87.5	139	1	VG39_BPML5	Q05249	mycobacteri
171	28	87.5	139	2	Q50LL6_ENTHI	Q50ll6	entamoeba h
172	28	87.5	141	2	Q5SJP1_THET8	Q5sjp1	thermus the
173	28	87.5	141	2	Q72K15_THET2	Q72k15	thermus the
174	28	87.5	144	2	Q8QNJ4_9PHYC	Q8qnj4	ectocarpus
175	28	87.5	151	2	Q9ETF6_ECOLI	Q9etf6	escherichia
176	28	87.5	151	2	Q9ETF7_ECOLI	Q9etf7	escherichia
177	28	87.5	151	2	Q9F143_ECOLI	Q9f143	escherichia
178	28	87.5	154	2	Q9RM01_HELPY	Q9rm01	helicobacte
179	28	87.5	157	2	Q6AD65_LEIXX	Q6ad65	leifsonia x
180	28	87.5	162	2	Q8GAY3_BURST	Q8gay3	burkholderi
181	28	87.5	162	2	Q9AQS3_9BURK	Q9aqs3	burkholderi
182	28	87.5	162	2	Q4LMI7_9BURK	Q4lmi7	burkholderi
183	28	87.5	165	2	Q5TUG6_ANOGA	Q5tug6	anopheles g
184	28	87.5	168	2	Q8SNF7_XIPHE	Q8snf7	xiphophorus
185	28	87.5	168	2	Q8SNI3_XIPHE	Q8sni3	xiphophorus
186	28	87.5	168	2	Q8SNI4_XIPHE	Q8sni4	xiphophorus
187	28	87.5	168	2	Q8SNI5_XIPHE	Q8sni5	xiphophorus
188	28	87.5	168	2	Q8SNI6_XIPHE	Q8sni6	xiphophorus
189	28	87.5	169	2	Q8SNI7_XIPMO	Q8sni7	xiphophorus
190	28	87.5	177	2	Q97M83_CLOAB	Q97m83	clostridium
191	28	87.5	179	2	Q4ZWG0_PSESY	Q4zwg0	pseudomonas
192	28	87.5	179	2	Q81AA9_BACCR	Q81aa9	bacillus ce
193	28	87.5	183	2	Q52DW5_MAGGR	Q52dw5	magnaporthe
194	28	87.5	184	2	Q4Q103_LEIMA	Q4q103	leishmania
195	28	87.5	186	1	YOSH_SCHPO	Q9p7k7	schizosacch
196	28	87.5	187	2	Q8TG38_EXODE	Q8tg38	exophiala d
197	28	87.5	187	2	Q5DBL5_SCHJA	Q5db15	schistosoma
198	28	87.5	188	2	Q6HCL9_BACHK	Q6hcl9	bacillus th
199	28	87.5	189	2	Q82WJ3_NITEU	Q82wj3	nitrosomona
200	28	87.5	194	2	Q6L311_PICTO	Q6l311	picrophilus
201	28	87.5	194	2	Q6J206_BRABE	Q6j206	branchiosto
202	28	87.5	199	2	Q6LNV1_PHOPR	Q6lnv1	photobacter
203	28	87.5	201	2	Q74IZ7_LACJO	Q74iz7	lactobacill
204	28	87.5	202	2	Q9FM12_ARATH	Q9fm12	arabidopsis
205	28	87.5	207	2	Q9HQF9_HALSA	Q9hqf9	halobacteri
206	28	87.5	207	2	Q92UT9_RHIME	Q92ut9	rhizobium m
207	28	87.5	216	2	Q96XB6_SULTO	Q96xb6	sulfolobus
208	28	87.5	223	2	Q6LSQ9_PHOPR	Q6lsq9	photobacter
209	28	87.5	225	2	Q4MNN8_BACCE	Q4mnn8	bacillus ce
210	28	87.5	225	2	Q6HFD0_BACHK	Q6hfd0	bacillus th
211	28	87.5	225	2	Q733F4_BACC1	Q733f4	bacillus ce
212	28	87.5	225	2	Q81Y26_BACAN	Q81y26	bacillus an
213	28	87.5	225	2	Q637F7_BACCZ	Q637f7	bacillus ce
214	28	87.5	229	1	Y3119_METAC	Q8tlb8	methanosarc
215	28	87.5	229	2	Q4X9Q5_PLACH	Q4x9q5	plasmodium
216	28	87.5	243	2	Q7TQM2_MOUSE	Q7tqm2	mus musculu
217	28	87.5	246	2	Q92QS0_RHIME	Q92qs0	rhizobium m
218	28	87.5	249	2	Q9YI30_CARAU	Q9yi30	carassius a
219	28	87.5	251	2	O66277_9SPHN	O66277	porphyrobac
220	28	87.5	253	2	Q6D2L2_ERWCT	Q6d212	erwinia car
221	28	87.5	255	2	Q4IX85_AZOVI	Q4ix85	azotobacter
222	28	87.5	256	2	Q5U2W7_RAT	Q5u2w7	rattus norv
223	28	87.5	262	2	Q9AGV6_CORAM	Q9agv6	corynebacte
224	28	87.5	263	2	Q69A98_RHIME	Q69a98	rhizobium m
225	28	87.5	269	2	Q8VYM8_ARATH	Q8vym8	arabidopsis
226	28	87.5	269	2	Q9FIQ5_ARATH	Q9fiq5	arabidopsis
227	28	87.5	269	2	Q837L9_ENTFA	Q837l9	enterococcu
228	28	87.5	270	2	Q93QI1_9LACT	Q93qi1	lactococcus
229	28	87.5	273	1	MCPT7_MOUSE	Q02844	mus musculu
230	28	87.5	273	1	MCPT7_RAT	P27435	rattus norv
231	28	87.5	273	2	Q6P6W8_RAT	Q6p6w8	rattus norv
232	28	87.5	273	2	Q921N4_MOUSE	Q921n4	mus musculu
233	28	87.5	281	2	Q9M6R4_GOSHI	Q9m6r4	gossypium h
234	28	87.5	282	2	Q5BMS4_9HYPO	Q5bms4	gibberella
235	28	87.5	282	2	Q8BJG2_MOUSE	Q8bjg2	m mus muscu
236	28	87.5	282	2	Q8BXN0_MOUSE	Q8bxn0	mus musculu
237	28	87.5	282	2	Q4FJQ2_MOUSE	Q4fjq2	mus musculu
238	28	87.5	288	1	KLRA2_MOUSE	Q60660	mus musculu
239	28	87.5	288	2	Q8U2S7_PYRFU	Q8u2s7	pyrococcus
240	28	87.5	288	2	Q548T4_MOUSE	Q548t4	mus musculu
241	28	87.5	290	2	Q4XMK1_PLACH	Q4xmk1	plasmodium
242	28	87.5	290	2	Q88EJ6_PSEPK	Q88ej6	pseudomonas
243	28	87.5	291	2	Q88RV9_PSEPK	Q88rv9	pseudomonas
244	28	87.5	294	2	Q5JHZ5_PYRKO	Q5jhz5	pyrococcus
245	28	87.5	295	2	Q8DUF1_STRMU	Q8duf1	streptococc
246	28	87.5	296	2	Q8VIH2_RAT	Q8vih2	rattus norv
247	28	87.5	299	2	Q87F82_XYLFT	Q87f82	xylella fas
248	28	87.5	300	2	Q4UNI4_RICFE	Q4uni4	rickettsia
249	28	87.5	301	1	SCO2_YEAST	P38072	saccharomyc
250	28	87.5	302	2	Q8U7F7_AGRT5	Q8u7f7	agrobacteri

251	28	87.5	305	2	O49685_ARATH	O49685	arabidopsis	324	28	87.5	473	1	RBL1_THIDE	Q56259	thiobacillu		
252	28	87.5	305	2	Q89PN9_BRAJA	Q89pn9	bradyrhizob	325	28	87.5	473	2	O85040_THINE	O85040	thiobacillu		
253	28	87.5	313	2	Q7CV33_AGRT5	Q7cv33	agrobacteri	326	28	87.5	473	2	Q6SH98_9BACT	Q6sh98	uncultured		
254	28	87.5	319	1	OPPB_LACLA	P0a4n7	lactococcus	327	28	87.5	473	2	Q9ZHZ1_THIIN	Q9zhz1	thiobacillu		
255	28	87.5	319	1	OPPB_LACLC	P0a4n8	lactococcus	328	28	87.5	478	2	Q8TL51_METAC	Q8tl51	methanosarc		
256	28	87.5	319	2	Q53DZ7_9LACT	Q53dz7	lactococcus	329	28	87.5	478	2	Q6PI81_HUMAN	Q6pi81	homo sapien		
257	28	87.5	323	2	Q4S9V0_TETNG	Q4s9v0	tetraodon n	330	28	87.5	481	2	Q89GP2_BRAJA	Q89gp2	bradyrhizob		
258	28	87.5	329	2	Q9EX48_STRCO	Q9ex48	streptomyce	331	28	87.5	492	2	Q5UR19_MIMIV	Q5ur19	mimivirus.		
259	28	87.5	329	2	Q8UEU1_AGRT5	Q8ueu1	agrobacteri	332	28	87.5	494	2	Q5AQH4_EMENI	Q5aqh4	aspergillus		
260	28	87.5	333	2	Q9PH76_XYLFA	Q9ph76	xylella fas	333	28	87.5	495	2	Q7NR94_CHRVO	Q7nr94	chromobacte		
261	28	87.5	346	2	Q4LZA8_9BURK	Q4lza8	burkholderi	334	28	87.5	496	2	Q4HAE4_9DEIO	Q4hae4	deinococcus		
262	28	87.5	350	2	Q5ZNU1_9VIRU	Q5znu1	cotesia con	335	28	87.5	499	2	Q6A5J2_PROAC	Q6a5j2	propionibac		
263	28	87.5	352	2	Q4J814_SULAC	Q4j814	sulfolobus	336	28	87.5	502	2	Q626C9_CAEBR	Q626c9	caenorhabdi		
264	28	87.5	355	2	Q55V21_CRYNE	Q55v21	cryptococcu	337	28	87.5	503	2	Q9KJ79_STRMU	Q9kj79	streptococc		
265	28	87.5	355	2	Q5KL62_CRYNE	Q5kl62	cryptococcu	338	28	87.5	507	1	SYFA_HUMAN	Q9y285	homo sapien		
266	28	87.5	362	2	Q86XE7_HUMAN	Q86xe7	homo sapien	339	28	87.5	507	2	Q7X9A9_CAMSI	Q7x9a9	camellia si		
267	28	87.5	364	2	Q5UHC3_SALET	Q5uhc3	salmonella	340	28	87.5	507	2	Q91WR4_MOUSE	Q91wr4	mus musculu		
268	28	87.5	364	2	Q9S5F7_ECOLI	Q9s5f7	escherichia	341	28	87.5	508	2	Q6IBR2_HUMAN	Q6ibr2	homo sapien		
269	28	87.5	364	2	Q7DBF3_ECO57	Q7dbf3	escherichia	342	28	87.5	508	2	Q5RFA2_PONPY	Q5rfa2	pongo pygma		
270	28	87.5	365	2	Q5UHD6_CITFR	Q5uhd6	citrobacter	343	28	87.5	508	2	Q8C0C7_MOUSE	Q8c0c7	m mus muscu		
271	28	87.5	366	2	Q615K2_CAEBR	Q615k2	caenorhabdi	344	28	87.5	508	2	Q922S1_MOUSE	Q922s1	mus musculu		
272	28	87.5	366	2	O07849_ECOLI	O07849	escherichia	345	28	87.5	508	2	Q505J8_RAT	Q505j8	rattus norv		
273	28	87.5	366	2	Q7ACQ1_ECO57	Q7acq1	escherichia	346	28	87.5	510	2	Q87T83_VIBPA	Q87t83	vibrio para		
274	28	87.5	368	2	Q4LED1_9CREN	Q4led1	uncultured	347	28	87.5	513	2	Q5WZR4_LEGPL	Q5wzr4	legionella		
275	28	87.5	369	2	Q5U3K4_MOUSE	Q5u3k4	mus musculu	348	28	87.5	513	2	Q5ZYU6_LEGPH	Q5zyu6	legionella		
276	28	87.5	371	2	Q83D30_COXBU	Q83d30	coxiella bu	349	28	87.5	515	1	C13A2_CAEEL	Q27518	caenorhabdi		
277	28	87.5	373	2	Q5FMK1_LACAC	Q5fmk1	lactobacill	350	28	87.5	515	2	Q5X8B4_LEGPA	Q5x8b4	legionella		
278	28	87.5	380	1	I13R2_HUMAN	Q14627	homo sapien	351	28	87.5	515	2	Q8ZKK1_SALTY	Q8zkk1	salmonella		
279	28	87.5	385	2	Q98K94_RHILO	Q98k94	rhizobium l	352	28	87.5	516	2	Q7N2R5_PHOLL	Q7n2r5	photorhabdu		
280	28	87.5	387	2	Q6EBW0_TRIIF	Q6ebw0	triatoma in	353	28	87.5	517	2	O64882_ARATH	O64882	arabidopsis		
281	28	87.5	392	2	Q9LUP5_ARATH	Q9lup5	arabidopsis	354	28	87.5	517	2	Q8GY78_ARATH	Q8gy78	arabidopsis		
282	28	87.5	395	2	Q6M689_CORGL	Q6m689	corynebacte	355	28	87.5	519	1	Y1005_HAEIN	P44974	haemophilus		
283	28	87.5	395	2	Q8NRH2_CORGL	Q8nrh2	corynebacte	356	28	87.5	519	2	Q5LDD2_BACFN	Q5ldd2	bacteroides		
284	28	87.5	397	2	Q4KC58_PSEF5	Q4kc58	pseudomonas	357	28	87.5	519	2	Q4QLQ7_HAEI8	Q4qlq7	haemophilus		
285	28	87.5	399	2	Q7QQA5_GIALA	Q7qqa5	giardia lam	358	28	87.5	519	2	Q64UF6_BACFR	Q64uf6	bacteroides		
286	28	87.5	399	2	Q8FQI6_COREF	Q8fqi6	corynebacte	359	28	87.5	519	2	Q65R72_MANSM	Q65r72	mannheimia		
287	28	87.5	401	1	MDTH_CANBF	Q7vqx5	candidatus	360	28	87.5	524	2	Q51WG5_MAGGR	Q51wg5	magnaporthe		
288	28	87.5	406	2	Q8IQ54_DROME	Q8iq54	drosophila	361	28	87.5	526	2	Q7UJB1_RHOBA	Q7ujb1	rhodopirell		
289	28	87.5	407	2	Q6MDT1_PARUW	Q6mdt1	parachlamyd	362	28	87.5	528	2	Q9M9X7_ARATH	Q9m9x7	arabidopsis		
290	28	87.5	408	2	Q9FGP1_ARATH	Q9fgp1	arabidopsis	363	28	87.5	528	2	Q8KLM4_STRTO	Q8klm4	streptomyce		
291	28	87.5	415	2	Q6C132_YARLI	Q6c132	yarrowia li	364	28	87.5	542	2	Q89ZH2_BACTN	Q89zh2	bacteroides		
292	28	87.5	419	2	Q6CHC7_YARLI	Q6chc7	yarrowia li	365	28	87.5	544	2	Q9N3Q7_CAEEL	Q9n3q7	caenorhabdi		
293	28	87.5	426	2	Q4H5E1_9DEIO	Q4h5e1	deinococcus	366	28	87.5	555	2	Q8KIV8_BACTI	Q8kiv8	bacillus th		
294	28	87.5	426	2	Q87Q13_VIBPA	Q87q13	vibrio para	367	28	87.5	562	2	Q55X35_CRYNE	Q55x35	cryptococcu		
295	28	87.5	432	2	Q4UEI0_THEAN	Q4uei0	theileria a	368	28	87.5	562	2	Q5KMU7_CRYNE	Q5kmu7	cryptococcu		
296	28	87.5	434	2	Q5BHW3_DROME	Q5bhw3	drosophila	369	28	87.5	562	2	Q8BJF3_MOUSE	Q8bjf3	mus musculu		
297	28	87.5	436	2	Q5BBM4_EMENI	Q5bbm4	aspergillus	370	28	87.5	562	2	Q5FWY0_MOUSE	Q5fwy0	mus musculu		
298	28	87.5	436	2	Q5LKW0_SILPO	Q5lkw0	silicibacte	371	28	87.5	563	2	Q88NT6_PSEPK	Q88nt6	pseudomonas		
299	28	87.5	438	2	Q9M5U3_CAPAN	Q9m5u3	capsicum an	372	28	87.5	565	1	ZN512_MACFA	Q95jv5	macaca fasc		
300	28	87.5	446	2	Q5WPB8_9DIPT	Q5wpb8	dermatobia	373	28	87.5	566	2	Q55TV8_CRYNE	Q55tv8	cryptococcu		
301	28	87.5	446	2	Q9B2I8_9DIPT	Q9b2i8	chrysomya p	374	28	87.5	566	2	Q5KIH9_CRYNE	Q5kih9	cryptococcu		
302	28	87.5	446	2	Q9MFP2_COLHO	Q9mfp2	cochliomyia	375	28	87.5	567	1	ZN512_HUMAN	Q96me7	homo sapien		
303	28	87.5	447	2	Q9XEM2_ORYSA	Q9xem2	oryza sativ	376	28	87.5	567	2	Q53RZ7_HUMAN	Q53rz7	homo sapien		
304	28	87.5	448	2	Q583Q1_9TRYP	Q583q1	trypanosoma	377	28	87.5	575	2	Q5LH65_BACFN	Q5lh65	bacteroides		
305	28	87.5	448	2	Q9LZV3_ARATH	Q9lzv3	arabidopsis	378	28	87.5	586	2	Q4HYM7_GIBZE	Q4hym7	gibberella		
306	28	87.5	452	2	Q6NB47_RHOPA	Q6nb47	rhodopseudo	379	28	87.5	587	2	Q64Y25_BACFR	Q64y25	bacteroides		
307	28	87.5	452	2	Q89VH5_BRAJA	Q89vh5	bradyrhizob	380	28	87.5	590	2	Q4SRY9_TETNG	Q4sry9	tetraodon n		
308	28	87.5	457	2	Q59SI6_CANAL	Q59si6	candida alb	381	28	87.5	591	2	Q69Z99_MOUSE	Q69z99	mus musculu		
309	28	87.5	457	2	Q73QT2_TREDE	Q73qt2	treponema d	382	28	87.5	594	2	Q61YE7_CAEBR	Q61ye7	caenorhabdi		
310	28	87.5	457	2	Q8YTA3_ANASP	Q8yta3	anabaena sp	383	28	87.5	595	2	O45934_CAEEL	O45934	caenorhabdi		
311	28	87.5	459	2	Q5GH77_HUMAN	Q5gh77	homo sapien	384	28	87.5	609	2	Q9C8W6_ARATH	Q9c8w6	arabidopsis		
312	28	87.5	459	2	Q8N7E1_HUMAN	Q8n7e1	homo sapien	385	28	87.5	613	2	Q87MT8_VIBPA	Q87mt8	vibrio para		
313	28	87.5	459	2	Q52PG8_HUMAN	Q52pg8	homo sapien	386	28	87.5	624	2	Q9K5T7_BACHD	Q9k5t7	bacillus ha		
314	28	87.5	459	2	O41926_MHV68	O41926	murid herpe	387	28	87.5	631	2	Q4ILB6_GIBZE	Q4ilb6	gibberella		
315	28	87.5	462	2	Q89Z38_BACTN	Q89z38	bacteroides	388	28	87.5	631	2	Q8A1H8_BACTN	Q8a1h8	bacteroides		
316	28	87.5	468	2	O55279_ADEGX	O55279	avian adeno	389	28	87.5	634	2	Q9VQP3_DROME	Q9vqp3	drosophila		
317	28	87.5	470	2	Q6PJA4_HUMAN	Q6pja4	homo sapien	390	28	87.5	647	2	Q8PXU3_METMA	Q8pxu3	methanosarc		
318	28	87.5	471	1	RBL1_CHRVI	P22849	chromatium	391	28	87.5	648	1	BGLR_MOUSE	P12265	mus musculu		
319	28	87.5	471	1	RBL_ALVHS	P24672	alvinoconch	392	28	87.5	648	2	Q8THR3_METAC	Q8thr3	methanosarc		
320	28	87.5	472	1	RBL1_HYDMR	Q59458	hydrogenovi	393	28	87.5	648	2	Q6IR10_MOUSE	Q6ir10	mus musculu		
321	28	87.5	472	2	Q9FFU7_ARATH	Q9ffu7	arabidopsis	394	28	87.5	650	2	Q8Z635_SALTI	Q8z635	salmonella		
322	28	87.5	472	2	Q75W45_HYDMR	Q75w45	hydrogenovi	395	28	87.5	650	2	Q57LB0_SALCH	Q57lb0	salmonella		
323	28	87.5	472	2	Q673V5_9GAMM	Q673v5	solemya vel	396	28	87.5	651	2	Q6MTX4_MYCMS	Q6mtx4	mycoplasma		

397	28	87.5	653	2	Q6G1I6_BARQU	Q6g1i6 bartonella
398	28	87.5	654	2	Q6FZY0_BARQU	Q6fzy0 bartonella
399	28	87.5	654	2	Q6G399_BARHE	Q6g399 bartonella
400	28	87.5	657	2	Q872Z1_NEUCR	Q872z1 neurospora
401	28	87.5	657	2	Q98KR7_RHILO	Q98kr7 rhizobium l
402	28	87.5	661	2	Q57DU0_BRUAB	Q57du0 brucella ab
403	28	87.5	661	2	Q8G1A6_BRUSU	Q8g1a6 brucella su
404	28	87.5	661	2	Q8YGL1_BRUME	Q8ygl1 brucella me
405	28	87.5	662	2	Q84TH5_ARATH	Q84th5 arabidopsis
406	28	87.5	662	2	Q949Y4_ARATH	Q949y4 arabidopsis
407	28	87.5	662	2	Q8Z7U3_SALTI	Q8z7u3 salmonella
408	28	87.5	664	2	Q92QP1_RHIME	Q92qp1 rhizobium m
409	28	87.5	672	2	Q9LI82_ARATH	Q9li82 arabidopsis
410	28	87.5	683	2	O83436_TREPA	O83436 treponema p
411	28	87.5	685	2	Q4Q937_LEIMA	Q4q937 leishmania
412	28	87.5	692	2	Q6UEH6_GALME	Q6ueh6 galleria me
413	28	87.5	693	2	Q9BLG6_BOMMO	Q9blg6 bombyx mori
414	28	87.5	694	2	Q65X41_ORYSA	Q65x41 oryza sativ
415	28	87.5	697	2	O76208_HYPCU	O76208 hyphantria
416	28	87.5	698	2	Q8B4P9_9VIRU	Q8b4p9 myzus persi
417	28	87.5	700	2	Q75HT8_ORYSA	Q75ht8 oryza sativ
418	28	87.5	706	2	Q5SUD9_MOUSE	Q5sud9 mus musculu
419	28	87.5	709	2	Q628K8_CAEBR	Q628k8 caenorhabdi
420	28	87.5	715	2	Q8Z0B6_ANASP	Q8z0b6 anabaena sp
421	28	87.5	738	2	Q9XEM3_ORYSA	Q9xem3 oryza sativ
422	28	87.5	782	2	Q23054_CAEEL	Q23054 caenorhabdi
423	28	87.5	791	2	Q6D7Q0_ERWCT	Q6d7q0 erwinia car
424	28	87.5	793	2	Q7RW19_NEUCR	Q7rw19 neurospora
425	28	87.5	851	2	Q9U2S3_CAEEL	Q9u2s3 caenorhabdi
426	28	87.5	852	1	SSY1_YEAST	Q03770 saccharomyc
427	28	87.5	854	2	Q9VQP4_DROME	Q9vqp4 drosophila
428	28	87.5	856	2	Q9GZ10_DROME	Q9gz10 drosophila
429	28	87.5	882	2	Q54PA1_DICDI	Q54pa1 dictyosteli
430	28	87.5	897	2	Q7NMZ8_GLOVI	Q7nmz8 gloeobacter
431	28	87.5	907	2	Q6MIL5_BDEBA	Q6mil5 bdellovibri
432	28	87.5	921	2	Q9FN05_ARATH	Q9fn05 arabidopsis
433	28	87.5	929	2	Q67WN0_ORYSA	Q67wn0 oryza sativ
434	28	87.5	931	2	Q4LEE4_9CREN	Q4lee4 uncultured
435	28	87.5	931	2	Q4P968_USTMA	Q4p968 ustilago ma
436	28	87.5	939	2	Q8YQR3_ANASP	Q8yqr3 anabaena sp
437	28	87.5	942	2	O13690_SCHPO	O13690 schizosacch
438	28	87.5	942	2	Q9SL18_ARATH	Q9sl18 arabidopsis
439	28	87.5	951	2	Q4WGB1_ASPFU	Q4wgb1 aspergillus
440	28	87.5	989	2	O80947_ARATH	O80947 arabidopsis
441	28	87.5	1011	2	Q7XHN9_ORYSA	Q7xhn9 oryza sativ
442	28	87.5	1017	2	Q7KU30_DROME	Q7ku30 drosophila
443	28	87.5	1038	2	Q7G6Q3_ORYSA	Q7g6q3 oryza sativ
444	28	87.5	1038	2	Q8RV24_ORYSA	Q8rv24 oryza sativ
445	28	87.5	1040	2	Q8A203_BACTN	Q8a203 bacteroides
446	28	87.5	1062	2	Q50NV1_ENTHI	Q50nv1 entamoeba h
447	28	87.5	1098	2	Q75EP5_ASHGO	Q75ep5 ashbya goss
448	28	87.5	1135	2	Q4WMK2_ASPFU	Q4wmk2 aspergillus
449	28	87.5	1172	2	Q88JL1_PSEPK	Q88jl1 pseudomonas
450	28	87.5	1254	1	DPOG_YEAST	P15801 saccharomyc
451	28	87.5	1284	2	Q6FV24_CANGA	Q6fv24 candida gla
452	28	87.5	1295	2	Q93SV6_CHLTE	Q93sv6 chlorobium
453	28	87.5	1307	2	Q8EV70_MYCPE	Q8ev70 mycoplasma
454	28	87.5	1327	2	Q517E4_ENTHI	Q517e4 entamoeba h
455	28	87.5	1337	2	Q4NAV7_9MICC	Q4nav7 arthrobacte
456	28	87.5	1357	2	Q8I7K7_CAEEL	Q8i7k7 caenorhabdi
457	28	87.5	1413	2	Q9NBD3_CAEEL	Q9nbd3 caenorhabdi
458	28	87.5	1438	2	Q4HWF2_GIBZE	Q4hwf2 gibberella
459	28	87.5	1483	2	Q62AQ9_BURMA	Q62aq9 burkholderi
460	28	87.5	1493	2	Q9N5D3_CAEEL	Q9n5d3 caenorhabdi
461	28	87.5	1526	2	Q19611_CAEEL	Q19611 caenorhabdi
462	28	87.5	1551	2	Q96WN4_VENIN	Q96wn4 venturia in
463	28	87.5	1589	2	Q7S3S0_NEUCR	Q7s3s0 neurospora
464	28	87.5	1702	2	Q95QK2_CAEEL	Q95qk2 caenorhabdi
465	28	87.5	1791	2	Q8ABE6_BACTN	Q8abe6 bacteroides
466	28	87.5	1814	2	Q60WH4_CAEBR	Q60wh4 caenorhabdi
467	28	87.5	1844	2	Q7S6Q1_NEUCR	Q7s6q1 neurospora
468	28	87.5	2210	2	Q4WF61_ASPFU	Q4wf61 aspergillus
469	28	87.5	2255	2	Q7YYS3_CRYPV	Q7yys3 cryptospori
470	28	87.5	2329	2	Q5CK63_CRYHO	Q5ck63 cryptospori
471	28	87.5	2330	2	Q5CWU8_CRYPV	Q5cwu8 cryptospori
472	28	87.5	2611	2	Q4HX44_GIBZE	Q4hx44 gibberella
473	28	87.5	2710	2	Q7R3A9_GIALA	Q7r3a9 giardia lam
474	28	87.5	3291	2	Q63JT0_BURPS	Q63jt0 burkholderi
475	28	87.5	3919	2	Q5CHS8_CRYHO	Q5chs8 cryptospori
476	28	87.5	5145	2	Q4UH33_THEAN	Q4uh33 theileria a
477	28	87.5	11696	2	Q5CV09_CRYPV	Q5cv09 cryptospori
478	27	84.4	18	2	Q4XG73_PLACH	Q4xg73 plasmodium
479	27	84.4	51	2	Q24623_DROPS	Q24623 drosophila
480	27	84.4	65	2	Q4RIX4_TETNG	Q4rix4 tetraodon n
481	27	84.4	67	2	Q9HN48_HALSA	Q9hn48 halobacteri
482	27	84.4	73	2	Q8PR71_XANAC	Q8pr71 xanthomonas
483	27	84.4	79	2	Q5NC26_MOUSE	Q5nc26 mus musculu
484	27	84.4	85	2	Q4V0L3_XANCP	Q4v0l3 xanthomonas
485	27	84.4	85	2	Q8PEB4_XANCP	Q8peb4 xanthomonas
486	27	84.4	89	1	RS16_NITEU	Q82u38 nitrosomona
487	27	84.4	105	2	Q6B715_RABIT	Q6b715 oryctolagus
488	27	84.4	105	2	Q56XS0_ARATH	Q56xs0 arabidopsis
489	27	84.4	108	2	Q59NN5_CANAL	Q59nn5 candida alb
490	27	84.4	108	2	Q7Z4E6_HUMAN	Q7z4e6 homo sapien
491	27	84.4	109	2	Q974A3_SULTO	Q974a3 sulfolobus
492	27	84.4	110	2	Q5DC70_SCHJA	Q5dc70 schistosoma
493	27	84.4	116	1	HV36_MOUSE	P01806 mus musculu
494	27	84.4	117	1	HV41_MOUSE	P01811 mus musculu
495	27	84.4	117	1	HV42_MOUSE	P01812 mus musculu
496	27	84.4	118	1	HV39_MOUSE	P01809 mus musculu
497	27	84.4	119	1	HV37_MOUSE	P01807 mus musculu
498	27	84.4	119	1	HV38_MOUSE	P01808 mus musculu
499	27	84.4	119	1	HV40_MOUSE	P01810 mus musculu
500	27	84.4	141	2	Q4Y0F5_PLACH	Q4y0f5 plasmodium
501	27	84.4	142	2	Q96K88_HUMAN	Q96k88 homo sapien
502	27	84.4	150	2	Q518M5_ENTHI	Q518m5 entamoeba h
503	27	84.4	156	2	Q9LKW3_LYCES	Q9lkw3 lycopersico
504	27	84.4	158	2	Q8GHP4_PSERE	Q8ghp4 pseudomonas
505	27	84.4	159	2	P73696_SYNY3	P73696 synechocyst
506	27	84.4	160	2	Q9Q8W6_9POXV	Q9q8w6 rabbit fibr
507	27	84.4	164	2	Q9Q8I8_9POXV	Q9q8i8 myxoma viru
508	27	84.4	167	2	Q959J2_9CRUS	Q959j2 excirolana
509	27	84.4	173	1	NU6M_LATCH	O03175 latimeria c
510	27	84.4	173	2	Q5DTD2_LATME	Q5dtd2 latimeria m
511	27	84.4	175	2	Q7PZ94_ANOGA	Q7pz94 anopheles g
512	27	84.4	176	2	Q8SEY3_BOMMA	Q8sey3 bombyx mand
513	27	84.4	176	2	Q6JV96_BOMMA	Q6jv96 bombyx mand
514	27	84.4	176	2	Q9MIE4_BOMMO	Q9mie4 bombyx mori
515	27	84.4	176	2	Q6HBU9_BACHK	Q6hbu9 bacillus th
516	27	84.4	176	2	Q632B1_BACCZ	Q632b1 bacillus ce
517	27	84.4	178	2	Q85MU8_ANTPE	Q85mu8 antheraea p
518	27	84.4	178	2	Q4FH05_SAMCR	Q4fh05 samia cynth
519	27	84.4	185	1	APC10_HUMAN	Q9um13 homo sapien
520	27	84.4	185	1	APC10_MOUSE	Q8k2h6 mus musculu
521	27	84.4	185	2	Q8XC52_ECO57	Q8xc52 escherichia
522	27	84.4	185	2	Q5ZL04_CHICK	Q5zl04 gallus gall
523	27	84.4	185	2	Q5EAZ2_XENLA	Q5eaz2 xenopus lae
524	27	84.4	185	2	Q5HZC0_XENLA	Q5hzc0 xenopus lae
525	27	84.4	186	2	Q4T330_TETNG	Q4t330 tetraodon n
526	27	84.4	188	2	Q9W3D8_DROME	Q9w3d8 drosophila
527	27	84.4	189	1	APC10_SCHPO	O42971 schizosacch
528	27	84.4	192	1	APC10_ARATH	Q9zpw2 arabidopsis
529	27	84.4	195	1	APC10_DROME	Q9v831 drosophila
530	27	84.4	196	1	CLPP_STRP3	P69885 streptococc
531	27	84.4	196	1	CLPP_STRP6	Q5xdm4 streptococc
532	27	84.4	196	1	CLPP_STRP8	P69886 streptococc
533	27	84.4	196	1	CLPP_STRPY	P69884 streptococc
534	27	84.4	198	2	Q57TW2_9TRYP	Q57tw2 trypanosoma
535	27	84.4	201	2	Q688U0_ORYSA	Q688u0 oryza sativ
536	27	84.4	202	2	Q95UQ7_BRABE	Q95uq7 branchiosto
537	27	84.4	207	2	Q27449_BRUMA	Q27449 brugia mala
538	27	84.4	212	2	Q86KC1_DICDI	Q86kc1 dictyosteli
539	27	84.4	216	2	Q4J395_AZOVI	Q4j395 azotobacter
540	27	84.4	217	2	Q6Z9I2_ORYSA	Q6z9i2 oryza sativ
541	27	84.4	221	2	Q7T3B3_BRARE	Q7t3b3 brachydanio
542	27	84.4	223	1	CLPP2_GLUOX	Q5fqt4 gluconobact

543	27	84.4	224	2	Q95YN3_HALRO	Q95yn3	halocynthia
544	27	84.4	228	2	Q7RFH8_PLAYO	Q7rfh8	plasmodium
545	27	84.4	229	2	Q4YU41_PLABE	Q4yu41	plasmodium
546	27	84.4	234	2	Q6P084_HUMAN	Q6p084	homo sapien
547	27	84.4	234	2	Q72N12_LEPIC	Q72n12	leptospira
548	27	84.4	234	2	Q8F8L7_LEPIN	Q8f8l7	leptospira
549	27	84.4	238	2	Q82E73_STRAW	Q82e73	streptomyce
550	27	84.4	239	2	Q9XHV6_ORYSA	Q9xhv6	oryza sativ
551	27	84.4	242	2	Q84MJ3_FAGSY	Q84mj3	fagus sylva
552	27	84.4	252	2	Q50ZK4_ENTHI	Q50zk4	entamoeba h
553	27	84.4	254	1	COAT_BCTV	P14984	beet curly
554	27	84.4	254	2	P73626_SYNY3	P73626	synechocyst
555	27	84.4	255	2	O74510_SCHPO	O74510	schizosacch
556	27	84.4	256	2	Q53WN0_ORYSA	Q53wn0	oryza sativ
557	27	84.4	262	2	Q4HYI8_GIBZE	Q4hyi8	gibberella
558	27	84.4	269	2	Q4I3G8_GIBZE	Q4i3g8	gibberella
559	27	84.4	270	2	Q53QL9_HUMAN	Q53ql9	homo sapien
560	27	84.4	270	2	Q833E0_ENTFA	Q833e0	enterococcu
561	27	84.4	274	2	Q6MJR0_BDEBA	Q6mjr0	bdellovibri
562	27	84.4	278	2	Q5P559_AZOSE	Q5p559	azoarcus sp
563	27	84.4	285	2	Q88W52_LACPL	Q88w52	lactobacill
564	27	84.4	286	2	O42290_CHICK	O42290	gallus gall
565	27	84.4	286	2	O57342_COTJA	O57342	coturnix co
566	27	84.4	286	2	Q8AWH8_CHICK	Q8awh8	gallus gall
567	27	84.4	289	2	Q4U1U2_XENTR	Q4u1u2	xenopus tro
568	27	84.4	290	2	Q66KH3_XENLA	Q66kh3	xenopus lae
569	27	84.4	297	2	Q8BJG7_MOUSE	Q8bjg7	mus musculu
570	27	84.4	299	2	Q9KBM0_BACHD	Q9kbm0	bacillus ha
571	27	84.4	301	2	Q9HXT0_PSEAE	Q9hxt0	pseudomonas
572	27	84.4	304	2	Q579G9_BRUAB	Q579g9	brucella ab
573	27	84.4	304	2	Q8FV94_BRUSU	Q8fv94	brucella su
574	27	84.4	306	1	HTPX_BIFLO	Q8g6t7	bifidobacte
575	27	84.4	308	2	Q6BZC4_DEBHA	Q6bzc4	debaryomyce
576	27	84.4	312	2	Q9G7W2_9ARAC	Q9g7w2	hypochilus
577	27	84.4	313	2	Q6DE84_XENLA	Q6de84	xenopus lae
578	27	84.4	313	2	Q9PUA6_XENLA	Q9pua6	xenopus lae
579	27	84.4	315	2	Q4ZSV1_PSESY	Q4zsv1	pseudomonas
580	27	84.4	316	2	Q4IY61_AZOVI	Q4iy61	azotobacter
581	27	84.4	316	2	Q4KFN2_PSEF5	Q4kfn2	pseudomonas
582	27	84.4	316	2	Q4KDQ7_PSEF5	Q4kdq7	pseudomonas
583	27	84.4	316	2	Q88JG2_PSEPK	Q88jg2	pseudomonas
584	27	84.4	316	2	Q8YD32_BRUME	Q8yd32	brucella me
585	27	84.4	317	2	Q9I306_PSEAE	Q9i306	pseudomonas
586	27	84.4	322	2	Q4IIQ2_GIBZE	Q4iiq2	gibberella
587	27	84.4	322	2	Q83F54_COXBU	Q83f54	coxiella bu
588	27	84.4	322	2	Q606G0_METCA	Q606g0	methylococc
589	27	84.4	324	2	Q54MS5_DICDI	Q54ms5	dictyosteli
590	27	84.4	325	2	Q8VQ45_ECOLI	Q8vq45	escherichia
591	27	84.4	327	2	Q9I8Z6_BRARE	Q9i8z6	brachydanio
592	27	84.4	333	2	Q8QRY0_9BETA	Q8qry0	pongine her
593	27	84.4	340	2	Q9G7V2_9ARAC	Q9g7v2	hypochilus
594	27	84.4	340	2	Q9G7V4_9ARAC	Q9g7v4	hypochilus
595	27	84.4	341	2	Q9G7V6_9ARAC	Q9g7v6	hypochilus
596	27	84.4	341	2	Q9G7V9_9ARAC	Q9g7v9	hypochilus
597	27	84.4	341	2	Q4TCX7_TETNG	Q4tcx7	tetraodon n
598	27	84.4	343	2	Q5RZ66_CRYNV	Q5rz66	cryptococcu
599	27	84.4	346	2	Q54MS8_DICDI	Q54ms8	dictyosteli
600	27	84.4	346	2	Q4U1U0_XENTR	Q4u1u0	xenopus tro
601	27	84.4	348	2	Q7UKP4_RHOBA	Q7ukp4	rhodopirell
602	27	84.4	349	2	Q6WC31_9ARAC	Q6wc31	sarinda sp.
603	27	84.4	349	2	Q9G7V1_9ARAC	Q9g7v1	hypochilus
604	27	84.4	349	2	Q9G7V5_9ARAC	Q9g7v5	hypochilus
605	27	84.4	349	2	Q9G7V7_9ARAC	Q9g7v7	hypochilus
606	27	84.4	349	2	Q9G7W1_9ARAC	Q9g7w1	hypochilus
607	27	84.4	349	2	Q9G7W3_9ARAC	Q9g7w3	hypochilus
608	27	84.4	351	2	Q4P800_USTMA	Q4p800	ustilago ma
609	27	84.4	352	2	Q8NHW3_HUMAN	Q8nhw3	homo sapien
610	27	84.4	352	2	Q7U2L8_MYCBO	Q7u2l8	mycobacteri
611	27	84.4	359	2	Q8CF90_MOUSE	Q8cf90	mus musculu
612	27	84.4	362	2	Q6FFE4_ACIAD	Q6ffe4	acinetobact
613	27	84.4	363	2	Q44878_PRERU	Q44878	prevotella
614	27	84.4	363	2	Q7N967_PHOLL	Q7n967	photorhabdu
615	27	84.4	366	2	Q8VKQ1_MYCTU	Q8vkq1	mycobacteri
616	27	84.4	366	2	O07436_MYCTU	O07436	mycobacteri
617	27	84.4	367	2	Q93NG6_ARTNI	Q93ng6	arthrobacte
618	27	84.4	369	2	Q4IDN0_GIBZE	Q4idn0	gibberella
619	27	84.4	371	2	Q5KFM3_CRYNE	Q5kfm3	cryptococcu
620	27	84.4	371	2	Q55QJ3_CRYNE	Q55qj3	cryptococcu
621	27	84.4	374	2	Q620H3_CAEBR	Q620h3	caenorhabdi
622	27	84.4	375	2	Q87KF5_VIBPA	Q87kf5	vibrio para
623	27	84.4	377	2	Q8AWR8_9TELE	Q8awr8	pollimyrus
624	27	84.4	377	2	Q9I867_9TELE	Q9i867	campylomorm
625	27	84.4	377	2	Q9IAD5_9TELE	Q9iad5	stomatorhin
626	27	84.4	377	2	Q9IAD6_9TELE	Q9iad6	stomatorhin
627	27	84.4	377	2	Q9IAD7_9TELE	Q9iad7	stomatorhin
628	27	84.4	377	2	Q9IAD8_9TELE	Q9iad8	stomatorhin
629	27	84.4	377	2	Q9IAD9_9TELE	Q9iad9	pollimyrus
630	27	84.4	377	2	Q9IAE0_9TELE	Q9iae0	pollimyrus
631	27	84.4	377	2	Q9IAE1_9TELE	Q9iae1	pollimyrus
632	27	84.4	377	2	Q9IAE6_9TELE	Q9iae6	paramormyro
633	27	84.4	377	2	Q9IAE9_9TELE	Q9iae9	mormyrus ru
634	27	84.4	377	2	Q9IAF0_9TELE	Q9iaf0	mormyrus ov
635	27	84.4	377	2	Q9IAF4_9TELE	Q9iaf4	marcusenius
636	27	84.4	377	2	Q9IAF5_9TELE	Q9iaf5	marcusenius
637	27	84.4	377	2	Q9IAF6_9TELE	Q9iaf6	marcusenius
638	27	84.4	377	2	Q9IAF7_9TELE	Q9iaf7	marcusenius
639	27	84.4	377	2	Q9IAF8_9TELE	Q9iaf8	marcusenius
640	27	84.4	377	2	Q9IAF9_9TELE	Q9iaf9	ivindomyrus
641	27	84.4	377	2	Q9IAG1_9TELE	Q9iag1	hyperopisus
642	27	84.4	377	2	Q9IAG2_9TELE	Q9iag2	hippopotamy
643	27	84.4	377	2	Q9IAG3_9TELE	Q9iag3	hippopotamy
644	27	84.4	377	2	Q9IAG4_9TELE	Q9iag4	hippopotamy
645	27	84.4	377	2	Q9IAG6_9TELE	Q9iag6	gnathonemus
646	27	84.4	377	2	Q9IAG7_9TELE	Q9iag7	genyomyrus
647	27	84.4	377	2	Q9IAG9_9TELE	Q9iag9	campylomorm
648	27	84.4	377	2	Q9IAH0_9TELE	Q9iah0	campylomorm
649	27	84.4	377	2	Q9IAH1_9TELE	Q9iah1	brienomyrus
650	27	84.4	377	2	Q9IAH2_9TELE	Q9iah2	brienomyrus
651	27	84.4	377	2	Q9IAH3_9TELE	Q9iah3	brienomyrus
652	27	84.4	377	2	Q9IAH4_9TELE	Q9iah4	brienomyrus
653	27	84.4	377	2	Q9IAH6_9TELE	Q9iah6	boulengerom
654	27	84.4	382	2	Q9N3M5_CAEEL	Q9n3m5	caenorhabdi
655	27	84.4	386	2	Q9U2Q3_CAEEL	Q9u2q3	caenorhabdi
656	27	84.4	395	2	Q4NHC4_9MICC	Q4nhc4	arthrobacte
657	27	84.4	396	2	Q9HKT4_THEAC	Q9hkt4	thermoplasm
658	27	84.4	396	2	Q7SY78_XENLA	Q7sy78	xenopus lae
659	27	84.4	397	2	Q8MZA1_DROME	Q8mza1	drosophila
660	27	84.4	399	2	Q6BRL7_DEBHA	Q6brl7	debaryomyce
661	27	84.4	400	2	Q6BNL8_DEBHA	Q6bnl8	debaryomyce
662	27	84.4	403	2	Q60CF5_METCA	Q60cf5	methylococc
663	27	84.4	411	2	Q8DAA2_VIBVU	Q8daa2	vibrio vuln
664	27	84.4	411	2	Q7MJX1_VIBVY	Q7mjx1	vibrio vuln
665	27	84.4	413	2	Q73WJ4_MYCPA	Q73wj4	mycobacteri
666	27	84.4	414	2	O06577_MYCTU	O06577	mycobacteri
667	27	84.4	414	2	Q7U0L4_MYCBO	Q7u0l4	mycobacteri
668	27	84.4	416	2	Q7RN32_PLAYO	Q7rn32	plasmodium
669	27	84.4	417	2	Q72YT8_BACC1	Q72yt8	bacillus ce
670	27	84.4	419	2	Q9SVT7_ARATH	Q9svt7	arabidopsis
671	27	84.4	419	2	Q89M23_BRAJA	Q89m23	bradyrhizob
672	27	84.4	420	2	Q7NGH0_GLOVI	Q7ngh0	gloeobacter
673	27	84.4	422	2	Q4SZ36_TETNG	Q4sz36	tetraodon n
674	27	84.4	423	1	TTLL1_HUMAN	O95922	homo sapien
675	27	84.4	423	1	TTLL1_MOUSE	Q91v51	mus musculu
676	27	84.4	423	2	Q8NC32_HUMAN	Q8nc32	homo sapien
677	27	84.4	423	2	Q543S4_MOUSE	Q543s4	mus musculu
678	27	84.4	423	2	Q5PPI9_RAT	Q5ppi9	rattus norv
679	27	84.4	424	2	Q5K860_CRYNE	Q5k860	cryptococcu
680	27	84.4	426	2	Q9XWL8_CAEEL	Q9xwl8	caenorhabdi
681	27	84.4	427	2	Q9ZP18_IPOBA	Q9zp18	ipomoea bat
682	27	84.4	431	2	Q4LYS4_9BURK	Q4lys4	burkholderi
683	27	84.4	437	2	Q4WB17_ASPFU	Q4wb17	aspergillus
684	27	84.4	439	2	Q8S3C1_9STRA	Q8s3c1	thraustochy
685	27	84.4	440	2	Q63KE2_BURPS	Q63ke2	burkholderi
686	27	84.4	442	2	Q5KPW8_CRYNE	Q5kpw8	cryptococcu
687	27	84.4	442	2	Q5WIT3_BACSK	Q5wit3	bacillus cl
688	27	84.4	444	1	CIT1_KLEPN	P16482	klebsiella

689	27	84.4	446	2	Q97XL4_SULSO	Q97xl4	sulfolobus
690	27	84.4	446	2	Q560W7_CRYNE	Q560w7	cryptococcu
691	27	84.4	446	2	Q4SA93_TETNG	Q4sa93	tetraodon n
692	27	84.4	458	2	Q92PD7_RHIME	Q92pd7	rhizobium m
693	27	84.4	459	2	Q61QU7_CAEBR	Q61qu7	caenorhabdi
694	27	84.4	459	2	Q8KF21_CHLTE	Q8kf21	chlorobium
695	27	84.4	461	2	Q749B5_GEOSL	Q749b5	geobacter s
696	27	84.4	461	2	Q7N4D3_PHOLL	Q7n4d3	photorhabdu
697	27	84.4	462	2	Q8TIS6_METAC	Q8tis6	methanosarc
698	27	84.4	464	2	Q8PYK9_METMA	Q8pyk9	methanosarc
699	27	84.4	464	2	Q6AKR1_DESPS	Q6akr1	desulfotale
700	27	84.4	465	2	Q6P6C4_HUMAN	Q6p6c4	homo sapien
701	27	84.4	465	2	Q9LR73_ARATH	Q9lr73	arabidopsis
702	27	84.4	465	2	Q8A7R9_BACTN	Q8a7r9	bacteroides
703	27	84.4	467	2	Q55IM0_CRYNE	Q55im0	cryptococcu
704	27	84.4	467	2	Q4KD66_PSEF5	Q4kd66	pseudomonas
705	27	84.4	468	2	Q88GJ5_PSEPK	Q88gj5	pseudomonas
706	27	84.4	469	2	Q9ZWB4_ARATH	Q9zwb4	arabidopsis
707	27	84.4	469	2	Q62D94_BURMA	Q62d94	burkholderi
708	27	84.4	470	2	Q4N513_THEPA	Q4n513	theileria p
709	27	84.4	470	2	Q28464_MONDO	Q28464	monodelphis
710	27	84.4	470	2	Q9HUI4_PSEAE	Q9hui4	pseudomonas
711	27	84.4	474	2	Q6P8D8_XENTR	Q6p8d8	xenopus tro
712	27	84.4	481	2	Q7Q9T5_ANOGA	Q7q9t5	anopheles g
713	27	84.4	485	2	Q54JG7_DICDI	Q54jg7	dictyosteli
714	27	84.4	489	2	Q4KT08_9NUCL	Q4kt08	chrysodeixi
715	27	84.4	491	2	Q6A5H4_PROAC	Q6a5h4	propionibac
716	27	84.4	493	2	Q5A4L3_CANAL	Q5a413	candida alb
717	27	84.4	493	2	Q9LYK2_ARATH	Q9lyk2	arabidopsis
718	27	84.4	498	2	Q6CL55_KLULA	Q6cl55	kluyveromyc
719	27	84.4	502	2	P93082_CAMAC	P93082	camptotheca
720	27	84.4	506	2	Q9XEG4_HORVU	Q9xeg4	hordeum vul
721	27	84.4	507	2	P93182_HORVU	P93182	hordeum vul
722	27	84.4	507	2	Q940R8_WHEAT	Q940r8	triticum ae
723	27	84.4	507	2	Q9ATG9_WHEAT	Q9atg9	triticum ae
724	27	84.4	507	2	Q9FYU4_WHEAT	Q9fyu4	triticum ae
725	27	84.4	507	2	Q9XEG5_HORVU	Q9xeg5	hordeum vul
726	27	84.4	509	2	Q8TVT3_METKA	Q8tvt3	methanopyru
727	27	84.4	509	2	P93183_HORVU	P93183	hordeum vul
728	27	84.4	510	1	YJY5_YEAST	P47090	saccharomyc
729	27	84.4	510	2	Q66R65_YEAST	Q66r65	saccharomyc
730	27	84.4	516	2	Q8F2W4_LEPIN	Q8f2w4	leptospira
731	27	84.4	516	2	Q72SP0_LEPIC	Q72sp0	leptospira
732	27	84.4	516	2	Q7SYI9_BRARE	Q7syi9	brachydanio
733	27	84.4	517	2	Q5KDT4_CRYNE	Q5kdt4	cryptococcu
734	27	84.4	517	2	Q55PM2_CRYNE	Q55pm2	cryptococcu
735	27	84.4	517	2	Q98523_CHVP1	Q98523	paramecium
736	27	84.4	520	2	Q4TAR0_TETNG	Q4tar0	tetraodon n
737	27	84.4	521	1	PHLB_MYCTU	P95246	mycobacteri
738	27	84.4	521	2	Q96Z01_SULTO	Q96z01	sulfolobus
739	27	84.4	522	2	Q5T7C7_HUMAN	Q5t7c7	homo sapien
740	27	84.4	522	2	O82412_ARATH	O82412	arabidopsis
741	27	84.4	522	2	Q9LMZ9_ARATH	Q9lmz9	arabidopsis
742	27	84.4	523	2	Q84LK4_PHRAU	Q841k4	phragmites
743	27	84.4	524	2	Q4WHM9_ASPFU	Q4whm9	aspergillus
744	27	84.4	524	2	Q84VI9_MAIZE	Q84vi9	zea mays (m
745	27	84.4	524	2	Q53CL7_MAIZE	Q53cl7	zea mays (m
746	27	84.4	527	2	Q9FJH8_ARATH	Q9fjh8	arabidopsis
747	27	84.4	528	2	Q5UUY8_ANTLO	Q5uuy8	antonospora
748	27	84.4	530	1	NTNG2_HUMAN	Q96cw9	homo sapien
749	27	84.4	530	2	Q5T7C8_HUMAN	Q5t7c8	homo sapien
750	27	84.4	530	2	O04431_NICPL	O04431	nicotiana p
751	27	84.4	530	2	O64999_SOYBN	O64999	glycine max
752	27	84.4	530	2	O82811_ARATH	O82811	arabidopsis
753	27	84.4	530	2	Q5K410_9ROSI	Q5k410	populus tre
754	27	84.4	530	2	Q76IH8_PRUPE	Q76ih8	prunus pers
755	27	84.4	530	2	Q76IJ7_PRUPE	Q76ij7	prunus pers
756	27	84.4	530	2	Q84MZ8_TOBAC	Q84mz8	nicotiana t
757	27	84.4	530	2	Q84MZ9_TOBAC	Q84mz9	nicotiana t
758	27	84.4	530	2	Q9ARC5_LOTJA	Q9arc5	lotus japon
759	27	84.4	530	2	Q9SQG6_LYCES	Q9sqg6	lycopersico
760	27	84.4	530	2	Q9SQG7_LYCES	Q9sqg7	lycopersico
761	27	84.4	531	2	Q93X79_LYCES	Q93x79	lycopersico
762	27	84.4	532	1	PHR_POTTR	Q28811	potorous tr
763	27	84.4	533	2	Q5ILJ4_POLPA	Q5ilj4	polysphondy
764	27	84.4	533	2	O81510_ARATH	O81510	arabidopsis
765	27	84.4	533	2	O82138_ORYSA	O82138	oryza sativ
766	27	84.4	533	2	Q6ZH34_ORYSA	Q6zh34	oryza sativ
767	27	84.4	535	2	Q8MKP1_DROME	Q8mkp1	drosophila
768	27	84.4	535	2	Q8RVG5_DAUCA	Q8rvg5	daucus caro
769	27	84.4	536	2	Q26373_DROME	Q26373	drosophila
770	27	84.4	543	1	Y9488_RHOBA	Q7uli3	rhodopirell
771	27	84.4	543	2	Q6FXQ2_CANGA	Q6fxq2	candida gla
772	27	84.4	544	2	Q9UK59_HUMAN	Q9uk59	homo sapien
773	27	84.4	544	2	Q96GH0_HUMAN	Q96gh0	homo sapien
774	27	84.4	545	2	Q6FSM9_CANGA	Q6fsm9	candida gla
775	27	84.4	546	2	O26601_METTH	O26601	methanobact
776	27	84.4	546	2	Q6WS77_9FILI	Q6ws77	pityrogramm
777	27	84.4	547	1	SNG1_YEAST	P46950	saccharomyc
778	27	84.4	547	2	Q76C05_PHYPA	Q76c05	physcomitre
779	27	84.4	548	2	Q76C03_PHYPA	Q76c03	physcomitre
780	27	84.4	548	2	Q76C06_PHYPA	Q76c06	physcomitre
781	27	84.4	553	2	Q9W430_DROME	Q9w430	drosophila
782	27	84.4	555	2	Q9V323_DROME	Q9v323	drosophila
783	27	84.4	556	1	PHR_CARAU	P34205	carassius a
784	27	84.4	565	2	Q5B921_EMENI	Q5b921	aspergillus
785	27	84.4	566	1	NAD3_CAEEL	Q21339	caenorhabdi
786	27	84.4	566	2	Q61JH2_CAEBR	Q61jh2	caenorhabdi
787	27	84.4	568	2	Q8MLB5_DROME	Q8mlb5	drosophila
788	27	84.4	572	2	Q51A71_ENTHI	Q51a71	entamoeba h
789	27	84.4	580	2	Q8BEQ1_9VIRU	Q8beq1	subterranea
790	27	84.4	580	2	Q5YL91_9VIRU	Q5yl91	subterranea
791	27	84.4	583	1	PHBC_AZOCA	O66392	a poly-beta
792	27	84.4	583	2	Q5WGM2_BACSK	Q5wgm2	bacillus cl
793	27	84.4	589	1	NTNG2_MOUSE	Q8r4f1	mus musculu
794	27	84.4	589	2	Q4J0Y2_AZOVI	Q4j0y2	azotobacter
795	27	84.4	593	2	Q8A460_BACTN	Q8a460	bacteroides
796	27	84.4	594	2	Q96HN9_HUMAN	Q96hn9	homo sapien
797	27	84.4	595	2	Q60RZ8_CAEBR	Q60rz8	caenorhabdi
798	27	84.4	598	1	YPC3_CAEEL	Q11180	caenorhabdi
799	27	84.4	599	2	Q5B5Q1_EMENI	Q5b5q1	aspergillus
800	27	84.4	600	2	Q9NL27_CIOIN	Q9nl27	ciona intes
801	27	84.4	612	2	Q9XHE2_CHLRE	Q9xhe2	chlamydomon
802	27	84.4	615	2	Q4RWK0_TETNG	Q4rwk0	tetraodon n
803	27	84.4	616	2	Q7QGS5_ANOGA	Q7qgs5	anopheles g
804	27	84.4	616	2	Q8VXX2_ARATH	Q8vxx2	arabidopsis
805	27	84.4	616	2	Q9FF13_ARATH	Q9ff13	arabidopsis
806	27	84.4	618	1	M3K2_HUMAN	Q9y2u5	homo sapien
807	27	84.4	618	2	Q5EAV4_XENLA	Q5eav4	xenopus lae
808	27	84.4	619	1	M3K2_MOUSE	Q61083	mus musculu
809	27	84.4	619	2	Q9NYK3_HUMAN	Q9nyk3	homo sapien
810	27	84.4	621	2	Q59GZ6_HUMAN	Q59gz6	homo sapien
811	27	84.4	621	2	Q5ZLW4_CHICK	Q5zlw4	gallus gall
812	27	84.4	626	1	M3K3_HUMAN	Q99759	homo sapien
813	27	84.4	626	1	M3K3_MOUSE	Q61084	mus musculu
814	27	84.4	626	2	Q5BKZ6_HUMAN	Q5bkz6	homo sapien
815	27	84.4	639	1	PAKM_DROME	Q9vxe5	drosophila
816	27	84.4	640	2	Q24443_DROME	Q24443	drosophila
817	27	84.4	642	2	Q7V3K6_PROMP	Q7v3k6	prochloroco
818	27	84.4	650	2	Q9NL28_CIOIN	Q9nl28	ciona intes
819	27	84.4	657	2	Q8N3I9_HUMAN	Q8n3i9	homo sapien
820	27	84.4	661	2	Q7VQU4_CANBF	Q7vqu4	candidatus
821	27	84.4	667	2	Q7M9D4_WOLSU	Q7m9d4	wolinella s
822	27	84.4	669	2	O87518_ECOLI	O87518	escherichia
823	27	84.4	670	2	Q95YK2_CIOSA	Q95yk2	ciona savig
824	27	84.4	673	2	Q5KLL2_CRYNE	Q5kll2	cryptococcu
825	27	84.4	673	2	Q55YC9_CRYNE	Q55yc9	cryptococcu
826	27	84.4	676	2	Q6FXI1_CANGA	Q6fxi1	candida gla
827	27	84.4	684	2	Q9N4Z3_CAEEL	Q9n4z3	caenorhabdi
828	27	84.4	695	2	Q6EZC5_ECOLI	Q6ezc5	escherichia
829	27	84.4	695	2	Q93SE1_ECOLI	Q93se1	escherichia
830	27	84.4	696	2	Q6KD36_ECOLI	Q6kd36	escherichia
831	27	84.4	696	2	Q8FDX2_ECOL6	Q8fdx2	escherichia
832	27	84.4	696	2	Q9LAP1_ECO57	Q9lap1	escherichia
833	27	84.4	702	2	Q4RMW8_TETNG	Q4rmw8	tetraodon n
834	27	84.4	721	2	Q9FRN4_ORYSA	Q9frn4	oryza sativ

835	27	84.4	721	2	Q7XBS0_ORYSA	Q7xbs0	oryza sativ
836	27	84.4	722	2	Q4ILN5_GIBZE	Q4iln5	gibberella
837	27	84.4	724	2	Q4P842_USTMA	Q4p842	ustilago ma
838	27	84.4	726	2	Q4S527_TETNG	Q4s527	tetraodon n
839	27	84.4	735	2	Q8ZD01_YERPE	Q8zd01	yersinia pe
840	27	84.4	735	2	Q66DI8_YERPS	Q66di8	yersinia ps
841	27	84.4	736	2	Q4PHE8_USTMA	Q4phe8	ustilago ma
842	27	84.4	739	2	Q99AQ3_9VIRU	Q99aq3	torque teno
843	27	84.4	754	2	Q6Z3V4_ORYSA	Q6z3v4	oryza sativ
844	27	84.4	771	2	Q8YNG0_ANASP	Q8yng0	anabaena sp
845	27	84.4	787	2	Q50RD6_ENTHI	Q50rd6	entamoeba h
846	27	84.4	800	2	Q6CHB1_YARLI	Q6chb1	yarrowia li
847	27	84.4	802	2	Q4WL16_ASPFU	Q4wl16	aspergillus
848	27	84.4	809	1	SYL_CAMJE	Q9pnk3	campylobact
849	27	84.4	809	1	SYL_CAMJR	Q5hu13	campylobact
850	27	84.4	818	2	Q9SLI6_ARATH	Q9sli6	arabidopsis
851	27	84.4	828	2	Q550C1_DICDI	Q550c1	dictyosteli
852	27	84.4	828	2	Q86K85_DICDI	Q86k85	dictyosteli
853	27	84.4	829	1	KSR2_HUMAN	Q6vab6	homo sapien
854	27	84.4	829	2	Q4HV89_GIBZE	Q4hv89	gibberella
855	27	84.4	830	2	Q9BKT7_CAEEL	Q9bkt7	caenorhabdi
856	27	84.4	832	2	Q9SLE5_ARATH	Q9sle5	arabidopsis
857	27	84.4	834	2	Q59LV8_CANAL	Q59lv8	candida alb
858	27	84.4	834	2	Q60PV4_CAEBR	Q60pv4	caenorhabdi
859	27	84.4	837	2	Q6AW03_CAEEL	Q6aw03	caenorhabdi
860	27	84.4	843	2	Q516X2_ENTHI	Q516x2	entamoeba h
861	27	84.4	848	2	Q9SCU9_ARATH	Q9scu9	arabidopsis
862	27	84.4	853	2	Q6FVK9_CANGA	Q6fvk9	candida gla
863	27	84.4	858	2	Q8IKI5_PLAF7	Q8iki5	plasmodium
864	27	84.4	877	2	Q648D9_9ARCH	Q648d9	uncultured
865	27	84.4	883	2	Q6Z7F7_ORYSA	Q6z7f7	oryza sativ
866	27	84.4	887	2	Q9SCU8_ARATH	Q9scu8	arabidopsis
867	27	84.4	894	2	Q4QBX4_LEIMA	Q4qbx4	leishmania
868	27	84.4	901	2	Q6BY30_DEBHA	Q6by30	debaryomyce
869	27	84.4	905	2	Q4NF83_9MICC	Q4nf83	arthrobacte
870	27	84.4	905	2	Q4RTX3_TETNG	Q4rtx3	tetraodon n
871	27	84.4	910	2	Q6CKL7_KLULA	Q6ckl7	kluyveromyc
872	27	84.4	912	2	Q759E8_ASHGO	Q759e8	ashbya goss
873	27	84.4	912	2	Q75EA4_ASHGO	Q75ea4	ashbya goss
874	27	84.4	924	2	O06842_PREBR	O06842	prevotella
875	27	84.4	926	2	Q7QBA4_ANOGA	Q7qba4	anopheles g
876	27	84.4	927	2	Q8T300_TRYCR	Q8t300	trypanosoma
877	27	84.4	927	2	Q8T304_TRYCR	Q8t304	trypanosoma
878	27	84.4	962	1	TSP3_BRARE	Q8jhw2	brachydanio
879	27	84.4	962	2	Q5U3J1_BRARE	Q5u3j1	brachydanio
880	27	84.4	966	2	Q8BEQ2_9VIRU	Q8beq2	subterranea
881	27	84.4	966	2	Q5YL92_9VIRU	Q5yl92	subterranea
882	27	84.4	973	2	Q7S904_NEUCR	Q7s904	neurospora
883	27	84.4	977	2	O97357_TRYCR	O97357	trypanosoma
884	27	84.4	992	2	Q59LU4_CANAL	Q59lu4	candida alb
885	27	84.4	1018	2	Q8T301_TRYCR	Q8t301	trypanosoma
886	27	84.4	1028	2	Q8SXA6_DROME	Q8sxa6	drosophila
887	27	84.4	1034	2	Q8FQ70_COREF	Q8fq70	corynebacte
888	27	84.4	1034	2	Q8NR89_CORGL	Q8nr89	corynebacte
889	27	84.4	1036	2	Q9SZN8_ARATH	Q9szn8	arabidopsis
890	27	84.4	1043	2	Q97E41_CLOAB	Q97e41	clostridium
891	27	84.4	1044	2	Q70CT4_ARATH	Q70ct4	arabidopsis
892	27	84.4	1096	2	Q5A2Y2_CANAL	Q5a2y2	candida alb
893	27	84.4	1098	2	Q8L262_PROVU	Q8l262	proteus vul
894	27	84.4	1142	2	Q8DKA7_SYNEL	Q8dka7	synechococc
895	27	84.4	1190	2	Q6CLJ2_KLULA	Q6clj2	kluyveromyc
896	27	84.4	1197	2	Q4RVM1_TETNG	Q4rvm1	tetraodon n
897	27	84.4	1210	2	Q4P998_USTMA	Q4p998	ustilago ma
898	27	84.4	1216	2	Q8NJW8_USTMA	Q8njw8	ustilago ma
899	27	84.4	1254	2	Q9VF51_DROME	Q9vf51	drosophila
900	27	84.4	1254	2	Q86NS1_DROME	Q86ns1	drosophila
901	27	84.4	1262	2	Q5AQK4_EMENI	Q5aqk4	aspergillus
902	27	84.4	1277	1	SM3L3_ARATH	Q9fiy7	arabidopsis
903	27	84.4	1294	2	Q8LGU1_ARATH	Q8lgu1	arabidopsis
904	27	84.4	1306	2	Q9LU34_ARATH	Q9lu34	arabidopsis
905	27	84.4	1330	1	XDH_RAT	P22985	rattus norv
906	27	84.4	1334	1	XDH_MOUSE	Q00519	mus musculu
907	27	84.4	1358	2	Q6AW15_CAEEL	Q6aw15	caenorhabdi
908	27	84.4	1361	2	Q6AW16_CAEEL	Q6aw16	caenorhabdi
909	27	84.4	1380	2	Q60VE7_CAEBR	Q60ve7	caenorhabdi
910	27	84.4	1414	2	Q8TH79_METAC	Q8th79	methanosarc
911	27	84.4	1433	2	P75020_STRLI	P75020	streptomyce
912	27	84.4	1433	2	Q9L040_STRCO	Q9l040	streptomyce
913	27	84.4	1474	2	Q53WJ5_ORYSA	Q53wj5	oryza sativ
914	27	84.4	1477	2	Q6Y3I1_MAIZE	Q6y3i1	zea mays (m
915	27	84.4	1576	2	Q70KN5_9NIDO	Q70kn5	porcine tor
916	27	84.4	1581	1	VGLP_BEV	P23052	berne virus
917	27	84.4	1583	2	O90304_9NIDO	O90304	breda virus
918	27	84.4	1584	2	Q70KN4_9NIDO	Q70kn4	bovine toro
919	27	84.4	1639	2	Q9X577_BACSU	Q9x577	bacillus su
920	27	84.4	1866	2	Q4FXZ8_LEIMA	Q4fxz8	leishmania
921	27	84.4	1906	2	Q51U68_MAGGR	Q51u68	magnaporthe
922	27	84.4	2006	2	Q5BGD9_EMENI	Q5bgd9	aspergillus
923	27	84.4	2090	2	Q6FVN7_CANGA	Q6fvn7	candida gla
924	27	84.4	2108	1	NOT1_YEAST	P25655	saccharomyc
925	27	84.4	2117	2	Q6A7B3_PROAC	Q6a7b3	propionibac
926	27	84.4	2272	2	Q9VZS7_DROME	Q9vzs7	drosophila
927	27	84.4	2397	1	MOK11_SCHPO	Q09854	schizosacch
928	27	84.4	2410	2	Q7PNQ7_ANOGA	Q7pnq7	anopheles g
929	27	84.4	2441	2	Q51K96_MAGGR	Q51k96	magnaporthe
930	27	84.4	2497	2	Q6FIZ0_CANGA	Q6fiz0	candida gla
931	27	84.4	2609	2	O74390_SCHPO	O74390	schizosacch
932	27	84.4	3149	2	Q7PUV8_ANOGA	Q7puv8	anopheles g
933	27	84.4	3269	2	Q7T7N5_9POTV	Q7t7n5	papaya leaf
934	27	84.4	3583	2	Q45675_BACSU	Q45675	bacillus su
935	27	84.4	3587	1	SRFAB_BACSU	Q04747	bacillus su
936	27	84.4	4540	1	DYHC_PARTE	Q27171	paramecium
937	27	84.4	4654	2	Q8D418_VIBVU	Q8d418	vibrio vuln
938	27	84.4	4656	2	Q7MFI9_VIBVY	Q7mfi9	vibrio vuln
939	27	84.4	5246	2	Q5CSZ3_CRYPV	Q5csz3	cryptospori
940	26	81.2	68	2	Q579A3_BRUAB	Q579a3	brucella ab
941	26	81.2	68	2	Q8FVG0_BRUSU	Q8fvg0	brucella su
942	26	81.2	68	2	Q8YCW6_BRUME	Q8ycw6	brucella me
943	26	81.2	69	2	Q89TR1_BRAJA	Q89tr1	bradyrhizob
944	26	81.2	74	2	Q5FKZ9_LACAC	Q5fkz9	lactobacill
945	26	81.2	76	2	Q9Y862_ASPVI	Q9y862	aspergillus
946	26	81.2	76	2	O68793_YERPE	O68793	yersinia pe
947	26	81.2	76	2	Q7ARC3_YERPE	Q7arc3	yersinia pe
948	26	81.2	88	2	Q89PC6_BRAJA	Q89pc6	bradyrhizob
949	26	81.2	93	2	Q5L8M8_BACFN	Q5l8m8	bacteroides
950	26	81.2	95	2	Q99SV0_STAAN	Q99sv0	staphylococ
951	26	81.2	99	2	Q6L720_9HEMI	Q6l720	tuberaphis
952	26	81.2	99	2	Q9GAD7_9CUCU	Q9gad7	diabrotica
953	26	81.2	99	2	Q9PE89_XYLFA	Q9pe89	xylella fas
954	26	81.2	100	2	Q69KH1_ORYSA	Q69kh1	oryza sativ
955	26	81.2	101	2	Q5BT47_SCHJA	Q5bt47	schistosoma
956	26	81.2	102	2	Q6G7Z4_STAAS	Q6g7z4	staphylococ
957	26	81.2	102	2	Q6GFB6_STAAR	Q6gfb6	staphylococ
958	26	81.2	102	2	Q8NVR3_STAAW	Q8nvr3	staphylococ
959	26	81.2	102	2	Q931M8_STAAM	Q931m8	staphylococ
960	26	81.2	106	2	Q7UXC8_RHOBA	Q7uxc8	rhodopirell
961	26	81.2	114	2	Q61150_MOUSE	Q61150	mus musculu
962	26	81.2	115	2	Q8ZMZ7_SALTY	Q8zmz7	salmonella
963	26	81.2	115	2	Q57Q86_SALCH	Q57q86	salmonella
964	26	81.2	118	2	Q56S09_AZOSA	Q56s09	azotobacter
965	26	81.2	125	2	Q7SDU5_NEUCR	Q7sdu5	neurospora
966	26	81.2	127	2	Q877N7_BACTN	Q877n7	bacteroides
967	26	81.2	129	2	Q6HWX3_BACAN	Q6hwx3	bacillus an
968	26	81.2	135	2	Q8BN36_MOUSE	Q8bn36	mus musculu
969	26	81.2	136	2	Q8NML2_CORGL	Q8nml2	corynebacte
970	26	81.2	140	2	Q8FKA9_ECOL6	Q8fka9	escherichia
971	26	81.2	141	2	Q9RR87_DEIRA	Q9rr87	deinococcus
972	26	81.2	144	2	Q5TY16_ANOGA	Q5ty16	anopheles g
973	26	81.2	148	2	Q9H1Z8_HUMAN	Q9h1z8	homo sapien
974	26	81.2	150	2	Q63N49_BURPS	Q63n49	burkholderi
975	26	81.2	150	2	Q747K4_GEOSL	Q747k4	geobacter s
976	26	81.2	152	2	Q5NYT5_AZOSE	Q5nyt5	azoarcus sp
977	26	81.2	153	2	Q970F5_SULTO	Q970f5	sulfolobus
978	26	81.2	155	2	O74054_CERSY	O74054	cenarchaeum
979	26	81.2	156	2	Q97Y35_SULSO	Q97y35	sulfolobus
980	26	81.2	157	2	Q8YMA5_ANASP	Q8yma5	anabaena sp

981	26	81.2	159	2	Q82A00_STRAW	Q82a00 streptomyce
982	26	81.2	162	1	LEC3_MEGRO	P07439 megabalanus
983	26	81.2	162	2	Q25459_MEGRO	Q25459 megabalanus
984	26	81.2	172	2	Q9US69_SCHPO	Q9us69 schizosacch
985	26	81.2	174	2	Q7PCT5_ANOGA	Q7pct5 anopheles g
986	26	81.2	174	2	Q4HTI1_CAMUP	Q4hti1 campylobact
987	26	81.2	174	2	Q81ZT9_NITEU	Q81zt9 nitrosomona
988	26	81.2	174	2	Q6MML7_BDEBA	Q6mml7 bdellovibri
989	26	81.2	178	2	Q60F71_CAEEL	Q60f71 caenorhabdi
990	26	81.2	180	2	Q4H7P0_9DEIO	Q4h7p0 deinococcus
991	26	81.2	181	2	Q6BSR1_DEBHA	Q6bsr1 debaryomyce
992	26	81.2	183	2	Q94881_DROME	Q94881 drosophila
993	26	81.2	185	2	Q4WE11_ASPFU	Q4we11 aspergillus
994	26	81.2	185	2	Q8KEK8_CHLTE	Q8kek8 chlorobium
995	26	81.2	186	2	Q9VIX1_DROME	Q9vix1 drosophila
996	26	81.2	186	2	Q6SHE1_9BACT	Q6she1 uncultured
997	26	81.2	191	2	Q6FDD5_ACIAD	Q6fdd5 acinetobact
998	26	81.2	195	2	Q9LHM8_ARATH	Q9lhm8 arabidopsis
999	26	81.2	198	2	Q7Z8Q5_SCLSC	Q7z8q5 sclerotinia
1000	26	81.2	199	1	YD63_SCHPO	Q10315 schizosacch

ALIGNMENTS

```
RESULT 1
LSPA_VIBVU
ID   LSPA_VIBVU     STANDARD;      PRT;   168 AA.
AC   Q8DES8;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Lipoprotein signal peptidase (EC 3.4.23.36) (Prolipoprotein signal
DE   peptidase) (Signal peptidase II) (SPase II).
GN   Name=lspA; OrderedLocusNames=VV10506;
OS   Vibrio vulnificus.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Vibrio.
OX   NCBI_TaxID=672;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=CMCP6;
RA   Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA   Choy H.E.;
RT   "Complete genome sequence of Vibrio vulnificus CMCP6.";
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: This protein specifically catalyzes the removal of
CC       signal peptides from prolipoproteins (By similarity).
CC   -!- CATALYTIC ACTIVITY: Release of signal peptides from bacterial
CC       membrane prolipoproteins. Hydrolyzes -Xaa-Yaa-Zaa-|-
CC       (S,diacylglyceryl)Cys-, in which Xaa is hydrophobic (preferably
CC       Leu), and Yaa (Ala or Ser) and Zaa (Gly or Ala) have small,
CC       neutral side chains.
CC   -!- PATHWAY: Lipoprotein biosynthesis; second step.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC       (By similarity).
CC   -!- SIMILARITY: Belongs to the peptidase A8 family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; AE016798; AAO09025.1; -; Genomic_DNA.
DR   MEROPS; A08.001; -.
DR   HAMAP; MF_00161; -; 1.
DR   InterPro; IPR001872; Peptidase_A8.
DR   Pfam; PF01252; Peptidase_A8; 1.
DR   PRINTS; PR00781; LIPOSIGPTASE.
DR   ProDom; PD004304; Peptidase_A8; 1.
DR   TIGRFAMs; TIGR00077; lspA; 1.
DR   PROSITE; PS00855; SPASE_II; 1.
KW   Aspartyl protease; Complete proteome; Hydrolase; Inner membrane;
KW   Membrane; Protease; Transmembrane.
FT   TRANSMEM     12     34       Potential.
FT   TRANSMEM     70     92       Potential.
FT   TRANSMEM    104    126       Potential.
FT   TRANSMEM    136    158       Potential.
FT   ACT_SITE    119    119       By similarity.
FT   ACT_SITE    146    146       By similarity.
SQ   SEQUENCE   168 AA;  19200 MW;  825297099B2D7BA3 CRC64;

  Query Match             100.0%;  Score 32;  DB 1;  Length 168;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         89 TYWMS 93


RESULT 2
LSPA_VIBVY
ID   LSPA_VIBVY     STANDARD;      PRT;   168 AA.
AC   Q7MNM7;
DT   25-OCT-2004 (Rel. 45, Created)
DT   25-OCT-2004 (Rel. 45, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Lipoprotein signal peptidase (EC 3.4.23.36) (Prolipoprotein signal
DE   peptidase) (Signal peptidase II) (SPase II).
GN   Name=lspA; OrderedLocusNames=VV0688;
OS   Vibrio vulnificus (strain YJ016).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Vibrio.
OX   NCBI_TaxID=196600;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=14656965; DOI=10.1101/gr.1295503;
RA   Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA   Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA   Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT   "Comparative genome analysis of Vibrio vulnificus, a marine
RT   pathogen.";
RL   Genome Res. 13:2577-2587(2003).
CC   -!- FUNCTION: This protein specifically catalyzes the removal of
CC       signal peptides from prolipoproteins (By similarity).
CC   -!- CATALYTIC ACTIVITY: Release of signal peptides from bacterial
CC       membrane prolipoproteins. Hydrolyzes -Xaa-Yaa-Zaa-|-
CC       (S,diacylglyceryl)Cys-, in which Xaa is hydrophobic (preferably
CC       Leu), and Yaa (Ala or Ser) and Zaa (Gly or Ala) have small,
CC       neutral side chains.
CC   -!- PATHWAY: Lipoprotein biosynthesis; second step.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC       (By similarity).
CC   -!- SIMILARITY: Belongs to the peptidase A8 family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; BA000037; BAC93452.1; -; Genomic_DNA.
DR   HAMAP; MF_00161; -; 1.
DR   InterPro; IPR001872; Peptidase_A8.
DR   Pfam; PF01252; Peptidase_A8; 1.
DR   PRINTS; PR00781; LIPOSIGPTASE.
DR   ProDom; PD004304; Peptidase_A8; 1.
DR   TIGRFAMs; TIGR00077; lspA; 1.
DR   PROSITE; PS00855; SPASE_II; 1.
KW   Aspartyl protease; Complete proteome; Hydrolase; Inner membrane;
KW   Membrane; Protease; Transmembrane.
FT   TRANSMEM     12     34       Potential.
FT   TRANSMEM     70     92       Potential.
FT   TRANSMEM    104    126       Potential.
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FT   TRANSMEM    136    158       Potential.
FT   ACT_SITE    119    119       By similarity.
FT   ACT_SITE    146    146       By similarity.
SQ   SEQUENCE   168 AA;  19200 MW;  825297099B2D7BA3 CRC64;

  Query Match            100.0%;  Score 32;  DB 1;  Length 168;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         89 TYWMS 93


RESULT 3
LSPA_VIBPA
ID   LSPA_VIBPA     STANDARD;      PRT;   169 AA.
AC   Q87S89;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Lipoprotein signal peptidase (EC 3.4.23.36) (Prolipoprotein signal
DE   peptidase) (Signal peptidase II) (SPase II).
GN   Name=lspA; OrderedLocusNames=VP0535;
OS   Vibrio parahaemolyticus.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Vibrio.
OX   NCBI_TaxID=670;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=RIMD 2210633 / Serotype O3:K6;
RX   MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA   Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA   Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA   Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT   "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT   distinct from that of V. cholerae.";
RL   Lancet 361:743-749(2003).
CC   -!- FUNCTION: This protein specifically catalyzes the removal of
CC       signal peptides from prolipoproteins (By similarity).
CC   -!- CATALYTIC ACTIVITY: Release of signal peptides from bacterial
CC       membrane prolipoproteins. Hydrolyzes -Xaa-Yaa-Zaa-|-
CC       (S,diacylglyceryl)Cys-, in which Xaa is hydrophobic (preferably
CC       Leu), and Yaa (Ala or Ser) and Zaa (Gly or Ala) have small,
CC       neutral side chains.
CC   -!- PATHWAY: Lipoprotein biosynthesis; second step.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC       (By similarity).
CC   -!- SIMILARITY: Belongs to the peptidase A8 family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; BA000031; BAC58798.1; -; Genomic_DNA.
DR   MEROPS; A08.001; -.
DR   HAMAP; MF_00161; -; 1.
DR   InterPro; IPR001872; Peptidase_A8.
DR   Pfam; PF01252; Peptidase_A8; 1.
DR   PRINTS; PR00781; LIPOSIGPTASE.
DR   ProDom; PD004304; Peptidase_A8; 1.
DR   TIGRFAMs; TIGR00077; lspA; 1.
DR   PROSITE; PS00855; SPASE_II; 1.
KW   Aspartyl protease; Complete proteome; Hydrolase; Inner membrane;
KW   Membrane; Protease; Transmembrane.
FT   TRANSMEM     15     34       Potential.
FT   TRANSMEM     47     66       Potential.
FT   TRANSMEM     70     92       Potential.
FT   TRANSMEM    104    126       Potential.
FT   TRANSMEM    136    158       Potential.
FT   ACT_SITE    119    119       By similarity.
FT   ACT_SITE    146    146       By similarity.
SQ   SEQUENCE   169 AA;  19266 MW;  F9FA101EC910A74F CRC64;

  Query Match            100.0%;  Score 32;  DB 1;  Length 169;
  Best Local Similarity   100.0%;  Pred. No. 4.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         89 TYWMS 93


RESULT 4
Q8WB24_9NEOP
ID   Q8WB24_9NEOP PRELIMINARY;      PRT;   178 AA.
AC   Q8WB24;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   NADH dehydrogenase subunit 6.
GN   Name=ND6;
OS   Ostrinia furnacalis (Asian corn borer).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC   Crambidae; Pyraustinae; Ostrinia.
OX   NCBI_TaxID=93504;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Coates B.S., Sumerford D.V., Hellmich R.L., Lewis L.C.;
RT   "Partial mitochondrial genome sequence of Ostrinia nubilalis and
RT   Ostrinia furnicalis.";
RL   Int. J. Biol. Sci. 1:13-18(2004).
DR   EMBL; AF467260; AAL66402.1; -; Genomic_DNA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
DR   GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR   InterPro; IPR001457; Oxidored_q3.
DR   Pfam; PF00499; Oxidored_q3; 1.
KW   Mitochondrion.
SQ   SEQUENCE   178 AA;  21024 MW;  2B5B7AEEAD908C88 CRC64;

  Query Match            100.0%;  Score 32;  DB 2;  Length 178;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         47 TYWMS 51


RESULT 5
Q8WBV3_OSTNU
ID   Q8WBV3_OSTNU PRELIMINARY;      PRT;   178 AA.
AC   Q8WBV3;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   NADH dehydrogenase subunit 6.
GN   Name=ND6;
OS   Ostrinia nubilalis (European corn borer).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;
OC   Crambidae; Pyraustinae; Ostrinia.
OX   NCBI_TaxID=29057;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Coates B.S., Sumerford D.V., Hellmich R.L., Lewis L.C.;
RT   "Partial mitochondrial genome sequence of Ostrinia nubilalis and
RT   Ostrinia furnicalis.";
RL   Int. J. Biol. Sci. 1:13-18(2004).
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RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Coates B.S., Sumerford D.V., Hellmich R.L.;
RT   "Geographic and voltinism differentiation among North American
RT   Ostrinia nubilalis (European corn borer) mitochondrial cytochrome c
RT   oxidase haplotypes.";
RL   J. Insect Sci. 4:1-9(2004).
DR   EMBL; AF442957; AAL66248.1; -; Genomic_DNA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
DR   GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . .; IEA.
DR   InterPro; IPR001457; Oxidored_q3.
DR   Pfam; PF00499; Oxidored_q3; 1.
KW   Mitochondrion.
SQ   SEQUENCE   178 AA;  20992 MW;  D04071FEAD8080E5 CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 178;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         47 TYWMS 51


RESULT 6
Q9XHV8_ORYSA
ID   Q9XHV8_ORYSA PRELIMINARY;      PRT;   236 AA.
AC   Q9XHV8;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   10A19I.8.
GN   Name=10A19I.8;
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Vysotskaia V.S., Schwartz J.R., Osborne B.I., Wing R., Yu G., Kwan A.,
RA   Liu S., Lee J., Toriumi M., Luros J., Li J., Kremenetskaia I., Oji O.,
RA   Theologis A.;
RL   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR   EMBL; AC007858; AAD39593.1; -; Genomic_DNA.
DR   Gramene; Q9XHV8; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   InterPro; IPR001005; Myb_DNA_bd.
DR   Pfam; PF00249; Myb_DNA-binding; 1.
DR   SMART; SM00717; SANT; 1.
KW   Nuclear protein; Repeat.
SQ   SEQUENCE   236 AA;  26681 MW;  0A33BE5977933E42 CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        200 TYWMS 204


RESULT 7
Q688U1_ORYSA
ID   Q688U1_ORYSA PRELIMINARY;      PRT;   236 AA.
AC   Q688U1;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein OSJNBa0017N18.10.
GN   Name=OSJNBa0017N18.10;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Chow T.-Y., Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA   Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA   Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA   Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA   Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA   Wu H.-P., Shaw J.-F.;
RT   "Oryza sativa BAC OSJNBa0017N18 genomic sequence.";
RL   Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
DR   EMBL; AC120988; AAU10697.1; -; Genomic_DNA.
DR   Gramene; Q688U1; -.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   InterPro; IPR001005; Myb_DNA_bd.
DR   Pfam; PF00249; Myb_DNA-binding; 1.
DR   SMART; SM00717; SANT; 1.
KW   Hypothetical protein; Nuclear protein; Repeat.
SQ   SEQUENCE   236 AA;  26681 MW;  0A33BE5977933E42 CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 5.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        200 TYWMS 204


RESULT 8
Q70EF4_9RHIZ
ID   Q70EF4_9RHIZ PRELIMINARY;      PRT;   256 AA.
AC   Q70EF4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Particulate Methane Monooxigenase subunit C.
GN   Name=pmoC;
OS   Methylocystis sp. SC2.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Methylocystaceae; Methylocystis.
OX   NCBI_TaxID=187303;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=SC2;
RX   PubMed=15128567; DOI=10.1128/AEM.70.5.3055-3063.2004;
RA   Ricke P., Erkel C., Kube M., Reinhardt R., Liesack W.;
RT   "Comparative Analysis of the Conventional and Novel pmo (Particulate
RT   Methane Monooxygenase) Operons from Methylocystis Strain SC2.";
RL   Appl. Environ. Microbiol. 70:3055-3063(2004).
DR   EMBL; AJ584611; CAE47799.1; -; Genomic_DNA.
DR   InterPro; IPR006980; AmoC.
DR   Pfam; PF04896; AmoC; 1.
SQ   SEQUENCE   256 AA;  29247 MW;  773BC00EE865439A CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 6.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         60 TYWMS 64


RESULT 9
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Q9KX37_9RHIZ
ID   Q9KX37_9RHIZ PRELIMINARY;      PRT;   256 AA.
AC   Q9KX37;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   PmoC.
GN   Name=pmoC;
OS   Methylocystis sp. M.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Methylocystaceae; Methylocystis.
OX   NCBI_TaxID=51782;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=M;
RX   MEDLINE=20163992; PubMed=10698759; DOI=10.1128/AEM.66.3.966-975.2000;
RA   Gilbert B., McDonald I.R., Finch R., Stafford G.P., Nielsen A.K.,
RA   Murrell J.C.;
RT   "Molecular analysis of the pmo (particulate methane monooxygenase)
RT   operons from two type II methanotrophs.";
RL   Appl. Environ. Microbiol. 66:966-975(2000).
DR   EMBL; U81596; AAF37896.1; -; Genomic_DNA.
DR   InterPro; IPR006980; AmoC.
DR   Pfam; PF04896; AmoC; 1.
SQ   SEQUENCE   256 AA;  29021 MW;  AC0A28882AB28131 CRC64;

  Query Match            100.0%;  Score 32;  DB 2;  Length 256;
  Best Local Similarity  100.0%;  Pred. No. 6.4e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         60 TYWMS 64


RESULT 10
YKO4_CAEEL
ID   YKO4_CAEEL     STANDARD;      PRT;   315 AA.
AC   P34292;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Hypothetical protein C05B5.4 in chromosome III.
GN   ORFNames=C05B5.4;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; Z32679; CAA83591.1; -; Genomic_DNA.
DR   PIR; B88571; B88571.
DR   Ensembl; C05B5.4; Caenorhabditis elegans.
DR   WormBase; WBGene00007321; C05B5.4.
DR   WormPep; C05B5.4; CE00880.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   315 AA;  35918 MW;  D6665F5FAB040BCF CRC64;

  Query Match            100.0%;  Score 32;  DB 1;  Length 315;
  Best Local Similarity  100.0%;  Pred. No. 7.8e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        281 TYWMS 285


RESULT 11
Q61J61_CAEBR
ID   Q61J61_CAEBR PRELIMINARY;      PRT;   322 AA.
AC   Q61J61;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein CBG09928.
GN   Name=CBG09928;
OS   Caenorhabditis briggsae.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6238;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RG   The C.briggsae Sequencing Consortium;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAC01000045; CAE65074.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   322 AA;  37000 MW;  DB16C2E29C4864CF CRC64;

  Query Match            100.0%;  Score 32;  DB 2;  Length 322;
  Best Local Similarity  100.0%;  Pred. No. 7.9e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        288 TYWMS 292


RESULT 12
Q8ED62_SHEON
ID   Q8ED62_SHEON PRELIMINARY;      PRT;   357 AA.
AC   Q8ED62;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   O-methyltransferase, putative.
GN   OrderedLocusNames=SO2905;
OS   Shewanella oneidensis.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC   Shewanellaceae; Shewanella.
OX   NCBI_TaxID=70863;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=MR-1;
RX   MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA   Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA   Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA   Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA   Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA   Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA   White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA   Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA   Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA   Venter J.C., Nealson K.H., Fraser C.M.;
RT   "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT   Shewanella oneidensis.";
RL   Nat. Biotechnol. 20:1118-1123(2002).
DR   EMBL; AE015729; AAN55921.1; -; Genomic_DNA.
DR   TIGR; SO2905; -.
DR   GO; GO:0008171; F:O-methyltransferase activity; IEA.
DR   GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.
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DR   GO; GO:0016740; F:transferase activity; IEA.
DR   InterPro; IPR001077; O_Met_trans2.
DR   InterPro; IPR000051; SAM_bind.
DR   Pfam; PF00891; Methyltransf_2; 1.
KW   Complete proteome; Methyltransferase; Transferase.
SQ   SEQUENCE   357 AA;  39951 MW;  AD1024E81756C98F CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 357;
  Best Local Similarity   100.0%;  Pred. No. 8.7e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        252 TYWMS 256


RESULT 13
Q9KEG6_BACHD
ID   Q9KEG6_BACHD PRELIMINARY;      PRT;   454 AA.
AC   Q9KEG6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   BH0886 protein.
GN   OrderedLocusNames=BH0886;
OS   Bacillus halodurans.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=86665;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C-125 / JCM 9153;
RX   MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA   Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA   Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA   Horikoshi K.;
RT   "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT   halodurans and genomic sequence comparison with Bacillus subtilis.";
RL   Nucleic Acids Res. 28:4317-4331(2000).
DR   EMBL; BA000004; BAB04605.1; -; Genomic_DNA.
DR   PIR; F83760; F83760.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0015297; F:antiporter activity; IEA.
DR   GO; GO:0015238; F:drug transporter activity; IEA.
DR   GO; GO:0006855; P:multidrug transport; IEA.
DR   InterPro; IPR002528; MatE.
DR   Pfam; PF01554; MatE; 2.
DR   TIGRFAMs; TIGR00797; matE; 1.
KW   Complete proteome.
SQ   SEQUENCE   454 AA;  49128 MW;  8484B16F4CE362BC CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 454;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        402 TYWMS 406


RESULT 14
Q7N2H2_PHOLL
ID   Q7N2H2_PHOLL PRELIMINARY;      PRT;   484 AA.
AC   Q7N2H2;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Similar to D-serine/D-alanine/glycine transporter.
GN   OrderedLocusNames=plu3105;
OS   Photorhabdus luminescens (subsp. laumondii).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Photorhabdus.
OX   NCBI_TaxID=141679;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=TT01;
RX   MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA   Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA   Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA   Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA   Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
RA   Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT   "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT   luminescens.";
RL   Nat. Biotechnol. 21:1307-1313(2003).
DR   EMBL; BX571869; CAE15479.1; -; Genomic_DNA.
DR   PhotoList; plu3105; -.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.
DR   GO; GO:0006865; P:amino acid transport; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR002293; AA/rel_permease1.
DR   InterPro; IPR004841; Permease_region.
DR   Pfam; PF00324; AA_permease; 1.
KW   Complete proteome.
SQ   SEQUENCE   484 AA;  53727 MW;  91DABD242DD4D98E CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 484;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        109 TYWMS 113


RESULT 15
Q8MS57_DROME
ID   Q8MS57_DROME PRELIMINARY;      PRT;   516 AA.
AC   Q8MS57;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   LP10535p.
GN   Name=CG7346; ORFNames=CG32091;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Berkeley;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.;
RL   Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY119083; AAM50943.1; -; mRNA.
DR   Ensembl; CG32091; Drosophila melanogaster.
DR   FlyBase; FBgn0052091; CG32091.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016887; F:ATPase activity; IEA.
DR   GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR000412; ABC_2.
DR   InterPro; IPR003439; ABC_transp_like.
DR   Pfam; PF01061; ABC2_membrane; 1.
DR   Pfam; PF00005; ABC_tran; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
SQ   SEQUENCE   516 AA;  58202 MW;  F67BF99048BE5258 CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 516;
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  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        362 TYWMS 366


RESULT 16
Q8SXX6_DROME
ID   Q8SXX6_DROME PRELIMINARY;      PRT;   623 AA.
AC   Q8SXX6;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   RE70153p.
GN   Name=CG7346; ORFNames=CG32091;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Berkeley;
RA   Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA   Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA   George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA   Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA   Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA   Celniker S.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the ABC transporter family.
DR   EMBL; AY075521; AAL68329.1; -; mRNA.
DR   FlyBase; FBgn0052091; CG32091.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016887; F:ATPase activity; IEA.
DR   GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR000412; ABC_2.
DR   InterPro; IPR003439; ABC_transp_like.
DR   Pfam; PF01061; ABC2_membrane; 1.
DR   Pfam; PF00005; ABC_tran; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   ATP-binding; Nucleotide-binding; Transmembrane; Transport.
SQ   SEQUENCE   623 AA;  70221 MW;  F6137DCC3196A133 CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 623;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        469 TYWMS 473


RESULT 17
Q9VTL3_DROME
ID   Q9VTL3_DROME PRELIMINARY;      PRT;   623 AA.
AC   Q9VTL3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CG32091-PB.
GN   Name=CG32091; ORFNames=CG32091;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RG   Berkeley Drosophila Genome Project;
RA   Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA   Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA   Yu C., Rubin G.;
RT   "Drosophila melanogaster release 4 sequence.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RG   FlyBase;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the ABC transporter family.
DR   EMBL; AE003544; AAF50035.2; -; Genomic_DNA.
DR   FlyBase; FBgn0052091; CG32091.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016887; F:ATPase activity; IEA.
DR   GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR000412; ABC_2.
DR   InterPro; IPR003439; ABC_transp_like.
DR   Pfam; PF01061; ABC2_membrane; 1.
DR   Pfam; PF00005; ABC_tran; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   ATP-binding; Nucleotide-binding; Transmembrane; Transport.
SQ   SEQUENCE   623 AA;  70235 MW;  82743BB91391D413 CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 623;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        469 TYWMS 473


RESULT 18
Q4S5S6_TETNG
ID   Q4S5S6_TETNG PRELIMINARY;      PRT;  1238 AA.
AC   Q4S5S6;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 9 SCAF14729, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00023606001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01014729; CAG04006.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER    1238   1238
SQ   SEQUENCE   1238 AA;  139685 MW;  86CFA13B09AD1724 CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 1238;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        133 TYWMS 137


RESULT 19
Q60V14_CAEBR
ID   Q60V14_CAEBR PRELIMINARY;      PRT;  1497 AA.
AC   Q60V14;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein CBG19737.
GN   Name=CBG19737;
OS   Caenorhabditis briggsae.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6238;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RG   The C.briggsae Sequencing Consortium;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAC01000102; CAE72553.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   1497 AA;  173495 MW;  6D65C6B8501AF112 CRC64;

  Query Match             100.0%;  Score 32;  DB 2;  Length 1497;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        581 TYWMS 585


RESULT 20
O62191_CAEEL
ID   O62191_CAEEL PRELIMINARY;      PRT;  2021 AA.
AC   O62191;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein F31C3.3.
GN   ORFNames=F31C3.3;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
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RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; Z92784; CAB07193.2; -; Genomic_DNA.
DR   PIR; T21588; T21588.
DR   Ensembl; F31C3.3; Caenorhabditis elegans.
DR   WormBase; WBGene00009285; F31C3.3.
DR   WormPep; F31C3.3; CE32399.
DR   InterPro; IPR001000; Glyco_hydro_10.
DR   PROSITE; PS00591; GLYCOSYL_HYDROL_F10; UNKNOWN_1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   2021 AA;  233800 MW;  F70E443EBF7428E7 CRC64;

  Query Match            100.0%;  Score 32;  DB 2;  Length 2021;
  Best Local Similarity  100.0%;  Pred. No. 4.6e+03;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db       1172 TYWMS 1176


RESULT 21
Q8VVS0_STAAU
ID   Q8VVS0_STAAU PRELIMINARY;      PRT;    30 AA.
AC   Q8VVS0;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   ORF25.
OS   Staphylococcus aureus.
OG   Plasmid ETB plasmid.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=1280;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=TY4;
RX   MEDLINE=21562640; PubMed=11705958;
RX   DOI=10.1128/IAI.69.12.7760-7771.2001;
RA   Yamaguchi T., Hayashi T., Takami H., Ohnisi M., Murata T.,
RA   Nakayama K., Asakawa K., Ohara M., Komatsuzawa H., Sugai M.;
RT   "Complete nucleotide sequence of a Staphylococcus aureus exfoliative
RT   toxin B plasmid and identification of a novel ADP-ribosyltransferase,
RT   EDIN-C.";
RL   Infect. Immun. 69:7760-7771(2001).
DR   EMBL; AP003088; BAB78423.1; -; Genomic_DNA.
KW   Plasmid.
SQ   SEQUENCE   30 AA;  3471 MW;  65BE5BFA5B43E97A CRC64;

  Query Match            90.6%;  Score 29;  DB 2;  Length 30;
  Best Local Similarity  80.0%;  Pred. No. 2.8e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         22 TYWLS 26


RESULT 22
Q79ZU4_STAAW
ID   Q79ZU4_STAAW PRELIMINARY;      PRT;    30 AA.
AC   Q79ZU4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein MWP005.
GN   OrderedLocusNames=MWP005;
OS   Staphylococcus aureus (strain MW2).
OG   Plasmid pMW2.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=196620;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA   Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA   Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA   Yamamoto K., Hiramatsu K.;
RT   "Genome and virulence determinants of high virulence community-
RT   acquired MRSA.";
RL   Lancet 359:1819-1827(2002).
DR   EMBL; AP004832; BAB96502.1; -; Genomic_DNA.
KW   Complete proteome.
SQ   SEQUENCE   30 AA;  3471 MW;  65BE5BFA5B43E97A CRC64;

  Query Match            90.6%;  Score 29;  DB 2;  Length 30;
  Best Local Similarity  80.0%;  Pred. No. 2.8e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         22 TYWLS 26


RESULT 23
Q6GIX8_STAAR
ID   Q6GIX8_STAAR PRELIMINARY;      PRT;    30 AA.
AC   Q6GIX8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Putative membrane protein.
GN   OrderedLocusNames=SAR0716;
OS   Staphylococcus aureus (strain MRSA252).
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=282458;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA   Holden M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA   Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA   Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA   Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA   Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA   James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA   Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,
RA   Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA   Spratt B.G., Parkhill J.;
RT   "Complete genomes of two clinical Staphylococcus aureus strains:
RT   evidence for the rapid evolution of virulence and drug resistance.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR   EMBL; BX571856; CAG39727.1; -; Genomic_DNA.
KW   Complete proteome.
SQ   SEQUENCE   30 AA;  3471 MW;  65BE5BFA5B43E97A CRC64;

  Query Match            90.6%;  Score 29;  DB 2;  Length 30;
  Best Local Similarity  80.0%;  Pred. No. 2.8e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         22 TYWLS 26


RESULT 24
Q9AC83_STAAN
ID   Q9AC83_STAAN PRELIMINARY;      PRT;    55 AA.
AC   Q9AC83;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein SAP007.
GN   OrderedLocusNames=SAP007;
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OS   Staphylococcus aureus (strain N315).
OG   Plasmid pN315.
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=158879;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=N315;
RX   MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA   Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA   Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA   Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA   Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA   Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA   Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA   Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT   "Whole genome sequencing of meticillin-resistant Staphylococcus
RT   aureus.";
RL   Lancet 357:1225-1240(2001).
DR   EMBL; AP003139; BAB43876.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein; Plasmid.
SQ   SEQUENCE   55 AA;  6260 MW;  328AC4114FB9A3B4 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 55;
  Best Local Similarity   80.0%;  Pred. No. 4.9e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         47 TYWLS 51


RESULT 25
RS16_PSEPK
ID   RS16_PSEPK     STANDARD;      PRT;    83 AA.
AC   Q88MV6;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   30S ribosomal protein S16.
GN   Name=rpsP; OrderedLocusNames=PP1462;
OS   Pseudomonas putida (strain KT2440).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=160488;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=22423060; PubMed=12534463;
RX   DOI=10.1046/j.1462-2920.2002.00366.x;
RA   Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA   Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA   Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA   Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA   Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA   Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA   Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA   Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA   Fraser C.M.;
RT   "Complete genome sequence and comparative analysis of the
RT   metabolically versatile Pseudomonas putida KT2440.";
RL   Environ. Microbiol. 4:799-808(2002).
CC   -!- SIMILARITY: Belongs to the ribosomal protein S16P family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; AE016779; AAN67084.1; ALT_INIT; Genomic_DNA.
DR   HSSP; P80379; 1EMW.
DR   TIGR; PP1462; -.
DR   HAMAP; MF_00385; -; 1.
DR   InterPro; IPR000307; Ribosomal_S16.
DR   PANTHER; PTHR12919; Ribosomal_S16; 1.
DR   Pfam; PF00886; Ribosomal_S16; 1.
DR   ProDom; PD003791; Ribosomal_S16; 1.
DR   TIGRFAMs; TIGR00002; S16; 1.
DR   PROSITE; PS00732; RIBOSOMAL_S16; FALSE_NEG.
KW   Complete proteome; Ribonucleoprotein; Ribosomal protein.
SQ   SEQUENCE   83 AA;  9189 MW;  9A724CD54A66A68E CRC64;

  Query Match             90.6%;  Score 29;  DB 1;  Length 83;
  Best Local Similarity   80.0%;  Pred. No. 7.3e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         58 TYWLS 62


RESULT 26
Q57A45_BRUAB
ID   Q57A45_BRUAB PRELIMINARY;      PRT;   102 AA.
AC   Q57A45;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=BruAb2_0038;
OS   Brucella abortus.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Brucellaceae; Brucella.
OX   NCBI_TaxID=235;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=9-941 / Biovar 1;
RX   PubMed=15805518; DOI=10.1128/JB.187.8.2715-2726.2005;
RA   Halling S.M., Peterson-Burch B.D., Bricker B.J., Zuerner R.L.,
RA   Qing Z., Li L.-L., Kapur V., Alt D.P., Olsen S.C.;
RT   "Completion of the genome sequence of Brucella abortus and comparison
RT   to the highly similar genomes of Brucella melitensis and Brucella
RT   suis.";
RL   J. Bacteriol. 187:2715-2726(2005).
DR   EMBL; AE017224; AAX75489.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   102 AA;  11724 MW;  4EDA516119F16CE6 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 102;
  Best Local Similarity   80.0%;  Pred. No. 8.9e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         65 TYWLS 69


RESULT 27
Q8FXM7_BRUSU
ID   Q8FXM7_BRUSU PRELIMINARY;      PRT;   116 AA.
AC   Q8FXM7;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=BRA0038;
OS   Brucella suis.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Brucellaceae; Brucella.
OX   NCBI_TaxID=29461;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=1330 / Biovar 1;
RX   MEDLINE=22247741; PubMed=12271122; DOI=10.1073/pnas.192319099;
RA   Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA   Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J.,
RA   Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
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RA   Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,
RA   Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,
RA   Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,
RA   Fraser C.M.;
RT   "The Brucella suis genome reveals fundamental similarities between
RT   animal and plant pathogens and symbionts.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR   EMBL; AE014292; AAN33250.1; -; Genomic_DNA.
DR   TIGR; BRA0038; -.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   116 AA;  13141 MW;  20FEA274A0E2DD86 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 116;
  Best Local Similarity   80.0%;  Pred. No. 1e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         79 TYWLS 83


RESULT 28
Q8YDW9_BRUME
ID   Q8YDW9_BRUME PRELIMINARY;      PRT;   116 AA.
AC   Q8YDW9;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein BMEII0055.
GN   OrderedLocusNames=BMEII0055;
OS   Brucella melitensis.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Brucellaceae; Brucella.
OX   NCBI_TaxID=29459;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=16M / ATCC 23456 / Biotype 1;
RX   PubMed=11756688; DOI=10.1073/pnas.221575398;
RA   DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
RA   Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
RA   Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA   Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA   Haselkorn R., Kyrpides N.C., Overbeek R.;
RT   "The genome sequence of the facultative intracellular pathogen
RT   Brucella melitensis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR   EMBL; AE009644; AAL53296.1; -; Genomic_DNA.
DR   PIR; AE3516; AE3516.
KW   Complete proteome.
SQ   SEQUENCE   116 AA;  13177 MW;  20FEA265A3232C86 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 116;
  Best Local Similarity   80.0%;  Pred. No. 1e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         79 TYWLS 83


RESULT 29
Q5N0Q1_SYNP6
ID   Q5N0Q1_SYNP6 PRELIMINARY;      PRT;   123 AA.
AC   Q5N0Q1;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=syc1929_d;
OS   Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX   NCBI_TaxID=269084;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PCC6301;
RA   Sugita M.;
RT   "Complete genome structure of the unicellular cyanobacterium Anacystis
RT   nidulans 6301 (Synechococcus sp. PCC6301).";
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP008231; BAD80119.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   123 AA;  13467 MW;  91EC1215ACBC3856 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 123;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         12 TYWLS 16


RESULT 30
Q9ZV01_ARATH
ID   Q9ZV01_ARATH PRELIMINARY;      PRT;   124 AA.
AC   Q9ZV01;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein At2g39070.
GN   Name=At2g39070;
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA   Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Town C.D., Kaul S.;
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC005770; AAC79617.1; -; Genomic_DNA.
DR   PIR; G84812; G84812.
KW   Hypothetical protein.
SQ   SEQUENCE   124 AA;  13991 MW;  79565D167C0DB681 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 124;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         16 TYWLS 20


RESULT 31
Q8WSW6_DUGTI
ID   Q8WSW6_DUGTI PRELIMINARY;      PRT;   145 AA.
AC   Q8WSW6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Scarf1.
GN   Name=scarf1;
OS   Dugesia tigrina (Planarian).
OC   Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
OC   Paludicola; Dugesiidae; Girardia.
OX   NCBI_TaxID=6162;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22140212; PubMed=12145187; DOI=10.1093/glycob/cwf056;
RA   Shagin D.A., Barsova E.V., Bogdanova E.A., Britanova O.V.,
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RA   Gurskaya N.G., Lukyanov K.A., Matz M.V., Punkova N.I., Usman N.Y.,
RA   Kopantzev E.P., Salo E., Lukyanov S.A.;
RT   "Identification and characterization of a new family of C-type lectin-
RT   like genes from planaria Girardia tigrina.";
RL   Glycobiology 12:463-472(2002).
DR   EMBL; AY057980; AAL29937.1; -; Genomic_DNA.
DR   HSSP; P05452; 1HTN.
DR   GO; GO:0005529; F:sugar binding; IEA.
DR   InterPro; IPR001304; Lectin_C.
DR   Pfam; PF00059; Lectin_C; 1.
DR   SMART; SM00034; CLECT; 1.
DR   PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
DR   PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SQ   SEQUENCE   145 AA;  16670 MW;  3D1337BBE477CB25 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 145;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db         68 TYWMN 72


RESULT 32
LUXS_BACHD
ID   LUXS_BACHD     STANDARD;      PRT;   158 AA.
AC   Q9K7K8;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   S-ribosylhomocysteine lyase (EC 4.4.1.21) (Autoinducer-2 production
DE   protein luxS) (AI-2 synthesis protein).
GN   Name=luxS; OrderedLocusNames=BH3353;
OS   Bacillus halodurans.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=86665;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=C-125 / JCM 9153;
RX   MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA   Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA   Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA   Horikoshi K.;
RT   "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT   halodurans and genomic sequence comparison with Bacillus subtilis.";
RL   Nucleic Acids Res. 28:4317-4331(2000).
CC   -!- FUNCTION: Involved in the synthesis of autoinducer 2 (AI-2) which
CC       is secreted by bacteria and is used to communicate both the cell
CC       density and the metabolic potential of the environment. The
CC       regulation of gene expression in response to changes in cell
CC       density is called quorum sensing. Catalyzes the transformation of
CC       S-ribosylhomocysteine (RHC) to homocysteine (HC) and 4,5-
CC       dihydroxy-2,3-pentadione (DPD) (By similarity).
CC   -!- CATALYTIC ACTIVITY: S-(5-deoxy-D-ribos-5-yl)-L-homocysteine = L-
CC       homocysteine + (S)-4,5-dihydroxypentan-2,3-dione.
CC   -!- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC   -!- SUBUNIT: Homodimer (By similarity).
CC   -!- SIMILARITY: Belongs to the luxS family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; BA000004; BAB07072.1; -; Genomic_DNA.
DR   PIR; A84069; A84069.
DR   HSSP; O34667; 1IE0.
DR   SMR; Q9K7K8; 2-156.
DR   HAMAP; MF_00091; -; 1.
DR   InterPro; IPR003815; LuxS.
DR   Pfam; PF02664; LuxS; 1.
DR   PIRSF; PIRSF006160; AI2; 1.
DR   PRINTS; PR01487; LUXSPROTEIN.
DR   ProDom; PD013172; LuxS; 1.
KW   Autoinducer synthesis; Complete proteome; Iron; Lyase; Metal-binding;
KW   Quorum sensing.
FT   METAL        54     54       Iron (By similarity).
FT   METAL        58     58       Iron (By similarity).
FT   METAL       126    126       Iron (By similarity).
SQ   SEQUENCE   158 AA;  17986 MW;  68101401BA079300 CRC64;

  Query Match             90.6%;  Score 29;  DB 1;  Length 158;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        142 TYWLS 146


RESULT 33
Q88MJ3_PSEPK
ID   Q88MJ3_PSEPK PRELIMINARY;      PRT;   159 AA.
AC   Q88MJ3;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=PP1578;
OS   Pseudomonas putida (strain KT2440).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=160488;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22423060; PubMed=12534463;
RX   DOI=10.1046/j.1462-2920.2002.00366.x;
RA   Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA   Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA   Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA   Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA   Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA   Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA   Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA   Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA   Fraser C.M.;
RT   "Complete genome sequence and comparative analysis of the
RT   metabolically versatile Pseudomonas putida KT2440.";
RL   Environ. Microbiol. 4:799-808(2002).
DR   EMBL; AE016779; AAN67199.1; -; Genomic_DNA.
DR   TIGR; PP1578; -.
KW   Complete proteome.
SQ   SEQUENCE   159 AA;  17547 MW;  8AF9EEA44C69C79D CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 159;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db         28 TYWMT 32


RESULT 34
P73017_SYNY3
ID   P73017_SYNY3 PRELIMINARY;      PRT;   170 AA.
AC   P73017;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Slr1052 protein.
GN   OrderedLocusNames=slr1052;
OS   Synechocystis sp. (strain PCC 6803).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
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OX   NCBI_TaxID=1148;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97061201; PubMed=8905231;
RA   Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA   Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
RA   Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA   Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA   Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT   entire genome and assignment of potential protein-coding regions.";
RL   DNA Res. 3:109-136(1996).
DR   EMBL; BA000022; BAA17037.1; -; Genomic_DNA.
DR   PIR; S74997; S74997.
DR   GO; GO:0005488; F:binding; IEA.
DR   GO; GO:0015979; P:photosynthesis; IEA.
DR   InterPro; IPR011990; TPR-like_helical.
KW   Complete proteome.
SQ   SEQUENCE   170 AA;  19470 MW;  996DCBE26E8599F1 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 170;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        166 TYWLS 170


RESULT 35
Q8QQT8_PRRSV
ID   Q8QQT8_PRRSV PRELIMINARY;      PRT;   173 AA.
AC   Q8QQT8;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Truncated envelope glycoprotein.
GN   Name=ORF5;
OS   Porcine reproductive and respiratory syndrome virus (PRRSV).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC   Arteriviridae; Arterivirus.
OX   NCBI_TaxID=28344;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=uab2;
RX   MEDLINE=22492680; PubMed=12604802; DOI=10.1099/vir.0.18478-0;
RA   Mateu E., Martin M., Vidal D.;
RT   "Genetic diversity and phylogenetic analysis of glycoprotein 5 of
RT   European-type porcine reproductive and respiratory virus strains in
RT   Spain.";
RL   J. Gen. Virol. 84:529-534(2003).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=uab2;
RA   Mateu E.M., Martin M., Vidal D.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF495514; AAM15952.1; -; Genomic_RNA.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   InterPro; IPR001332; Arteri_glycop.
DR   InterPro; IPR003239; Porcine_RR_virus.
DR   Pfam; PF00951; Arteri_Gl; 1.
DR   ProDom; PD001151; Porcine_RR_virus; 1.
KW   Envelope protein.
SQ   SEQUENCE   173 AA;  19581 MW;  52F6C92C3FF75629 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 173;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         55 TYWLS 59


RESULT 36
Q950U9_HYACU
ID   Q950U9_HYACU PRELIMINARY;      PRT;   182 AA.
AC   Q950U9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Orf182.
GN   Name=orf182;
OS   Hyaloraphidium curvatum.
OG   Mitochondrion.
OC   Eukaryota; Fungi; Fungi incertae sedis; Hyaloraphidium.
OX   NCBI_TaxID=82268;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21851207; PubMed=11861890;
RA   Forget L., Ustinova J., Wang Z., Huss V.A.R., Lang B.F.;
RT   "Hyaloraphidium curvatum: a linear mitochondrial genome, tRNA editing,
RT   and an evolutionary link to lower fungi.";
RL   Mol. Biol. Evol. 19:310-319(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Lang F.B.F.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF402142; AAK83417.1; -; Genomic_DNA.
DR   GO; GO:0005739; C:mitochondrion; IEA.
KW   Mitochondrion.
SQ   SEQUENCE   182 AA;  21371 MW;  2E9A3ED397C95ED1 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 182;
  Best Local Similarity   80.0%;  Pred. No. 1.6e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db        103 TYWMT 107


RESULT 37
Q7V8H5_PROMM
ID   Q7V8H5_PROMM PRELIMINARY;      PRT;   195 AA.
AC   Q7V8H5;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hemolysin-type calcium-binding protein.
GN   OrderedLocusNames=PMT0372;
OS   Prochlorococcus marinus (strain MIT 9313).
OC   Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC   Prochlorococcus.
OX   NCBI_TaxID=74547;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
RA   Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P.,
RA   Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
RA   Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
RA   Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
RA   Webb E.A., Zinser E.R., Chisholm S.W.;
RT   "Genome divergence in two Prochlorococcus ecotypes reflects oceanic
RT   niche differentiation.";
RL   Nature 424:1042-1047(2003).
DR   EMBL; BX572096; CAE20547.1; -; Genomic_DNA.
DR   HSSP; P16317; 1K7I.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   InterPro; IPR001343; Hemlysn_Ca_bind.
DR   Pfam; PF00353; HemolysinCabind; 2.
DR   PRINTS; PR00313; CABNDNGRPT.
KW   Complete proteome.
SQ   SEQUENCE   195 AA;  20591 MW;  A8B74E78124975BB CRC64;
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  Query Match             90.6%;  Score 29;  DB 2;  Length 195;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        129 TYWLS 133


RESULT 38
Q6TF35_PRRSV
ID   Q6TF35_PRRSV PRELIMINARY;      PRT;   201 AA.
AC   Q6TF35;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   GP5 protein.
GN   Name=ORF5;
OS   Porcine reproductive and respiratory syndrome virus (PRRSV).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC   Arteriviridae; Arterivirus.
OX   NCBI_TaxID=28344;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15016889; DOI=10.1128/JVI.78.7.3684-3703.2004;
RA   Ropp S.L., Mahlum Wees C.E., Fang Y., Nelson E.A., Rossow K.D.,
RA   Bien M., Arndt B., Preszler S., Steen P., Christopher-Hennings J.,
RA   Collins J.E., Benfield D.A., Faaberg K.S.;
RT   "Characterization of emerging European-like porcine reproductive and
RT   respiratory syndrome virus isolates in the United States.";
RL   J. Virol. 78:3684-3703(2004).
DR   EMBL; AY422808; AAR84063.1; -; Genomic_RNA.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   InterPro; IPR001332; Arteri_glycop.
DR   InterPro; IPR003239; Porcine_RR_virus.
DR   Pfam; PF00951; Arteri_Gl; 1.
DR   ProDom; PD001151; Porcine_RR_virus; 1.
SQ   SEQUENCE   201 AA;  22347 MW;  2AA829080ADBEF80 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 201;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         55 TYWLS 59


RESULT 39
Q8JJF4_PRRSV
ID   Q8JJF4_PRRSV PRELIMINARY;      PRT;   201 AA.
AC   Q8JJF4;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Major envelope glycoprotein GP5.
OS   Porcine reproductive and respiratory syndrome virus (PRRSV).
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC   Arteriviridae; Arterivirus.
OX   NCBI_TaxID=28344;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=1/93, and 1751/93;
RA   Storgaard T., Nielsen H.S.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY035926; AAK61646.1; -; Genomic_RNA.
DR   EMBL; AY035927; AAK61647.1; -; Genomic_RNA.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   InterPro; IPR001332; Arteri_glycop.
DR   InterPro; IPR003239; Porcine_RR_virus.
DR   Pfam; PF00951; Arteri_Gl; 1.
DR   ProDom; PD001151; Porcine_RR_virus; 1.
KW   Envelope protein.
SQ   SEQUENCE   201 AA;  22490 MW;  A7FCD201AE73A909 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 201;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         55 TYWLS 59


RESULT 40
Q5WG47_BACSK
ID   Q5WG47_BACSK PRELIMINARY;      PRT;   228 AA.
AC   Q5WG47;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Multidrug ABC transporter permease.
GN   OrderedLocusNames=ABC2123;
OS   Bacillus clausii (strain KSM-K16).
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=66692;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=KSM-K16;
RA   Takaki Y., Kageyama Y., Shimamura S., Suzuki H., Nishi S., Hatada Y.,
RA   Kawai S., Ito S., Horikoshi K.;
RT   "The complete genome sequence of the alkaliphilic Bacillus clausii
RT   KSM-K16.";
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP006627; BAD64658.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR000412; ABC_2.
DR   Pfam; PF01061; ABC2_membrane; 1.
KW   Complete proteome.
SQ   SEQUENCE   228 AA;  25755 MW;  033334E294648A33 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 228;
  Best Local Similarity   80.0%;  Pred. No. 1.9e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        185 TYWLS 189


RESULT 41
Q8XXM7_RALSO
ID   Q8XXM7_RALSO PRELIMINARY;      PRT;   231 AA.
AC   Q8XXM7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   PUTATIVE TRANSCRIPTION REGULATOR PROTEIN.
GN   OrderedLocusNames=RSc2086; ORFNames=RS03651;
OS   Ralstonia solanacearum (Pseudomonas solanacearum).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Ralstonia.
OX   NCBI_TaxID=305;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=GMI1000;
RX   MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA   Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA   Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA   Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
RA   Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA   Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA   Weissenbach J., Boucher C.A.;
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RT   "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL   Nature 415:497-502(2002).
CC   -!- FUNCTION: Repressor involved in choline regulation of the bet
CC       genes (By similarity).
CC   -!- PATHWAY: Betaine biosynthesis from choline; regulation.
DR   EMBL; AL646068; CAD15793.1; -; Genomic_DNA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   InterPro; IPR012287; Homeodomain-rel.
DR   InterPro; IPR001647; HTH_TetR.
DR   Pfam; PF00440; TetR_N; 1.
DR   PRINTS; PR00455; HTHTETR.
DR   PROSITE; PS50977; HTH_TETR_2; 1.
KW   Complete proteome; DNA-binding; Transcription;
KW   Transcription regulation.
SQ   SEQUENCE   231 AA;  27210 MW;  85B03FB6072F4DF8 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 231;
  Best Local Similarity   80.0%;  Pred. No. 2e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        166 TYWLS 170


RESULT 42
Q5F6W3_NEIG1
ID   Q5F6W3_NEIG1 PRELIMINARY;      PRT;   233 AA.
AC   Q5F6W3;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=NGO1431;
OS   Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC   Neisseriaceae; Neisseria.
OX   NCBI_TaxID=242231;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA   Lewis L.A., Gillaspy A.F., McLaughlin R.E., Gipson M., Ducey T.F.,
RA   Ownbey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
RA   Song L., Lin S., Yuan X., Najar F., Zhan M., Ren Q., Zhu H., Qi S.,
RA   Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
RT   "The complete genome sequence of Neisseria gonorrhoeae.";
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE004969; AAW90074.1; -; Genomic_DNA.
DR   InterPro; IPR010917; TonB_recept_C.
DR   PROSITE; PS01156; TONB_DEPENDENT_REC_2; UNKNOWN_1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   233 AA;  25731 MW;  49C9857E07ACBBD6 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 233;
  Best Local Similarity   80.0%;  Pred. No. 2e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        224 TYWLS 228


RESULT 43
Q62IL2_BURMA
ID   Q62IL2_BURMA PRELIMINARY;      PRT;   239 AA.
AC   Q62IL2;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Transcriptional reguator, TetR family.
GN   OrderedLocusNames=BMA1857;
OS   Burkholderia mallei (Pseudomonas mallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia.
OX   NCBI_TaxID=13373;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 23344;
RX   PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA   Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA   Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA   Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA   Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA   Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M.,
RA   Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA   Zafar N., Zhou L., Fraser C.M.;
RT   "Structural flexibility in the Burkholderia mallei genome.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
CC   -!- FUNCTION: Repressor involved in choline regulation of the bet
CC       genes (By similarity).
CC   -!- PATHWAY: Betaine biosynthesis from choline; regulation.
DR   EMBL; CP000010; AAU49406.1; -; Genomic_DNA.
DR   TIGR; BMA1857; -.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0006350; P:transcription; IEA.
DR   InterPro; IPR001647; HTH_TetR.
DR   Pfam; PF00440; TetR_N; 1.
DR   PRINTS; PR00455; HTHTETR.
DR   PROSITE; PS50977; HTH_TETR_2; 1.
KW   Complete proteome; DNA-binding; Transcription;
KW   Transcription regulation.
SQ   SEQUENCE   239 AA;  28373 MW;  05BA809ED09A47B6 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 239;
  Best Local Similarity   80.0%;  Pred. No. 2e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        162 TYWLS 166


RESULT 44
Q63VQ6_BURPS
ID   Q63VQ6_BURPS PRELIMINARY;      PRT;   239 AA.
AC   Q63VQ6;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Putative TetR-family transcriptional regulator.
GN   OrderedLocusNames=BPSL1188;
OS   Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia; pseudomallei group.
OX   NCBI_TaxID=28450;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=K96243;
RX   PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA   Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA   Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA   Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
RA   Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA   Chillingworth T., Cronin A., Crossett B., Davis P., DeShazer D.,
RA   Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA   Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA   Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA   Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA   Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT   "Genomic plasticity of the causative agent of melioidosis,
RT   Burkholderia pseudomallei.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
CC   -!- FUNCTION: Repressor involved in choline regulation of the bet
CC       genes (By similarity).
CC   -!- PATHWAY: Betaine biosynthesis from choline; regulation.
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DR   EMBL; BX571965; CAH35183.1; -; Genomic_DNA.
DR   GO; GO:0003700; F:transcription factor activity; IEA.
DR   GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR   GO; GO:0006350; P:transcription; IEA.
DR   InterPro; IPR001647; HTH_TetR.
DR   Pfam; PF00440; TetR_N; 1.
DR   PRINTS; PR00455; HTHTETR.
DR   PROSITE; PS50977; HTH_TETR_2; 1.
KW   Complete proteome; DNA-binding; Transcription;
KW   Transcription regulation.
SQ   SEQUENCE   239 AA;  28472 MW;  4839ED5ED09D2A74 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 239;
  Best Local Similarity   80.0%;  Pred. No. 2e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        162 TYWLS 166


RESULT 45
Q7SC34_NEUCR
ID   Q7SC34_NEUCR PRELIMINARY;      PRT;   245 AA.
AC   Q7SC34;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   Name=NCU05341.1;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=OR74A;
RA   Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA   Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA   Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA   Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA   Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA   Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA   Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA   Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA   Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
RA   Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA   DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA   Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA   Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA   Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT   "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL   Nature 0:0-0(2003).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AABX01000141; EAA34037.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   245 AA;  27349 MW;  C8417E953E9583AD CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 245;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        113 TYWLS 117


RESULT 46
Q96UB7_NEUCR
ID   Q96UB7_NEUCR PRELIMINARY;      PRT;   249 AA.
AC   Q96UB7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein 68B2.050.
GN   Name=68B2.050;
OS   Neurospora crassa.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX   NCBI_TaxID=5141;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA   Nyakatura G., Mewes H.W., Mannhaupt G.;
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   German Neurospora genome project;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL353821; CAD01106.1; -; Genomic_DNA.
DR   PIR; T48821; T48821.
KW   Hypothetical protein.
SQ   SEQUENCE   249 AA;  28773 MW;  F2D3EAB0F95BEAB8 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 249;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        114 TYWLS 118


RESULT 47
Q525H6_MAGGR
ID   Q525H6_MAGGR PRELIMINARY;      PRT;   252 AA.
AC   Q525H6;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=MG09230.4;
OS   Magnaporthe grisea 70-15.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
OX   NCBI_TaxID=242507;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=70-15;
RA   Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA   Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA   Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA   Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA   Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA   Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA   Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA   David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA   Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA   Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA   Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA   Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA   Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA   Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA   Jaffe D., Jones C., Kamal M., Kamat A., Kamvysselis M., Karlsson E.,
RA   Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
RA   Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA   Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
RA   Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA   Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA   Mccarthy M., Mcdonough S., Mcghee T., Meldrim J., Meneus L.,
RA   Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA   Mozes J., Mulrain L., Munson G., Naylor J., Newes C., Nguyen C.,
RA   Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA   Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
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RA   O'neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piqani B.,
RA   Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA   Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA   Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA   Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA   Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA   Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA   Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA   Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA   Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA   Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA   Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA   Zimmer A., Zody M., Lander E.;
RT   "The genome sequence of Magnaporthe grisea.";
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=70-15;
RA   Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=70-15;
RA   Zhu H., Blackmon B.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AACU01000647; EAA55423.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   252 AA;  27585 MW;  D094F00029CC9066 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 252;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         70 TYWLS 74


RESULT 48
Q7QC09_ANOGA
ID   Q7QC09_ANOGA PRELIMINARY;      PRT;   252 AA.
AC   Q7QC09;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ENSANGP00000014852 (Fragment).
GN   ORFNames=ENSANGG00000012363;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RT   "Anopheles gambiae re-annotation.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008859; EAA08097.2; -; Genomic_DNA.
DR   InterPro; IPR000195; RabGAP_TBC.
DR   PROSITE; PS50086; TBC_RABGAP; 1.
FT   NON_TER     252    252
SQ   SEQUENCE   252 AA;  29726 MW;  3D65BA25C3037977 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 252;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
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Db        152 TYWMA 156


RESULT 49
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AC   Q4LZS7;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Regulatory protein, TetR precursor.
GN   ORFNames=Bcen2424DRAFT_6582;
OS   Burkholderia cenocepacia HI2424.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX   NCBI_TaxID=331272;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=HI2424;
RG   US DOE Joint Genome Institute (JGI-PGF);
RA   Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA   Hammon N., Israni S., Pitluck S., Richardson P.;
RT   "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT   HI2424.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=HI2424;
RG   US DOE Joint Genome Institute (JGI-ORNL);
RA   Larimer F., Land M.;
RT   "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT   HI2424.";
RL   Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAHL01000002; EAM21695.1; -; Genomic_DNA.
KW   Signal.
FT   SIGNAL      252    252       Potential.
SQ   SEQUENCE   252 AA;  29694 MW;  3B3308DFD6C32039 CRC64;

  Query Match             90.6%;  Score 29;  DB 2;  Length 252;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        162 TYWLS 166


RESULT 50
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AC   Q9XDB7;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Particulate methane monooxygenase subunit PmoC3.
GN   Name=pmoC3;
OS   Methylococcus capsulatus.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
OC   Methylococcaceae; Methylococcus.
OX   NCBI_TaxID=414;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
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RC STRAIN=Bath;
RX MEDLINE=99303333; PubMed=10376840;
RA Stolyar S., Costello A.M., Peeples T.L., Lidstrom M.E.;
RT "Role of multiple gene copies in particulate methane monooxygenase
RT activity in the methane-oxidizing bacterium Methylococcus capsulatus
RT Bath.";
RL Microbiology 145:1235-1244(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Bath;
RA Stolyar S.M., Lidstrom M.E.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF091320; AAD43965.2; -; Genomic_DNA.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
DR InterPro; IPR006980; AmoC.
DR Pfam; PF04896; AmoC; 1.
KW Monooxygenase.
SQ SEQUENCE 253 AA; 29605 MW; 7AE3CC01FF661298 CRC64;

Query Match 90.6%; Score 29; DB 2; Length 253;
Best Local Similarity 80.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:
Db 58 TYWMN 62

Search completed: March 23, 2006, 02:04:05
Job time : 80.1566 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:05:22 ; Search time 10.8219 Seconds
(without alignments)
38.198 Million cell updates/sec

Title: US-10-755-382-23
Perfect score: 32
Sequence: 1 TYWMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	5	1	US-08-318-157B-23	Sequence 23, Appl
2	32	100.0	5	2	US-09-253-794-23	Sequence 23, Appl
3	32	100.0	119	1	US-08-318-157B-2	Sequence 2, Appli
4	32	100.0	119	1	US-08-318-157B-8	Sequence 8, Appli
5	32	100.0	119	1	US-08-318-157B-9	Sequence 9, Appli
6	32	100.0	119	1	US-08-318-157B-10	Sequence 10, Appl
7	32	100.0	119	1	US-08-318-157B-11	Sequence 11, Appl
8	32	100.0	119	1	US-08-318-157B-12	Sequence 12, Appl
9	32	100.0	119	1	US-08-318-157B-13	Sequence 13, Appl
10	32	100.0	119	1	US-08-318-157B-14	Sequence 14, Appl
11	32	100.0	119	1	US-08-318-157B-15	Sequence 15, Appl
12	32	100.0	119	1	US-08-318-157B-17	Sequence 17, Appl
13	32	100.0	119	1	US-08-318-157B-57	Sequence 57, Appl
14	32	100.0	119	1	US-08-318-157B-58	Sequence 58, Appl
15	32	100.0	119	2	US-09-253-794-2	Sequence 2, Appli
16	32	100.0	119	2	US-09-253-794-8	Sequence 8, Appli
17	32	100.0	119	2	US-09-253-794-9	Sequence 9, Appli
18	32	100.0	119	2	US-09-253-794-10	Sequence 10, Appl
19	32	100.0	119	2	US-09-253-794-11	Sequence 11, Appl
20	32	100.0	119	2	US-09-253-794-12	Sequence 12, Appl
21	32	100.0	119	2	US-09-253-794-13	Sequence 13, Appl
22	32	100.0	119	2	US-09-253-794-14	Sequence 14, Appl
23	32	100.0	119	2	US-09-253-794-15	Sequence 15, Appl
24	32	100.0	119	2	US-09-253-794-17	Sequence 17, Appl
25	32	100.0	119	2	US-09-253-794-57	Sequence 57, Appl
26	32	100.0	119	2	US-09-253-794-58	Sequence 58, Appl
27	32	100.0	157	2	US-09-270-767-33788	Sequence 33788, A
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30	29	90.6	261	2	US-09-489-039A-11728	Sequence 11728, A
31	29	90.6	479	2	US-09-489-039A-13978	Sequence 13978, A
32	29	90.6	543	2	US-09-543-681A-6901	Sequence 6901, Ap
33	29	90.6	546	2	US-09-252-991A-19089	Sequence 19089, A
34	28	87.5	98	1	US-07-942-245-37	Sequence 37, Appl
35	28	87.5	98	2	US-10-194-975-15	Sequence 15, Appl
36	28	87.5	98	2	US-09-534-717-664	Sequence 664, App
37	28	87.5	98	2	US-09-534-717-666	Sequence 666, App
38	28	87.5	117	2	US-09-065-059-15	Sequence 15, Appl
39	28	87.5	117	2	US-08-545-809A-95	Sequence 95, Appl
40	28	87.5	117	2	US-09-515-697-95	Sequence 95, Appl
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42	28	87.5	220	2	US-09-949-016-7266	Sequence 7266, Ap
43	28	87.5	240	2	US-09-252-991A-28028	Sequence 28028, A
44	28	87.5	247	2	US-09-902-540-11435	Sequence 11435, A
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48	28	87.5	273	1	US-08-978-404B-6	Sequence 6, Appli
49	28	87.5	296	2	US-09-134-000C-6205	Sequence 6205, Ap
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52	28	87.5	364	1	US-08-423-564-6	Sequence 6, Appli
53	28	87.5	380	1	US-08-609-572-4	Sequence 4, Appli
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55	28	87.5	380	2	US-08-846-340-4	Sequence 4, Appli
56	28	87.5	380	2	US-08-846-344-4	Sequence 4, Appli
57	28	87.5	380	2	US-09-301-808-4	Sequence 4, Appli
58	28	87.5	429	2	US-09-914-841A-1	Sequence 1, Appli
59	28	87.5	458	2	US-09-248-796A-17958	Sequence 17958, A
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61	28	87.5	507	2	US-09-914-841A-15	Sequence 15, Appl
62	28	87.5	648	2	US-09-715-858-4	Sequence 4, Appli
63	28	87.5	914	2	US-09-437-054A-8	Sequence 8, Appli
64	27	84.4	5	1	US-08-244-626-12	Sequence 12, Appl
65	27	84.4	5	1	US-08-480-434-32	Sequence 32, Appl
66	27	84.4	5	1	US-08-053-451B-32	Sequence 32, Appl
67	27	84.4	5	2	US-10-226-795-23	Sequence 23, Appl
68	27	84.4	24	2	US-08-525-539A-19	Sequence 19, Appl
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70	27	84.4	31	2	US-09-871-889A-6	Sequence 6, Appli
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73	27	84.4	98	2	US-09-840-459-52	Sequence 52, Appl
74	27	84.4	98	2	US-09-497-625A-47	Sequence 47, Appl
75	27	84.4	98	2	US-09-497-625A-52	Sequence 52, Appl
76	27	84.4	99	1	US-08-244-626-10	Sequence 10, Appl
77	27	84.4	100	2	US-09-840-459-36	Sequence 36, Appl
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79	27	84.4	101	2	US-10-004-381-7	Sequence 7, Appli
80	27	84.4	103	2	US-10-630-406-2	Sequence 2, Appli
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86	27	84.4	117	4	PCT-US93-09166-3	Sequence 3, Appli
87	27	84.4	118	2	US-09-232-290-53	Sequence 53, Appl
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89	27	84.4	120	1	US-08-053-451B-30	Sequence 30, Appl
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91	27	84.4	122	1	US-08-335-573-7	Sequence 7, Appli
92	27	84.4	124	1	US-07-958-140-4	Sequence 4, Appli
93	27	84.4	124	4	PCT-US93-09166-4	Sequence 4, Appli
94	27	84.4	143	2	US-09-270-767-39830	Sequence 39830, A
95	27	84.4	143	2	US-09-270-767-55047	Sequence 55047, A
96	27	84.4	150	2	US-10-226-795-22	Sequence 22, Appl
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104	27	84.4	185	2	US-09-562-737-120	Sequence 120, App
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112	27	84.4	298	2	US-09-883-758-2	Sequence 2, Appli
113	27	84.4	301	2	US-09-927-738-15	Sequence 15, Appl
114	27	84.4	342	2	US-09-252-991A-18101	Sequence 18101, A
115	27	84.4	439	2	US-09-769-863-29	Sequence 29, Appl
116	27	84.4	460	2	US-10-630-406-5	Sequence 5, Appli
117	27	84.4	466	2	US-09-489-039A-14325	Sequence 14325, A
118	27	84.4	477	2	US-09-248-796A-15439	Sequence 15439, A
119	27	84.4	485	2	US-09-252-991A-32881	Sequence 32881, A
120	27	84.4	561	2	US-09-252-991A-23786	Sequence 23786, A
121	27	84.4	580	2	US-09-252-991A-30180	Sequence 30180, A
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146	27	84.4	641	2	US-09-543-681A-4359	Sequence 4359, Ap
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148	27	84.4	687	1	US-08-702-367A-29	Sequence 29, Appl
149	27	84.4	696	1	US-08-765-081-5	Sequence 5, Appli
150	27	84.4	696	2	US-09-098-082-5	Sequence 5, Appli
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154	27	84.4	739	2	US-09-543-681A-6688	Sequence 6688, Ap
155	27	84.4	2108	2	US-09-538-092-87	Sequence 87, Appl
156	26	81.2	72	2	US-09-248-796A-21147	Sequence 21147, A
157	26	81.2	77	2	US-09-513-999C-7466	Sequence 7466, Ap
158	26	81.2	110	6	5514582-9	Patent No. 5514582
159	26	81.2	117	2	US-10-104-047-3157	Sequence 3157, Ap
160	26	81.2	145	2	US-09-828-995B-55	Sequence 55, Appl
161	26	81.2	148	2	US-10-012-231A-336	Sequence 336, App
162	26	81.2	148	2	US-10-015-389A-336	Sequence 336, App
163	26	81.2	148	2	US-10-006-768A-336	Sequence 336, App
164	26	81.2	148	2	US-10-015-671A-336	Sequence 336, App
165	26	81.2	148	2	US-10-015-393A-336	Sequence 336, App
166	26	81.2	148	2	US-10-011-833A-336	Sequence 336, App
167	26	81.2	148	2	US-10-006-041A-336	Sequence 336, App
168	26	81.2	148	2	US-10-012-064A-336	Sequence 336, App
169	26	81.2	150	2	US-09-270-767-32604	Sequence 32604, A
170	26	81.2	150	2	US-09-270-767-47821	Sequence 47821, A
171	26	81.2	155	2	US-09-408-020-78	Sequence 78, Appl
172	26	81.2	197	2	US-09-328-352-5731	Sequence 5731, Ap
173	26	81.2	213	2	US-09-408-020-64	Sequence 64, Appl
174	26	81.2	260	2	US-09-248-796A-14604	Sequence 14604, A
175	26	81.2	279	2	US-09-489-039A-10161	Sequence 10161, A
176	26	81.2	291	2	US-09-252-991A-28294	Sequence 28294, A
177	26	81.2	313	2	US-09-902-540-15660	Sequence 15660, A
178	26	81.2	316	2	US-09-248-796A-18830	Sequence 18830, A
179	26	81.2	318	2	US-09-828-995B-69	Sequence 69, Appl
180	26	81.2	325	2	US-09-328-352-5100	Sequence 5100, Ap
181	26	81.2	333	2	US-09-902-540-12170	Sequence 12170, A
182	26	81.2	335	2	US-09-489-039A-11298	Sequence 11298, A
183	26	81.2	339	2	US-09-719-243-2	Sequence 2, Appli
184	26	81.2	358	2	US-09-719-243-3	Sequence 3, Appli
185	26	81.2	365	2	US-09-828-995B-66	Sequence 66, Appl
186	26	81.2	370	2	US-09-303-518D-110	Sequence 110, App
187	26	81.2	372	2	US-09-252-991A-30132	Sequence 30132, A
188	26	81.2	386	2	US-09-828-995B-61	Sequence 61, Appl
189	26	81.2	405	2	US-09-710-279-2962	Sequence 2962, Ap
190	26	81.2	462	2	US-09-976-594-427	Sequence 427, App
191	26	81.2	465	2	US-09-134-001C-4428	Sequence 4428, Ap
192	26	81.2	554	2	US-09-543-681A-6886	Sequence 6886, Ap
193	26	81.2	561	2	US-09-828-995B-72	Sequence 72, Appl
194	26	81.2	561	2	US-09-828-995B-81	Sequence 81, Appl
195	26	81.2	563	2	US-09-828-995B-78	Sequence 78, Appl
196	26	81.2	565	2	US-09-489-039A-8414	Sequence 8414, Ap
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206	26	81.2	716	2	US-09-303-518D-108	Sequence 108, App
207	26	81.2	716	2	US-09-303-518D-112	Sequence 112, App
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212	26	81.2	1063	2	US-09-248-796A-14361	Sequence 14361, A
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216	26	81.2	1223	2	US-09-538-092-777	Sequence 777, App
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219	26	81.2	1501	2	US-09-487-558B-346	Sequence 346, App
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334	25	78.1	347	2	US-09-435-242-13	Sequence 13, Appl
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447	24	75.0	15	2	US-09-688-188B-126	Sequence 126, App
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459	24	75.0	22	1	US-08-471-282A-75	Sequence 75, Appl
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594	24	75.0	142	2	US-09-855-632-13	Sequence 13, Appl
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710	24	75.0	242	2	US-09-443-213-23	Sequence 23, Appl
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ALIGNMENTS

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RESULT 1
US-08-318-157B-23
; Sequence 23, Applicatiqn US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-23

  Query Match           100.0%;  Score 32;  DB 1;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 4.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db          1 TYWMS 5


RESULT 2
US-09-253-794-23
; Sequence 23, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 23:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 5 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-253-794-23

  Query Match           100.0%;  Score 32;  DB 2;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 4.6e+05;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db          1 TYWMS 5


RESULT 3
US-08-318-157B-2
; Sequence 2, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
```

```
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-2

  Query Match             100.0%;  Score 32;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 4
US-08-318-157B-8
; Sequence 8, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-8

  Query Match             100.0%;  Score 32;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 5
US-08-318-157B-9
; Sequence 9, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-9

  Query Match             100.0%;  Score 32;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35
```

```
RESULT 6
US-08-318-157B-10
; Sequence 10, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-10

  Query Match             100.0%;  Score 32;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 7
US-08-318-157B-11
; Sequence 11, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-11

  Query Match             100.0%;  Score 32;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 8
US-08-318-157B-12
; Sequence 12, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-12
```

```
  Query Match           100.0%;  Score 32;  DB 1;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 9
US-08-318-157B-13
; Sequence 13, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-13

  Query Match           100.0%;  Score 32;  DB 1;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 10
US-08-318-157B-14
; Sequence 14, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-14

  Query Match           100.0%;  Score 32;  DB 1;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 11
US-08-318-157B-15
; Sequence 15, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
```

```
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-15

  Query Match             100.0%;  Score 32;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 12
US-08-318-157B-17
; Sequence 17, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-17

  Query Match             100.0%;  Score 32;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 13
US-08-318-157B-57
; Sequence 57, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-318-157B-57

  Query Match             100.0%;  Score 32;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 14
US-08-318-157B-58
; Sequence 58, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
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;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-318-157B-58

  Query Match             100.0%;  Score 32;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 15
US-09-253-794-2
; Sequence 2, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-253-794-2

  Query Match             100.0%;  Score 32;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 16
US-09-253-794-8
; Sequence 8, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-253-794-8

  Query Match             100.0%;  Score 32;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 17
US-09-253-794-9
; Sequence 9, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
```

```
;                          MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-253-794-9

  Query Match             100.0%;  Score 32;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 18
US-09-253-794-10
; Sequence 10, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 10:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-253-794-10

  Query Match             100.0%;  Score 32;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 19
US-09-253-794-11
; Sequence 11, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 11:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;
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;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-253-794-11

  Query Match           100.0%;  Score 32;  DB 2;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 20
US-09-253-794-12
; Sequence 12, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-253-794-12

  Query Match           100.0%;  Score 32;  DB 2;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 21
US-09-253-794-13
; Sequence 13, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-253-794-13

  Query Match           100.0%;  Score 32;  DB 2;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 22
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
```

```
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

  Query Match             100.0%;  Score 32;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 23
US-09-253-794-15
; Sequence 15, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-253-794-15

  Query Match             100.0%;  Score 32;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 24
US-09-253-794-17
; Sequence 17, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-253-794-17

  Query Match             100.0%;  Score 32;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35
```

```
RESULT 25
US-09-253-794-57
; Sequence 57, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 57:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-253-794-57

  Query Match             100.0%;  Score 32;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 26
US-09-253-794-58
; Sequence 58, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 58:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-253-794-58

  Query Match             100.0%;  Score 32;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 27
US-09-270-767-33788
; Sequence 33788, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33788
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-33788

  Query Match             100.0%;  Score 32;  DB 2;  Length 157;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        143 TYWMS 147


RESULT 28
US-09-270-767-49005
; Sequence 49005, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
```

; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49005
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-49005

Query Match 100.0%; Score 32; DB 2; Length 157;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||||
Db 143 TYWMS 147

RESULT 29
US-09-252-991A-21716
; Sequence 21716, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21716
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21716

Query Match 90.6%; Score 29; DB 2; Length 125;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 40 TYWLS 44

RESULT 30
US-09-489-039A-11728
; Sequence 11728, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11728
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11728

Query Match 90.6%; Score 29; DB 2; Length 261;
Best Local Similarity 80.0%; Pred. No. 7.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
||||:
Db 207 TYWMA 211

RESULT 31
US-09-489-039A-13978
; Sequence 13978, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13978
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13978

Query Match 90.6%; Score 29; DB 2; Length 479;
Best Local Similarity 80.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 110 TYWLS 114

RESULT 32
US-09-543-681A-6901
; Sequence 6901, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6901
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6901

Query Match 90.6%; Score 29; DB 2; Length 543;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 313 TYWLS 317

RESULT 33
US-09-252-991A-19089
; Sequence 19089, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136

```
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 19089
;   LENGTH: 546
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19089

  Query Match             90.6%;  Score 29;  DB 2;  Length 546;
  Best Local Similarity   80.0%;  Pred. No. 1.5e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db        541 TYWMA 545


RESULT 34
US-07-942-245-37
; Sequence 37, Application US/07942245
; Patent No. 5639641
;  GENERAL INFORMATION:
;    APPLICANT:  PEDERSEN, Jan T.
;    APPLICANT:  SEARLE,   Stephen M.J.
;    APPLICANT:  REES,     Anthony R.
;    APPLICANT:  ROGUSKA,  Michael A.
;    APPLICANT:  GUILD,    Braydon C.
;    TITLE OF INVENTION:  SURFACE RESIDUE VENEERING OF RODENT
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  522
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sughrue, Mion, Zinn, Macpeak & Seas
;      STREET:  2100 Pensylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States
;      ZIP:  20037-3202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  HP 9000/700 Workstation
;      OPERATING SYSTEM:  UNIX
;      SOFTWARE:  In house
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/942,245
;      FILING DATE:  09-SEP-1992
;      CLASSIFICATION:  530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;      TELEX:  6491103
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  98 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-942-245-37

  Query Match             87.5%;  Score 28;  DB 1;  Length 98;
  Best Local Similarity   80.0%;  Pred. No. 4.7e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         31 SYWMS 35


RESULT 35
US-10-194-975-15
; Sequence 15, Application US/10194975
; Patent No. 6881557
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: Super Humanized Antibodies
;  FILE REFERENCE: 501231.01
;  CURRENT APPLICATION NUMBER: US/10/194,975
;  CURRENT FILING DATE:  2002-10-10
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 122
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-194-975-15

  Query Match             87.5%;  Score 28;  DB 2;  Length 98;
  Best Local Similarity   80.0%;  Pred. No. 4.7e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         31 SYWMS 35


RESULT 36
US-09-534-717-664
; Sequence 664, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
;  APPLICANT: Jochen, Salfeld et al.
;  TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
;  FILE REFERENCE: BBI-093CP
;  CURRENT APPLICATION NUMBER: US/09/534,717
;  CURRENT FILING DATE: 2000-03-24
;  EARLIER APPLICATION NUMBER: 60/126,603
;  EARLIER FILING DATE: March 25, 1999
;  NUMBER OF SEQ ID NOS: 675
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 664
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-534-717-664

  Query Match             87.5%;  Score 28;  DB 2;  Length 98;
  Best Local Similarity   80.0%;  Pred. No. 4.7e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         31 SYWMS 35


RESULT 37
US-09-534-717-666
; Sequence 666, Application US/09534717
; Patent No. 6914128
; GENERAL INFORMATION:
;  APPLICANT: Jochen, Salfeld et al.
;  TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
;  FILE REFERENCE: BBI-093CP
;  CURRENT APPLICATION NUMBER: US/09/534,717
;  CURRENT FILING DATE: 2000-03-24
;  EARLIER APPLICATION NUMBER: 60/126,603
;  EARLIER FILING DATE: March 25, 1999
;  NUMBER OF SEQ ID NOS: 675
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 666
;   LENGTH: 98
```

```
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-534-717-666

  Query Match             87.5%;  Score 28;  DB 2;  Length 98;
  Best Local Similarity   80.0%;  Pred. No. 4.7e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         31 SYWMS 35


RESULT 38
US-09-065-059-15
; Sequence 15, Application US/09065059
; Patent No. 6068841
;  GENERAL INFORMATION:
;    APPLICANT:  SEINO, Ken-ichiro
;    APPLICANT:  KAYAGAKI, No. 6068841uhiko
;    APPLICANT:  YAGITA, Hideo
;    APPLICANT:  OKUMURA, Ko
;    APPLICANT:  NAKATA, Motomi
;    TITLE OF INVENTION:  THERAPEUTIC AGENT FOR HEPATITIS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDermott, Will & Emery
;      STREET:  99 Canal Center Plaza
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/065,059
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bucca Ph.D., Daniel
;      REGISTRATION NUMBER:  P-42,368
;      REFERENCE/DOCKET NUMBER:  50356-151
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-518-5100
;      TELEFAX:  703-684-1124
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-065-059-15

  Query Match             87.5%;  Score 28;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWM 4
              ||||
Db         30 TYWM 33


RESULT 39
US-08-545-809A-95
; Sequence 95, Application US/08545809A
; Patent No. 6096878
;  GENERAL INFORMATION:
;    APPLICANT:  Honjo, Tasuku
;    APPLICANT:  Matsuda, Fumihiko
;    TITLE OF INVENTION:  HUMAN IMMUNOGLOBULIN VH GENE
;    TITLE OF INVENTION:  SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;    NUMBER OF SEQUENCES:  145
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  225 Franklin Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02110-2804
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/545,809A
;      FILING DATE:  27-MAR-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP93/00603
;      FILING DATE:  10-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Freeman, John W.
;      REGISTRATION NUMBER:  29,066
;      REFERENCE/DOCKET NUMBER:  06501/004001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-542-5070
;      TELEFAX:  617-542-8906
;      TELEX:  200154
;  INFORMATION FOR SEQ ID NO:  95:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-545-809A-95

  Query Match             87.5%;  Score 28;  DB 2;  Length 117;
  Best Local Similarity   80.0%;  Pred. No. 5.5e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         50 SYWMS 54


RESULT 40
US-09-515-697-95
; Sequence 95, Application US/09515697
; Patent No. 6936705
;  GENERAL INFORMATION:
;       APPLICANT: Honjo, Tasuku
;                  Matsuda, Fumihiko
;       TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
;                           SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
;       NUMBER OF SEQUENCES: 145
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson, P.C.
;            STREET: 225 Franklin Street
;            CITY: Boston
;            STATE: MA
;            COUNTRY: US
;            ZIP: 02110-2804
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/515,697
;            FILING DATE: 29-Feb-2000
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/545,809
```

; FILING DATE: 27-MAR-1996
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 95:
US-09-515-697-95

Query Match 87.5%; Score 28; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
:||||
Db 50 SYWMS 54

RESULT 41
US-08-913-555-15
; Sequence 15, Application US/08913555
; Patent No. 6946255
; GENERAL INFORMATION:
; APPLICANT: KAYAGAKI, No. 6946255uhiko
; APPLICANT: YAGITA, Kideo
; APPLICANT: OKUMURA, Ko
; APPLICANT: NAKATA, Motomi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFICALLY
; TITLE OF INVENTION: REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDermott, Will & Emery
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/913,555
; FILING DATE: 19-SEP-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Bucca Ph.D., Daniel
; REGISTRATION NUMBER: 42,368
; REFERENCE/DOCKET NUMBER: 50356-150
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-756-8600
; TELEFAX: 202-756-8699
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-913-555-15

Query Match 87.5%; Score 28; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWM 4
||||
Db 30 TYWM 33

RESULT 42
US-09-949-016-7266
; Sequence 7266, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7266
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7266

Query Match 87.5%; Score 28; DB 2; Length 220;
Best Local Similarity 80.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 152 TYWIS 156

RESULT 43
US-09-252-991A-28028
; Sequence 28028, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28028
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28028

Query Match 87.5%; Score 28; DB 2; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWM 4
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Db 131 TYWM 134

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RESULT 44
US-09-902-540-11435
; Sequence 11435, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11435
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-11435

  Query Match             87.5%;  Score 28;  DB 2;  Length 247;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        165 TYWVS 169


RESULT 45
US-09-270-767-47468
; Sequence 47468, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47468
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-47468

  Query Match             87.5%;  Score 28;  DB 2;  Length 248;
  Best Local Similarity   80.0%;  Pred. No. 1.1e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        128 TYWIS 132


RESULT 46
US-09-543-681A-4210
; Sequence 4210, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
;  APPLICANT: GARY BRETON
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
;  TITLE OF INVENTION:  DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 2709.1002-001
;  CURRENT APPLICATION NUMBER: US/09/543,681A
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 60/128,706
;  PRIOR FILING DATE: 1999-04-09
;  NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4210
;   LENGTH: 263
;   TYPE: PRT
;   ORGANISM: Proteus mirabilis
US-09-543-681A-4210

  Query Match             87.5%;  Score 28;  DB 2;  Length 263;
  Best Local Similarity   80.0%;  Pred. No. 1.2e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |:|||
Db        193 TFWMS 197


RESULT 47
US-08-978-404B-3
; Sequence 3, Application US/08978404B
; Patent No. 5968782
;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  273 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 5968782e
US-08-978-404B-3

  Query Match             87.5%;  Score 28;  DB 1;  Length 273;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWM 4
              ||||
Db         51 TYWM 54


RESULT 48
US-08-978-404B-6
; Sequence 6, Application US/08978404B
; Patent No. 5968782
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;  GENERAL INFORMATION:
;    APPLICANT:  Stevens, Richard L.
;    TITLE OF INVENTION:  MAST CELL PROTEASE THAT CLEAVES
;    TITLE OF INVENTION:  FIBRINOGEN
;    NUMBER OF SEQUENCES:  74
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/978,404B
;      FILING DATE:  25-NOV-97
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/032,354
;      FILING DATE:  04-DEC-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plumer, Elizabeth R.
;      REGISTRATION NUMBER:  36,637
;      REFERENCE/DOCKET NUMBER:  B0801/7090
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  273 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  No. 5968782e
US-08-978-404B-6

  Query Match             87.5%;  Score 28;  DB 1;  Length 273;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWM 4
              ||||
Db         51 TYWM 54


RESULT 49
US-09-134-000C-6205
; Sequence 6205, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;  TITLE OF INVENTION:  ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 032796-032
;  CURRENT APPLICATION NUMBER: US/09/134,000C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/055,778
;  PRIOR FILING DATE: 1997-08-15
;  NUMBER OF SEQ ID NOS: 6812
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6205
;   LENGTH: 296
;   TYPE: PRT
;   ORGANISM: Enterococcus faecalis
US-09-134-000C-6205

  Query Match             87.5%;  Score 28;  DB 2;  Length 296;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWM 4
              ||||
Db        264 TYWM 267


RESULT 50
US-09-079-029-10
; Sequence 10, Application US/09079029
; Patent No. 6342369
;  GENERAL INFORMATION:
;    APPLICANT:  Adams, Camilia W.
;    APPLICANT:  Ashkenazi, Avi J.
;    APPLICANT:  Chuntharapai, Anan
;    APPLICANT:  Kim, Kyung J.
;    TITLE OF INVENTION:  Apo-2 Receptor
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  1 DNA Way
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 1.44 Mb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WinPatin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,029
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Marschang, Diane L.
;      REGISTRATION NUMBER:  35,600
;      REFERENCE/DOCKET NUMBER:  P1101R2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650/225-5416
;      TELEFAX:  650/952-9881
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  312 amino acids
;      TYPE:  Amino Acid
;      TOPOLOGY:  Linear
US-09-079-029-10

  Query Match             87.5%;  Score 28;  DB 2;  Length 312;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+03;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
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Db         70 SYWMS 74


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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:42:16 ; Search time 35.0685 Seconds
(without alignments)
59.573 Million cell updates/sec

Title: US-10-755-382-23
Perfect score: 32
Sequence: 1 TYWMS 5

Scoring table: BLOSUM62
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	32	100.0	5	3	US-09-253-794-23	Sequence 23, Appl
2	32	100.0	5	3	US-09-977-797A-76	Sequence 76, Appl
3	32	100.0	5	4	US-10-680-734-23	Sequence 23, Appl
4	32	100.0	5	5	US-10-755-382-23	Sequence 23, Appl
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6	32	100.0	118	4	US-10-270-073-3	Sequence 3, Appli
7	32	100.0	119	3	US-09-253-794-2	Sequence 2, Appli
8	32	100.0	119	3	US-09-253-794-8	Sequence 8, Appli
9	32	100.0	119	3	US-09-253-794-9	Sequence 9, Appli
10	32	100.0	119	3	US-09-253-794-10	Sequence 10, Appl
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13	32	100.0	119	3	US-09-253-794-13	Sequence 13, Appl
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15	32	100.0	119	3	US-09-253-794-15	Sequence 15, Appl
16	32	100.0	119	3	US-09-253-794-17	Sequence 17, Appl
17	32	100.0	119	3	US-09-253-794-57	Sequence 57, Appl
18	32	100.0	119	3	US-09-253-794-58	Sequence 58, Appl
19	32	100.0	119	4	US-10-680-734-2	Sequence 2, Appli
20	32	100.0	119	4	US-10-680-734-8	Sequence 8, Appli
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24	32	100.0	119	4	US-10-680-734-12	Sequence 12, Appl
25	32	100.0	119	4	US-10-680-734-13	Sequence 13, Appl
26	32	100.0	119	4	US-10-680-734-14	Sequence 14, Appl
27	32	100.0	119	4	US-10-680-734-15	Sequence 15, Appl
28	32	100.0	119	4	US-10-680-734-17	Sequence 17, Appl
29	32	100.0	119	4	US-10-680-734-26	Sequence 26, Appl
30	32	100.0	119	4	US-10-680-734-27	Sequence 27, Appl
31	32	100.0	119	5	US-10-755-382-2	Sequence 2, Appli
32	32	100.0	119	5	US-10-755-382-8	Sequence 8, Appli
33	32	100.0	119	5	US-10-755-382-9	Sequence 9, Appli
34	32	100.0	119	5	US-10-755-382-10	Sequence 10, Appl
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37	32	100.0	119	5	US-10-755-382-13	Sequence 13, Appl
38	32	100.0	119	5	US-10-755-382-14	Sequence 14, Appl
39	32	100.0	119	5	US-10-755-382-15	Sequence 15, Appl
40	32	100.0	119	5	US-10-755-382-17	Sequence 17, Appl
41	32	100.0	119	5	US-10-755-382-57	Sequence 57, Appl
42	32	100.0	119	5	US-10-755-382-58	Sequence 58, Appl
43	32	100.0	138	4	US-10-006-771A-4	Sequence 4, Appli
44	32	100.0	236	4	US-10-697-787-10	Sequence 10, Appl
45	32	100.0	236	5	US-10-512-600-10	Sequence 10, Appl
46	32	100.0	256	4	US-10-270-073-6	Sequence 6, Appli
47	32	100.0	257	4	US-10-270-073-8	Sequence 8, Appli
48	32	100.0	261	4	US-10-270-071-18	Sequence 18, Appl
49	32	100.0	261	4	US-10-270-073-2	Sequence 2, Appli
50	32	100.0	261	4	US-10-328-190-6	Sequence 6, Appli
51	32	100.0	267	4	US-10-270-071-22	Sequence 22, Appl
52	32	100.0	267	4	US-10-270-071-26	Sequence 26, Appl
53	32	100.0	267	4	US-10-270-071-30	Sequence 30, Appl
54	32	100.0	267	4	US-10-270-071-36	Sequence 36, Appl
55	32	100.0	358	5	US-10-829-388-12	Sequence 12, Appl
56	32	100.0	363	5	US-10-829-388-2	Sequence 2, Appli
57	32	100.0	364	5	US-10-829-388-11	Sequence 11, Appl
58	32	100.0	370	5	US-10-829-388-1	Sequence 1, Appli
59	32	100.0	415	4	US-10-328-190-12	Sequence 12, Appl
60	32	100.0	443	4	US-10-006-773-2	Sequence 2, Appli
61	32	100.0	443	4	US-10-006-771A-2	Sequence 2, Appli
62	32	100.0	448	4	US-10-369-493-21148	Sequence 21148, A
63	32	100.0	464	4	US-10-369-493-406	Sequence 406, App
64	32	100.0	468	4	US-10-377-109-2	Sequence 2, Appli
65	32	100.0	597	4	US-10-267-502-306	Sequence 306, App
66	32	100.0	597	6	US-11-097-143-16407	Sequence 16407, A
67	32	100.0	669	5	US-10-900-928-3	Sequence 3, Appli
68	29	90.6	5	5	US-10-842-011-9	Sequence 9, Appli
69	29	90.6	62	4	US-10-424-599-174559	Sequence 174559,
70	29	90.6	89	4	US-10-424-599-185639	Sequence 185639,
71	29	90.6	95	4	US-10-424-599-276103	Sequence 276103,
72	29	90.6	109	4	US-10-282-122A-68018	Sequence 68018, A
73	29	90.6	115	5	US-10-938-992-11	Sequence 11, Appl
74	29	90.6	120	5	US-10-842-011-3	Sequence 3, Appli
75	29	90.6	151	4	US-10-425-115-309649	Sequence 309649,
76	29	90.6	156	4	US-10-424-599-254161	Sequence 254161,
77	29	90.6	158	5	US-10-823-396-14	Sequence 14, Appl
78	29	90.6	168	4	US-10-425-115-235854	Sequence 235854,
79	29	90.6	231	3	US-09-729-838-12	Sequence 12, Appl
80	29	90.6	231	4	US-10-398-424-12	Sequence 12, Appl
81	29	90.6	236	4	US-10-425-115-231775	Sequence 231775,
82	29	90.6	319	4	US-10-425-115-309660	Sequence 309660,
83	29	90.6	443	5	US-10-739-930-8504	Sequence 8504, Ap
84	29	90.6	449	3	US-09-768-781-7	Sequence 7, Appli
85	29	90.6	462	3	US-09-768-781-4	Sequence 4, Appli
86	29	90.6	462	4	US-10-282-122A-51118	Sequence 51118, A
87	29	90.6	462	5	US-10-994-727-5	Sequence 5, Appli
88	29	90.6	478	3	US-09-815-242-5719	Sequence 5719, Ap
89	29	90.6	478	3	US-09-815-242-12480	Sequence 12480, A
90	29	90.6	478	4	US-10-282-122A-43985	Sequence 43985, A
91	29	90.6	485	4	US-10-282-122A-58395	Sequence 58395, A
92	29	90.6	488	3	US-09-790-099-2	Sequence 2, Appli
93	29	90.6	488	4	US-10-237-852-2	Sequence 2, Appli
94	29	90.6	490	4	US-10-437-963-162301	Sequence 162301,
95	29	90.6	497	4	US-10-237-852-11	Sequence 11, Appl
96	29	90.6	497	4	US-10-437-963-192602	Sequence 192602,
97	29	90.6	508	4	US-10-431-273-71	Sequence 71, Appl
98	29	90.6	543	4	US-10-282-122A-69157	Sequence 69157, A
99	29	90.6	671	4	US-10-320-797-3275	Sequence 3275, Ap
100	29	90.6	827	4	US-10-437-963-177840	Sequence 177840,

101	29	90.6	1051	4	US-10-425-115-338413	Sequence 338413,
102	29	90.6	1081	4	US-10-369-493-3989	Sequence 3989, Ap
103	29	90.6	1139	4	US-10-369-493-6212	Sequence 6212, Ap
104	29	90.6	1382	6	US-11-097-143-18990	Sequence 18990, A
105	29	90.6	1463	6	US-11-097-143-12621	Sequence 12621, A
106	29	90.6	1981	6	US-11-097-143-11763	Sequence 11763, A
107	28	87.5	5	3	US-09-832-312-61	Sequence 61, Appl
108	28	87.5	5	3	US-09-829-495-61	Sequence 61, Appl
109	28	87.5	5	4	US-10-703-714-37	Sequence 37, Appl
110	28	87.5	5	4	US-10-703-714-49	Sequence 49, Appl
111	28	87.5	5	5	US-10-850-034-61	Sequence 61, Appl
112	28	87.5	6	4	US-10-741-481-50	Sequence 50, Appl
113	28	87.5	10	4	US-10-327-598-458	Sequence 458, App
114	28	87.5	11	5	US-10-879-994-99	Sequence 99, Appl
115	28	87.5	37	4	US-10-424-599-251683	Sequence 251683,
116	28	87.5	49	4	US-10-424-599-186870	Sequence 186870,
117	28	87.5	49	5	US-10-719-993-517	Sequence 517, App
118	28	87.5	49	5	US-10-719-993-518	Sequence 518, App
119	28	87.5	53	4	US-10-424-599-259490	Sequence 259490,
120	28	87.5	73	4	US-10-424-599-220280	Sequence 220280,
121	28	87.5	73	5	US-10-450-763-34771	Sequence 34771, A
122	28	87.5	75	5	US-10-450-763-52088	Sequence 52088, A
123	28	87.5	76	4	US-10-424-599-236367	Sequence 236367,
124	28	87.5	81	4	US-10-425-115-335705	Sequence 335705,
125	28	87.5	82	4	US-10-425-115-208263	Sequence 208263,
126	28	87.5	88	4	US-10-425-114-69079	Sequence 69079, A
127	28	87.5	88	4	US-10-425-115-279972	Sequence 279972,
128	28	87.5	92	4	US-10-424-599-176507	Sequence 176507,
129	28	87.5	93	4	US-10-437-963-180393	Sequence 180393,
130	28	87.5	94	3	US-09-864-761-38424	Sequence 38424, A
131	28	87.5	98	4	US-10-194-975-15	Sequence 15, Appl
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133	28	87.5	98	4	US-10-032-037B-85	Sequence 85, Appl
134	28	87.5	98	4	US-10-029-988B-85	Sequence 85, Appl
135	28	87.5	98	4	US-10-032-423A-85	Sequence 85, Appl
136	28	87.5	98	4	US-10-424-599-263641	Sequence 263641,
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138	28	87.5	98	4	US-10-029-926B-85	Sequence 85, Appl
139	28	87.5	98	4	US-10-379-392-14	Sequence 14, Appl
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141	28	87.5	98	5	US-10-884-830-666	Sequence 666, App
142	28	87.5	98	5	US-10-911-838-19	Sequence 19, Appl
143	28	87.5	99	4	US-10-703-714-22	Sequence 22, Appl
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147	28	87.5	117	3	US-09-982-992A-6	Sequence 6, Appli
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151	28	87.5	120	3	US-09-995-529-8	Sequence 8, Appli
152	28	87.5	120	3	US-09-995-529-8	Sequence 8, Appli
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154	28	87.5	123	4	US-10-450-295-13	Sequence 13, Appl
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159	28	87.5	157	5	US-10-473-287-63	Sequence 63, Appl
160	28	87.5	163	4	US-10-693-629-60	Sequence 60, Appl
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168	28	87.5	212	5	US-10-482-914-3	Sequence 3, Appli
169	28	87.5	212	6	US-11-090-448-29	Sequence 29, Appl
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171	28	87.5	236	4	US-10-369-493-8557	Sequence 8557, Ap
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175	28	87.5	241	4	US-10-293-418-1889	Sequence 1889, Ap
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177	28	87.5	243	5	US-10-610-452-10	Sequence 10, Appl
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182	28	87.5	247	5	US-10-981-621-48	Sequence 48, Appl
183	28	87.5	247	5	US-10-981-673-48	Sequence 48, Appl
184	28	87.5	247	5	US-10-981-691-48	Sequence 48, Appl
185	28	87.5	247	6	US-11-090-847-129	Sequence 129, App
186	28	87.5	249	5	US-10-732-923-14003	Sequence 14003, A
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188	28	87.5	251	4	US-10-293-418-1594	Sequence 1594, Ap
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223	28	87.5	380	5	US-10-671-034-4	Sequence 4, Appli
224	28	87.5	380	5	US-10-868-373-6	Sequence 6, Appli
225	28	87.5	380	5	US-10-631-467-557	Sequence 557, App
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229	28	87.5	402	4	US-10-369-493-7376	Sequence 7376, Ap
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236	28	87.5	512	5	US-10-839-896-69	Sequence 69, Appl
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253	28	87.5	852	4	US-10-369-493-1645	Sequence 1645, Ap
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262	27	84.4	5	5	US-10-783-311-315	Sequence 315, App
263	27	84.4	5	5	US-10-842-011-15	Sequence 15, Appl
264	27	84.4	5	5	US-10-842-011-30	Sequence 30, Appl
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266	27	84.4	10	3	US-09-995-529-43	Sequence 43, Appl
267	27	84.4	10	3	US-09-995-529-26	Sequence 26, Appl
268	27	84.4	10	3	US-09-995-529-43	Sequence 43, Appl
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270	27	84.4	10	4	US-10-327-598-457	Sequence 457, App
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272	27	84.4	24	5	US-10-965-616-19	Sequence 19, Appl
273	27	84.4	31	4	US-10-151-569-12	Sequence 12, Appl
274	27	84.4	31	4	US-10-151-569-13	Sequence 13, Appl
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277	27	84.4	63	4	US-10-425-115-246917	Sequence 246917,
278	27	84.4	64	4	US-10-242-355-367	Sequence 367, App
279	27	84.4	65	4	US-10-437-963-188018	Sequence 188018,
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287	27	84.4	98	3	US-09-840-459-52	Sequence 52, Appl
288	27	84.4	98	4	US-10-766-773-47	Sequence 47, Appl
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290	27	84.4	98	4	US-10-766-610-47	Sequence 47, Appl
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292	27	84.4	98	4	US-10-733-563-47	Sequence 47, Appl
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295	27	84.4	100	4	US-10-766-773-36	Sequence 36, Appl
296	27	84.4	100	4	US-10-766-610-36	Sequence 36, Appl
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310	27	84.4	115	4	US-10-425-115-258974	Sequence 258974,
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315	27	84.4	119	5	US-10-842-011-40	Sequence 40, Appl
316	27	84.4	119	5	US-10-842-011-44	Sequence 44, Appl
317	27	84.4	119	5	US-10-842-011-46	Sequence 46, Appl
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325	27	84.4	132	5	US-10-783-311-311	Sequence 311, App
326	27	84.4	134	3	US-09-811-737-3	Sequence 3, Appli
327	27	84.4	137	4	US-10-425-115-206504	Sequence 206504,
328	27	84.4	137	5	US-10-842-011-27	Sequence 27, Appl
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330	27	84.4	142	6	US-11-013-537-35	Sequence 35, Appl
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333	27	84.4	156	5	US-10-805-177-116	Sequence 116, App
334	27	84.4	159	4	US-10-437-963-200943	Sequence 200943,
335	27	84.4	161	4	US-10-424-599-192382	Sequence 192382,
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337	27	84.4	180	4	US-10-106-698-6125	Sequence 6125, Ap
338	27	84.4	183	3	US-09-836-392-18	Sequence 18, Appl
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340	27	84.4	185	4	US-10-211-962-117	Sequence 117, App
341	27	84.4	185	4	US-10-211-962-118	Sequence 118, App
342	27	84.4	185	4	US-10-211-962-119	Sequence 119, App
343	27	84.4	185	4	US-10-211-962-120	Sequence 120, App
344	27	84.4	185	4	US-10-424-599-241851	Sequence 241851,
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354	27	84.4	223	4	US-10-437-963-105581	Sequence 105581,
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357	27	84.4	252	4	US-10-239-656-55	Sequence 55, Appl
358	27	84.4	254	4	US-10-369-493-2699	Sequence 2699, Ap
359	27	84.4	256	4	US-10-239-656-57	Sequence 57, Appl
360	27	84.4	258	4	US-10-239-656-71	Sequence 71, Appl
361	27	84.4	258	4	US-10-437-963-105580	Sequence 105580,
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363	27	84.4	262	4	US-10-277-471A-5	Sequence 5, Appli
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368	27	84.4	286	4	US-10-258-951-62	Sequence 62, Appl
369	27	84.4	286	5	US-10-990-000-62	Sequence 62, Appl
370	27	84.4	290	4	US-10-406-676-18	Sequence 18, Appl
371	27	84.4	290	4	US-10-406-676-19	Sequence 19, Appl
372	27	84.4	290	4	US-10-406-676-20	Sequence 20, Appl
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377	27	84.4	348	4	US-10-320-797-3136	Sequence 3136, Ap
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383	27	84.4	378	4	US-10-369-493-5608	Sequence 5608, Ap
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385	27	84.4	423	4	US-10-635-977-8	Sequence 8, Appli
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389	27	84.4	439	4	US-10-431-952-29	Sequence 29, Appl
390	27	84.4	439	5	US-10-840-579-123	Sequence 123, App
391	27	84.4	460	4	US-10-630-406-5	Sequence 5, Appli
392	27	84.4	460	6	US-11-073-453-5	Sequence 5, Appli

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395	27	84.4	470	4	US-10-282-122A-66767	Sequence 66767, A
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397	27	84.4	503	4	US-10-239-656-75	Sequence 75, Appl
398	27	84.4	504	4	US-10-437-963-128079	Sequence 128079,
399	27	84.4	505	4	US-10-239-656-79	Sequence 79, Appl
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403	27	84.4	533	4	US-10-258-951-63	Sequence 63, Appl
404	27	84.4	533	5	US-10-990-000-63	Sequence 63, Appl
405	27	84.4	536	4	US-10-424-599-266554	Sequence 266554,
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410	27	84.4	555	6	US-11-097-143-23430	Sequence 23430, A
411	27	84.4	559	4	US-10-369-493-5740	Sequence 5740, Ap
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413	27	84.4	598	5	US-10-732-923-1770	Sequence 1770, Ap
414	27	84.4	600	4	US-10-282-122A-69214	Sequence 69214, A
415	27	84.4	607	5	US-10-501-282-2302	Sequence 2302, Ap
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422	27	84.4	619	4	US-10-456-422-8	Sequence 8, Appli
423	27	84.4	619	4	US-10-456-422-10	Sequence 10, Appl
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426	27	84.4	626	3	US-09-771-161A-202	Sequence 202, App
427	27	84.4	626	4	US-10-000-864-6	Sequence 6, Appli
428	27	84.4	626	4	US-10-000-864-12	Sequence 12, Appl
429	27	84.4	626	4	US-10-408-765A-451	Sequence 451, App
430	27	84.4	635	4	US-10-134-102-2	Sequence 2, Appli
431	27	84.4	639	4	US-10-134-102-6	Sequence 6, Appli
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435	27	84.4	721	4	US-10-437-963-144813	Sequence 144813,
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438	27	84.4	830	5	US-10-812-232-5	Sequence 5, Appli
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442	27	84.4	965	5	US-10-840-512-225	Sequence 225, App
443	27	84.4	982	4	US-10-618-941-120	Sequence 120, App
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972	26	81.2	143	4	US-10-179-508-510	Sequence 510, App
973	26	81.2	143	4	US-10-179-512-510	Sequence 510, App
974	26	81.2	143	4	US-10-179-515-510	Sequence 510, App
975	26	81.2	143	4	US-10-173-692-510	Sequence 510, App
976	26	81.2	143	4	US-10-173-702-510	Sequence 510, App

977	26	81.2	143	4	US-10-173-703-510	Sequence 510, App
978	26	81.2	143	4	US-10-173-704-510	Sequence 510, App
979	26	81.2	143	4	US-10-174-574-510	Sequence 510, App
980	26	81.2	143	4	US-10-176-486-510	Sequence 510, App
981	26	81.2	143	4	US-10-176-490-510	Sequence 510, App
982	26	81.2	143	4	US-10-176-752-510	Sequence 510, App
983	26	81.2	143	4	US-10-176-981-510	Sequence 510, App
984	26	81.2	143	4	US-10-176-983-510	Sequence 510, App
985	26	81.2	143	4	US-10-176-988-510	Sequence 510, App
986	26	81.2	143	4	US-10-179-517-510	Sequence 510, App
987	26	81.2	143	4	US-10-179-521-510	Sequence 510, App
988	26	81.2	143	4	US-10-202-475-510	Sequence 510, App
989	26	81.2	143	4	US-10-195-887-510	Sequence 510, App
990	26	81.2	143	4	US-10-195-893-510	Sequence 510, App
991	26	81.2	143	4	US-10-179-509-510	Sequence 510, App
992	26	81.2	143	4	US-10-194-486-510	Sequence 510, App
993	26	81.2	143	4	US-10-195-900-510	Sequence 510, App
994	26	81.2	143	4	US-10-198-759-510	Sequence 510, App
995	26	81.2	143	4	US-10-205-506-510	Sequence 510, App
996	26	81.2	143	4	US-10-174-570-510	Sequence 510, App
997	26	81.2	143	4	US-10-183-005-510	Sequence 510, App
998	26	81.2	143	4	US-10-179-523-510	Sequence 510, App
999	26	81.2	143	4	US-10-199-463-510	Sequence 510, App
1000	26	81.2	143	4	US-10-202-471-510	Sequence 510, App

ALIGNMENTS

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RESULT 1
US-09-253-794-23
; Sequence 23, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 23:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 5 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-253-794-23

  Query Match           100.0%;  Score 32;  DB 3;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db          1 TYWMS 5


RESULT 2
US-09-977-797A-76
; Sequence 76, Application US/09977797A
; Publication No. US20030044772A1
; GENERAL INFORMATION:
;  APPLICANT: Watkins, Jeffrey D.
;  APPLICANT:  Huse, William D.
;  APPLICANT:  Wu, Herren
;  TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
;  FILE REFERENCE: AME-06805
;  CURRENT APPLICATION NUMBER: US/09/977,797A
;  CURRENT FILING DATE:  2002-06-25
;  PRIOR APPLICATION NUMBER: 09/129,026
;  PRIOR FILING DATE: 1998-08-04
;  PRIOR APPLICATION NUMBER: 08/905,825
;  PRIOR FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 136
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-977-797A-76

  Query Match           100.0%;  Score 32;  DB 3;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db          1 TYWMS 5


RESULT 3
US-10-680-734-23
; Sequence 23, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 23
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-680-734-23

  Query Match           100.0%;  Score 32;  DB 4;  Length 5;
  Best Local Similarity  100.0%;  Pred. No. 1.7e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 TYWMS 5
              |||||
Db          1 TYWMS 5


RESULT 4
US-10-755-382-23
; Sequence 23, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 23:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 5 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-755-382-23

  Query Match             100.0%;  Score 32;  DB 5;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.7e+06;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db          1 TYWMS 5


RESULT 5
US-10-425-115-230946
; Sequence 230946, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
;  APPLICANT: La Rosa, Thomas J.
;  APPLICANT:  Kovalic, David K.
;  APPLICANT:  Zhou, Yihua
;  APPLICANT:  Cao, Yongwei
;  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
;  TITLE OF INVENTION:  Plants
;  FILE REFERENCE: 38-21(53222)B
;  CURRENT APPLICATION NUMBER: US/10/425,115
;  CURRENT FILING DATE:  2003-04-28
;  NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 230946
;   LENGTH: 99
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Clone ID: MRT4577_142216C.1.pep
US-10-425-115-230946

  Query Match             100.0%;  Score 32;  DB 4;  Length 99;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         94 TYWMS 98


RESULT 6
US-10-270-073-3
; Sequence 3, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14VH deduced amino acid sequence
US-10-270-073-3

  Query Match             100.0%;  Score 32;  DB 4;  Length 118;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 7
US-09-253-794-2
; Sequence 2, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
```

```
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-253-794-2

  Query Match             100.0%;  Score 32;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 8
US-09-253-794-8
; Sequence 8, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-253-794-8

  Query Match             100.0%;  Score 32;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 9
US-09-253-794-9
; Sequence 9, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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US-09-253-794-9

  Query Match             100.0%;  Score 32;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 10
US-09-253-794-10
; Sequence 10, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-253-794-10

  Query Match             100.0%;  Score 32;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 11
US-09-253-794-11
; Sequence 11, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-253-794-11

  Query Match             100.0%;  Score 32;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 12
US-09-253-794-12
; Sequence 12, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
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;           APPLICATION NUMBER: US/09/253,794
;           FILING DATE: 22-Feb-1999
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US 08/318,157
;           FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;           NAME: SAXE, Bernhard D.
;           REGISTRATION NUMBER: 28,665
;           REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 119 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-253-794-12

  Query Match             100.0%;  Score 32;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 13
US-09-253-794-13
; Sequence 13, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Foley & Lardner
;           STREET: 3000 K Street, N.W., Suite 500
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/253,794
;           FILING DATE: 22-Feb-1999
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US 08/318,157
;           FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;           NAME: SAXE, Bernhard D.
;           REGISTRATION NUMBER: 28,665
;           REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 119 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-253-794-13

  Query Match             100.0%;  Score 32;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 14
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Foley & Lardner
;           STREET: 3000 K Street, N.W., Suite 500
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/253,794
;           FILING DATE: 22-Feb-1999
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US 08/318,157
;           FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;           NAME: SAXE, Bernhard D.
;           REGISTRATION NUMBER: 28,665
;           REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 119 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

  Query Match             100.0%;  Score 32;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 15
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US-09-253-794-15
; Sequence 15, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-253-794-15

  Query Match             100.0%;  Score 32;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 16
US-09-253-794-17
; Sequence 17, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-253-794-17

  Query Match             100.0%;  Score 32;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 17
US-09-253-794-57
; Sequence 57, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
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;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 57:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-253-794-57

  Query Match            100.0%;  Score 32;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 18
US-09-253-794-58
; Sequence 58, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 58:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-253-794-58

  Query Match            100.0%;  Score 32;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 19
US-10-680-734-2
; Sequence 2, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-680-734-2

  Query Match            100.0%;  Score 32;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 20
US-10-680-734-8
; Sequence 8, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-8

  Query Match            100.0%;  Score 32;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 21
US-10-680-734-9
; Sequence 9, Application US/10680734
; Publication No. US20040191248A1
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; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-9

  Query Match           100.0%;  Score 32;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 22
US-10-680-734-10
; Sequence 10, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-10

  Query Match           100.0%;  Score 32;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 23
US-10-680-734-11
; Sequence 11, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 11
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-11

  Query Match           100.0%;  Score 32;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 24
US-10-680-734-12
; Sequence 12, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-12

  Query Match           100.0%;  Score 32;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 25
US-10-680-734-13
; Sequence 13, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
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;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-13

  Query Match           100.0%;  Score 32;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 26
US-10-680-734-14
; Sequence 14, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-14

  Query Match           100.0%;  Score 32;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 27
US-10-680-734-15
; Sequence 15, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-15

  Query Match           100.0%;  Score 32;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 28
US-10-680-734-17
; Sequence 17, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-17

  Query Match           100.0%;  Score 32;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 29
US-10-680-734-26
; Sequence 26, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 26
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-26
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  Query Match             100.0%;  Score 32;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 30
US-10-680-734-27
; Sequence 27, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 27
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-27

  Query Match             100.0%;  Score 32;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 31
US-10-755-382-2
; Sequence 2, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-755-382-2

  Query Match             100.0%;  Score 32;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 32
US-10-755-382-8
; Sequence 8, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
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;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-755-382-8

  Query Match             100.0%;  Score 32;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 33
US-10-755-382-9
; Sequence 9, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/755,382
;            FILING DATE: 13-Jan-2004
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-755-382-9

  Query Match             100.0%;  Score 32;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 34
US-10-755-382-10
; Sequence 10, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/755,382
;            FILING DATE: 13-Jan-2004
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 10:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-755-382-10

  Query Match             100.0%;  Score 32;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 35
US-10-755-382-11
; Sequence 11, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
```

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;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-755-382-11

  Query Match             100.0%;  Score 32;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 36
US-10-755-382-12
; Sequence 12, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-755-382-12

  Query Match             100.0%;  Score 32;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 37
US-10-755-382-13
; Sequence 13, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
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US-10-755-382-13

  Query Match             100.0%;  Score 32;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 38
US-10-755-382-14
; Sequence 14, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-755-382-14

  Query Match             100.0%;  Score 32;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 39
US-10-755-382-15
; Sequence 15, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-755-382-15

  Query Match             100.0%;  Score 32;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 40
US-10-755-382-17
; Sequence 17, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
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;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-755-382-17

  Query Match           100.0%;  Score 32;  DB 5;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 41
US-10-755-382-57
; Sequence 57, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 57:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-755-382-57

  Query Match           100.0%;  Score 32;  DB 5;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 42
US-10-755-382-58
; Sequence 58, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 58:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-755-382-58

  Query Match           100.0%;  Score 32;  DB 5;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 4.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 TYWMS 5
              |||||
Db         31 TYWMS 35


RESULT 43
US-10-006-771A-4
; Sequence 4, Application US/10006771A
; Publication No. US20020165360A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen
;  FILE REFERENCE: 002
;  CURRENT APPLICATION NUMBER: US/10/006,771A
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: 60/250,090
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 138
;   TYPE: PRT
;   ORGANISM: Homo sapiens and Mus sp.
US-10-006-771A-4

  Query Match             100.0%;  Score 32;  DB 4;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 4.8e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         50 TYWMS 54


RESULT 44
US-10-697-787-10
; Sequence 10, Application US/10697787
; Publication No. US20040216182A1
; GENERAL INFORMATION:
;  APPLICANT: Agrinomics, LLC
;  TITLE OF INVENTION: Generation of Plants with Improved Pathogen  Resistance and
;  TITLE OF INVENTION:  Drought Tolerance
;  FILE REFERENCE: AG03-071C
;  CURRENT APPLICATION NUMBER: US/10/697,787
;  CURRENT FILING DATE:  2003-10-29
;  PRIOR APPLICATION NUMBER: US 60/375,333
;  PRIOR FILING DATE: 2002-04-24
;  PRIOR APPLICATION NUMBER: PCT/US03/12981
;  PRIOR FILING DATE: 2003-04-24
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-697-787-10

  Query Match             100.0%;  Score 32;  DB 4;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 7.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        200 TYWMS 204


RESULT 45
US-10-512-600-10
; Sequence 10, Application US/10512600
; Publication No. US20050210546A1
; GENERAL INFORMATION:
;  APPLICANT: AGRINOMICS, LLC
;  TITLE OF INVENTION: GENERATION OF PLANTS WITH IMPROVED PATHOGEN RESISTANCE
;  FILE REFERENCE: AG03-033C-US
;  CURRENT APPLICATION NUMBER: US/10/512,600
;  CURRENT FILING DATE:  2004-10-22
;  PRIOR APPLICATION NUMBER: US 60/375,333
;  PRIOR FILING DATE: 2002-04-24
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 236
;   TYPE: PRT
;   ORGANISM: Oryza sativa
US-10-512-600-10

  Query Match             100.0%;  Score 32;  DB 5;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 7.6e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db        200 TYWMS 204


RESULT 46
US-10-270-073-6
; Sequence 6, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14-0 amino acid sequence
US-10-270-073-6

  Query Match             100.0%;  Score 32;  DB 4;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 8.1e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         54 TYWMS 58


RESULT 47
US-10-270-073-8
; Sequence 8, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
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;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 257
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14-1G amino acid sequence
US-10-270-073-8

  Query Match           100.0%;  Score 32;  DB 4;  Length 257;
  Best Local Similarity  100.0%;  Pred. No. 8.2e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         54 TYWMS 58


RESULT 48
US-10-270-071-18
; Sequence 18, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of hMN14VK
US-10-270-071-18

  Query Match           100.0%;  Score 32;  DB 4;  Length 261;
  Best Local Similarity  100.0%;  Pred. No. 8.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         54 TYWMS 58


RESULT 49
US-10-270-073-2
; Sequence 2, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14scFv-L5 amino acid sequence
US-10-270-073-2

  Query Match           100.0%;  Score 32;  DB 4;  Length 261;
  Best Local Similarity  100.0%;  Pred. No. 8.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         54 TYWMS 58


RESULT 50
US-10-328-190-6
; Sequence 6, Application US/10328190
; Publication No. US20030162709A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID M.
;  TITLE OF INVENTION: METHODS OF GENERATING MULTISPECIFIC, MULTIVALENT AGENTS
;  TITLE OF INVENTION:  FROM VH AND VL DOMAINS
;  FILE REFERENCE: 042418/0115
;  CURRENT APPLICATION NUMBER: US/10/328,190
;  CURRENT FILING DATE:  2003-04-03
;  PRIOR APPLICATION NUMBER: 60/342,103
;  PRIOR FILING DATE: 2001-12-26
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: hMN14-scFv-L5
;   OTHER INFORMATION: protein sequence
US-10-328-190-6

  Query Match           100.0%;  Score 32;  DB 4;  Length 261;
  Best Local Similarity  100.0%;  Pred. No. 8.3e+02;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||||
Db         54 TYWMS 58


Search completed: March 23, 2006, 02:52:23
Job time : 48.2113 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:44:01 ; Search time 4.24658 Seconds
(without alignments)
33.701 Million cell updates/sec

Title: US-10-755-382-23
Perfect score: 32
Sequence: 1 TYWMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
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8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	29	90.6	5	6	US-10-982-357-9	Sequence 9, Appli
2	29	90.6	120	6	US-10-982-357-3	Sequence 3, Appli
3	29	90.6	214	5	US-09-995-493-62	Sequence 62, Appl
4	29	90.6	233	6	US-10-467-657-12	Sequence 12, Appl
5	29	90.6	233	6	US-10-467-657-5530	Sequence 5530, Ap
6	29	90.6	293	7	US-11-096-568A-32269	Sequence 32269, A
7	29	90.6	351	7	US-11-096-568A-32268	Sequence 32268, A
8	29	90.6	378	7	US-11-096-568A-32267	Sequence 32267, A
9	29	90.6	391	7	US-11-096-568A-26756	Sequence 26756, A
10	29	90.6	416	7	US-11-096-568A-18081	Sequence 18081, A
11	29	90.6	416	7	US-11-096-568A-26755	Sequence 26755, A
12	29	90.6	443	7	US-11-096-568A-26754	Sequence 26754, A
13	29	90.6	444	7	US-11-096-568A-11404	Sequence 11404, A
14	29	90.6	456	7	US-11-087-099-1360	Sequence 1360, Ap
15	29	90.6	456	7	US-11-096-568A-18080	Sequence 18080, A
16	29	90.6	478	7	US-11-096-568A-18079	Sequence 18079, A
17	29	90.6	493	7	US-11-096-568A-11403	Sequence 11403, A
18	29	90.6	522	7	US-11-096-568A-11402	Sequence 11402, A
19	28	87.5	5	6	US-10-850-635-54	Sequence 54, Appl
20	28	87.5	97	7	US-11-093-274-35	Sequence 35, Appl
21	28	87.5	98	7	US-11-054-669-15	Sequence 15, Appl
22	28	87.5	98	7	US-11-084-554-44	Sequence 44, Appl
23	28	87.5	98	7	US-11-004-590-14	Sequence 14, Appl
24	28	87.5	98	7	US-11-136-250-44	Sequence 44, Appl
25	28	87.5	129	6	US-10-850-635-12	Sequence 12, Appl
26	28	87.5	213	7	US-11-137-465-59	Sequence 59, Appl
27	28	87.5	225	7	US-11-087-099-4770	Sequence 4770, Ap
28	28	87.5	241	7	US-11-054-515-1889	Sequence 1889, Ap
29	28	87.5	247	7	US-11-054-515-1470	Sequence 1470, Ap
30	28	87.5	251	7	US-11-054-515-1594	Sequence 1594, Ap
31	28	87.5	251	7	US-11-054-515-3245	Sequence 3245, Ap
32	28	87.5	257	7	US-11-056-825-10	Sequence 10, Appl
33	28	87.5	259	7	US-11-096-568A-5086	Sequence 5086, Ap
34	28	87.5	273	7	US-11-096-568A-28944	Sequence 28944, A
35	28	87.5	281	7	US-11-087-099-3415	Sequence 3415, Ap
36	28	87.5	312	7	US-11-245-053-10	Sequence 10, Appl
37	28	87.5	363	7	US-11-096-568A-28943	Sequence 28943, A
38	28	87.5	378	7	US/11/185	Sequence 12, Appl
39	28	87.5	378	7	US-11-182-384A-12	Sequence 12, Appl
40	28	87.5	378	7	US-11-183-599A-12	Sequence 12, Appl
41	28	87.5	380	6	US-10-989-313-4	Sequence 4, Appli
42	28	87.5	380	7	US-11-185-230-2	Sequence 2, Appli
43	28	87.5	380	7	US-11-182-384A-2	Sequence 2, Appli
44	28	87.5	380	7	US-11-183-599A-2	Sequence 2, Appli
45	28	87.5	408	7	US-11-096-568A-28942	Sequence 28942, A
46	28	87.5	438	7	US-11-087-099-6826	Sequence 6826, Ap
47	28	87.5	508	6	US-10-878-556A-154	Sequence 154, App
48	28	87.5	793	7	US-11-087-099-2968	Sequence 2968, Ap
49	28	87.5	992	7	US-11-098-686-10761	Sequence 10761, A
50	27	84.4	5	6	US-10-982-357-15	Sequence 15, Appl
51	27	84.4	5	6	US-10-982-357-30	Sequence 30, Appl
52	27	84.4	10	6	US-10-880-238-60	Sequence 60, Appl
53	27	84.4	103	7	US-11-096-568A-24919	Sequence 24919, A
54	27	84.4	119	6	US-10-982-357-5	Sequence 5, Appli
55	27	84.4	119	6	US-10-982-357-38	Sequence 38, Appl
56	27	84.4	119	6	US-10-982-357-41	Sequence 41, Appl
57	27	84.4	119	6	US-10-982-357-45	Sequence 45, Appl
58	27	84.4	119	6	US-10-982-357-47	Sequence 47, Appl
59	27	84.4	137	6	US-10-982-357-27	Sequence 27, Appl
60	27	84.4	163	7	US-11-096-568A-5260	Sequence 5260, Ap
61	27	84.4	192	7	US-11-096-568A-5259	Sequence 5259, Ap
62	27	84.4	353	6	US-10-055-877-30	Sequence 30, Appl
63	27	84.4	439	7	US-11-112-882-18	Sequence 18, Appl
64	27	84.4	439	7	US-11-146-428-62	Sequence 62, Appl
65	27	84.4	459	7	US-11-087-099-3117	Sequence 3117, Ap
66	27	84.4	462	7	US-11-087-099-2301	Sequence 2301, Ap
67	27	84.4	462	7	US-11-087-099-2409	Sequence 2409, Ap
68	27	84.4	464	7	US-11-087-099-6274	Sequence 6274, Ap
69	27	84.4	468	7	US-11-087-099-10268	Sequence 10268, A
70	27	84.4	470	7	US-11-087-099-7728	Sequence 7728, Ap
71	27	84.4	516	7	US-11-087-099-3958	Sequence 3958, Ap
72	27	84.4	530	7	US-11-183-136-44	Sequence 44, Appl
73	27	84.4	558	7	US-11-096-568A-23953	Sequence 23953, A
74	27	84.4	589	7	US-11-183-136-42	Sequence 42, Appl
75	27	84.4	593	7	US-11-096-568A-23952	Sequence 23952, A
76	27	84.4	606	7	US-11-096-568A-23951	Sequence 23951, A
77	27	84.4	612	7	US-11-087-099-8397	Sequence 8397, Ap
78	27	84.4	619	7	US-11-210-471-4	Sequence 4, Appli
79	27	84.4	619	7	US-11-210-471-10	Sequence 10, Appl
80	27	84.4	626	7	US-11-210-471-6	Sequence 6, Appli
81	27	84.4	626	7	US-11-210-471-12	Sequence 12, Appl
82	27	84.4	1248	7	US-11-096-568A-29804	Sequence 29804, A
83	27	84.4	1295	7	US-11-096-568A-29803	Sequence 29803, A
84	27	84.4	1305	7	US-11-096-568A-29802	Sequence 29802, A
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87	26	81.2	219	7	US-11-112-481C-4	Sequence 4, Appli
88	26	81.2	283	6	US-10-499-246-7	Sequence 7, Appli
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92	26	81.2	306	7	US-11-096-568A-16824	Sequence 16824, A
93	26	81.2	321	6	US-10-467-657-2352	Sequence 2352, Ap
94	26	81.2	332	7	US-11-096-568A-20663	Sequence 20663, A
95	26	81.2	333	7	US-11-096-568A-31931	Sequence 31931, A
96	26	81.2	334	7	US-11-096-568A-32123	Sequence 32123, A
97	26	81.2	396	7	US-11-096-568A-31930	Sequence 31930, A
98	26	81.2	405	6	US-10-793-626-2962	Sequence 2962, Ap

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103	26	81.2	459	7	US-11-087-099-8941	Sequence 8941, Ap
104	26	81.2	594	7	US-11-012-762-4	Sequence 4, Appli
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106	26	81.2	666	7	US-11-096-568A-14636	Sequence 14636, A
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119	26	81.2	833	7	US-11-208-701-2	Sequence 2, Appli
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124	26	81.2	1073	6	US-10-537-002-11	Sequence 11, Appl
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127	25	78.1	103	7	US-11-096-568A-40	Sequence 40, Appl
128	25	78.1	118	6	US-10-793-626-2630	Sequence 2630, Ap
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130	25	78.1	121	6	US-10-507-662-26	Sequence 26, Appl
131	25	78.1	125	7	US-11-116-144-157	Sequence 157, App
132	25	78.1	133	7	US-11-069-834-2	Sequence 2, Appli
133	25	78.1	139	7	US-11-072-512-2633	Sequence 2633, Ap
134	25	78.1	186	7	US-11-072-512-2159	Sequence 2159, Ap
135	25	78.1	211	7	US-11-090-878-46	Sequence 46, Appl
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138	25	78.1	229	6	US-10-948-429A-2	Sequence 2, Appli
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141	25	78.1	244	7	US-11-090-878-69	Sequence 69, Appl
142	25	78.1	245	6	US-10-948-429A-10	Sequence 10, Appl
143	25	78.1	249	7	US-11-087-099-2814	Sequence 2814, Ap
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148	25	78.1	327	7	US-11-096-568A-5412	Sequence 5412, Ap
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160	25	78.1	446	7	US-11-087-099-9985	Sequence 9985, Ap
161	25	78.1	449	7	US-11-087-099-1645	Sequence 1645, Ap
162	25	78.1	452	7	US-11-087-099-9683	Sequence 9683, Ap
163	25	78.1	467	6	US-10-821-234-904	Sequence 904, App
164	25	78.1	467	7	US-11-087-099-8408	Sequence 8408, Ap
165	25	78.1	469	7	US-11-087-099-3950	Sequence 3950, Ap
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185	24	75.0	5	7	US-11-105-708-20	Sequence 20, Appl
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191	24	75.0	10	6	US-10-880-238-54	Sequence 54, Appl
192	24	75.0	10	6	US-10-880-238-57	Sequence 57, Appl
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196	24	75.0	17	7	US-11-066-967-101	Sequence 101, App
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203	24	75.0	21	7	US-11-066-967-94	Sequence 94, Appl
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206	24	75.0	27	7	US-11-004-399-3610	Sequence 3610, Ap
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209	24	75.0	33	7	US-11-066-967-106	Sequence 106, App
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213	24	75.0	98	7	US-11-004-590-37	Sequence 37, Appl
214	24	75.0	98	7	US-11-004-590-50	Sequence 50, Appl
215	24	75.0	98	7	US-11-136-250-47	Sequence 47, Appl
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223	24	75.0	111	7	US-11-097-812-36	Sequence 36, Appl
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235	24	75.0	113	7	US-11-177-648-85	Sequence 85, Appl
236	24	75.0	113	7	US-11-177-648-86	Sequence 86, Appl
237	24	75.0	113	7	US-11-177-648-87	Sequence 87, Appl
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239	24	75.0	113	7	US-11-177-648-89	Sequence 89, Appl
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249	24	75.0	121	6	US-10-982-357-7	Sequence 7, Appli
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254	24	75.0	123	6	US-10-932-334-92	Sequence 92, Appl
255	24	75.0	124	6	US-10-932-334-7	Sequence 7, Appli
256	24	75.0	124	6	US-10-932-334-13	Sequence 13, Appl
257	24	75.0	124	6	US-10-932-334-70	Sequence 70, Appl
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259	24	75.0	128	7	US-11-173-071-14	Sequence 14, Appl
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262	24	75.0	143	6	US-10-932-334-52	Sequence 52, Appl
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264	24	75.0	154	7	US-11-096-568A-536	Sequence 536, App
265	24	75.0	159	7	US-11-156-084-151	Sequence 151, App
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274	24	75.0	188	7	US-11-000-463-867	Sequence 867, App
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285	24	75.0	242	7	US-11-054-515-2084	Sequence 2084, Ap
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287	24	75.0	243	7	US-11-054-515-1916	Sequence 1916, Ap
288	24	75.0	243	7	US-11-054-515-2051	Sequence 2051, Ap
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295	24	75.0	249	7	US-11-054-515-2065	Sequence 2065, Ap
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297	24	75.0	250	7	US-11-054-515-1851	Sequence 1851, Ap
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308	24	75.0	276	7	US-11-043-788-277	Sequence 277, App
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310	24	75.0	283	7	US-11-096-568A-5213	Sequence 5213, Ap
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312	24	75.0	292	7	US-11-092-140-32	Sequence 32, Appl
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317	24	75.0	311	6	US-10-980-388-113	Sequence 113, App
318	24	75.0	311	6	US-10-055-877-181	Sequence 181, App
319	24	75.0	311	6	US-10-055-877-182	Sequence 182, App
320	24	75.0	314	7	US-11-108-172-1110	Sequence 1110, Ap
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347	24	75.0	418	7	US-11-082-389-50	Sequence 50, Appl
348	24	75.0	419	7	US-11-096-568A-19366	Sequence 19366, A
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350	24	75.0	420	6	US-10-973-115B-290	Sequence 290, App
351	24	75.0	422	6	US-10-336-263A-4	Sequence 4, Appli
352	24	75.0	422	6	US-10-336-263A-12	Sequence 12, Appl
353	24	75.0	423	6	US-10-336-263A-10	Sequence 10, Appl
354	24	75.0	425	6	US-10-336-263A-2	Sequence 2, Appli
355	24	75.0	425	7	US-11-096-568A-24469	Sequence 24469, A
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357	24	75.0	429	7	US-11-087-099-7496	Sequence 7496, Ap
358	24	75.0	434	7	US-11-087-099-755	Sequence 755, App
359	24	75.0	434	7	US-11-087-099-6812	Sequence 6812, Ap
360	24	75.0	434	7	US-11-087-099-8234	Sequence 8234, Ap
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363	24	75.0	459	7	US-11-087-099-8021	Sequence 8021, Ap
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369	24	75.0	462	7	US-11-177-648-26	Sequence 26, Appl
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371	24	75.0	462	7	US-11-177-648-28	Sequence 28, Appl
372	24	75.0	462	7	US-11-177-648-29	Sequence 29, Appl
373	24	75.0	462	7	US-11-177-648-30	Sequence 30, Appl
374	24	75.0	462	7	US-11-177-648-31	Sequence 31, Appl
375	24	75.0	462	7	US-11-177-648-32	Sequence 32, Appl
376	24	75.0	462	7	US-11-177-648-33	Sequence 33, Appl
377	24	75.0	462	7	US-11-177-648-79	Sequence 79, Appl
378	24	75.0	462	7	US-11-177-648-92	Sequence 92, Appl
379	24	75.0	462	7	US-11-177-648-93	Sequence 93, Appl
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382	24	75.0	462	7	US-11-177-648-96	Sequence 96, Appl
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384	24	75.0	462	7	US-11-177-648-98	Sequence 98, Appl
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395	24	75.0	474	7	US-11-087-099-6217	Sequence 6217, Ap
396	24	75.0	475	7	US-11-087-099-7087	Sequence 7087, Ap
397	24	75.0	476	7	US-11-087-099-1256	Sequence 1256, Ap
398	24	75.0	476	7	US-11-096-568A-7304	Sequence 7304, Ap
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403	24	75.0	479	7	US-11-087-099-9765	Sequence 9765, Ap
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418	24	75.0	535	7	US-11-106-672A-44	Sequence 44, Appl
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439	24	75.0	707	7	US-11-044-640-2	Sequence 2, Appli
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444	24	75.0	755	7	US-11-067-121-6	Sequence 6, Appli
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446	24	75.0	757	7	US-11-186-284-41	Sequence 41, Appl
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458	24	75.0	997	6	US-10-995-561-896	Sequence 896, App
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477	24	75.0	2333	6	US-10-453-372-170	Sequence 170, App
478	24	75.0	2662	6	US-10-453-372-114	Sequence 114, App
479	24	75.0	2724	6	US-10-453-372-148	Sequence 148, App
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487	24	75.0	2733	6	US-10-453-372-154	Sequence 154, App
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494	24	75.0	3570	6	US-10-453-372-198	Sequence 198, App
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496	24	75.0	3570	6	US-10-453-372-202	Sequence 202, App
497	24	75.0	3570	6	US-10-453-372-204	Sequence 204, App
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531	23	71.9	11	6	US-10-919-492-14	Sequence 14, Appl
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546	23	71.9	32	6	US-10-537-002-137	Sequence 137, App
547	23	71.9	34	6	US-10-982-727-80	Sequence 80, Appl
548	23	71.9	35	7	US-11-096-725-33	Sequence 33, Appl
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552	23	71.9	49	7	US-11-226-325-135	Sequence 135, App
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568	23	71.9	49	7	US-11-226-325-153	Sequence 153, App
569	23	71.9	49	7	US-11-226-325-154	Sequence 154, App
570	23	71.9	49	7	US-11-226-325-155	Sequence 155, App
571	23	71.9	49	7	US-11-129-741-625	Sequence 625, App
572	23	71.9	58	6	US-10-613-744-32	Sequence 32, Appl
573	23	71.9	60	6	US-10-475-075-869	Sequence 869, App
574	23	71.9	64	7	US-11-096-568A-8330	Sequence 8330, Ap
575	23	71.9	68	7	US-11-096-568A-8329	Sequence 8329, Ap
576	23	71.9	72	7	US-11-096-568A-1528	Sequence 1528, Ap
577	23	71.9	87	7	US-11-087-099-6705	Sequence 6705, Ap
578	23	71.9	95	7	US-11-098-686-10589	Sequence 10589, A
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581	23	71.9	107	6	US-10-678-790-61	Sequence 61, Appl
582	23	71.9	108	7	US-11-049-536-244	Sequence 244, App
583	23	71.9	112	7	US/11/020	Sequence 24, Appl
584	23	71.9	112	7	US-11-076-728-24	Sequence 24, Appl
585	23	71.9	113	7	US-11-206-587-28	Sequence 28, Appl
586	23	71.9	115	7	US-11-182-016-46	Sequence 46, Appl
587	23	71.9	115	7	US-11-072-512-2136	Sequence 2136, Ap
588	23	71.9	116	7	US-11-055-163-17	Sequence 17, Appl
589	23	71.9	116	7	US-11-072-512-3301	Sequence 3301, Ap
590	23	71.9	116	7	US-11-096-568A-4136	Sequence 4136, Ap
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592	23	71.9	119	7	US-11-096-568A-8649	Sequence 8649, Ap
593	23	71.9	120	6	US-10-925-366A-286	Sequence 286, App
594	23	71.9	120	7	US-11-226-325-198	Sequence 198, App
595	23	71.9	120	7	US-11-226-325-201	Sequence 201, App
596	23	71.9	120	7	US-11-226-325-202	Sequence 202, App
597	23	71.9	120	7	US-11-195-095-1	Sequence 1, Appli
598	23	71.9	120	7	US-11-096-568A-5045	Sequence 5045, Ap
599	23	71.9	121	6	US-10-678-790-63	Sequence 63, Appl
600	23	71.9	121	7	US-11-096-568A-922	Sequence 922, App
601	23	71.9	122	6	US-10-678-790-60	Sequence 60, Appl
602	23	71.9	122	7	US-11-049-536-278	Sequence 278, App
603	23	71.9	123	6	US-10-910-463-16	Sequence 16, Appl
604	23	71.9	124	7	US-11-096-568A-6759	Sequence 6759, Ap
605	23	71.9	125	7	US-11-096-568A-4135	Sequence 4135, Ap
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607	23	71.9	128	6	US-10-993-543-72	Sequence 72, Appl
608	23	71.9	129	7	US-11-052-554A-363	Sequence 363, App
609	23	71.9	130	6	US-10-993-543-56	Sequence 56, Appl
610	23	71.9	130	7	US-11-096-568A-20611	Sequence 20611, A
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612	23	71.9	133	7	US-11-087-099-4031	Sequence 4031, Ap
613	23	71.9	133	7	US-11-096-568A-5044	Sequence 5044, Ap
614	23	71.9	134	6	US-10-986-501-114	Sequence 114, App
615	23	71.9	134	6	US-10-986-501-199	Sequence 199, App
616	23	71.9	136	6	US-10-475-075-855	Sequence 855, App
617	23	71.9	137	6	US-10-993-543-76	Sequence 76, Appl
618	23	71.9	138	7	US-11-096-568A-4375	Sequence 4375, Ap
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621	23	71.9	139	7	US-11-226-325-18	Sequence 18, Appl
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623	23	71.9	139	7	US-11-226-325-22	Sequence 22, Appl
624	23	71.9	139	7	US-11-226-325-24	Sequence 24, Appl
625	23	71.9	139	7	US-11-226-325-26	Sequence 26, Appl
626	23	71.9	139	7	US-11-226-325-28	Sequence 28, Appl
627	23	71.9	139	7	US-11-226-325-30	Sequence 30, Appl
628	23	71.9	139	7	US-11-226-325-32	Sequence 32, Appl
629	23	71.9	139	7	US-11-226-325-34	Sequence 34, Appl
630	23	71.9	139	7	US-11-226-325-36	Sequence 36, Appl
631	23	71.9	139	7	US-11-226-325-38	Sequence 38, Appl
632	23	71.9	139	7	US-11-226-325-40	Sequence 40, Appl
633	23	71.9	139	7	US-11-226-325-42	Sequence 42, Appl
634	23	71.9	139	7	US-11-226-325-44	Sequence 44, Appl
635	23	71.9	139	7	US-11-226-325-46	Sequence 46, Appl
636	23	71.9	139	7	US-11-226-325-48	Sequence 48, Appl
637	23	71.9	139	7	US-11-226-325-50	Sequence 50, Appl
638	23	71.9	139	7	US-11-226-325-98	Sequence 98, Appl
639	23	71.9	139	7	US-11-226-325-100	Sequence 100, App
640	23	71.9	139	7	US-11-226-325-127	Sequence 127, App
641	23	71.9	139	7	US-11-230-251-31	Sequence 31, Appl
642	23	71.9	140	6	US-10-063-703-90	Sequence 90, Appl
643	23	71.9	140	7	US-11-102-240-90	Sequence 90, Appl
644	23	71.9	140	7	US-11-103-195-90	Sequence 90, Appl
645	23	71.9	141	7	US-11-072-175-202	Sequence 202, App
646	23	71.9	141	7	US-11-072-175-229	Sequence 229, App
647	23	71.9	147	7	US-11-055-822-466	Sequence 466, App
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649	23	71.9	148	7	US-11-096-568A-18883	Sequence 18883, A
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653	23	71.9	157	7	US-11-096-568A-4245	Sequence 4245, Ap
654	23	71.9	157	7	US-11-096-568A-14660	Sequence 14660, A
655	23	71.9	158	7	US-11-087-099-5896	Sequence 5896, Ap
656	23	71.9	161	7	US-11-096-568A-6589	Sequence 6589, Ap
657	23	71.9	161	7	US-11-096-568A-30692	Sequence 30692, A
658	23	71.9	162	7	US-11-096-568A-4134	Sequence 4134, Ap
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660	23	71.9	163	7	US-11-096-568A-30691	Sequence 30691, A
661	23	71.9	164	6	US-10-131-826A-314	Sequence 314, App
662	23	71.9	164	6	US-10-432-483-11	Sequence 11, Appl
663	23	71.9	164	6	US-10-973-115B-314	Sequence 314, App
664	23	71.9	167	7	US-11-210-316-18	Sequence 18, Appl
665	23	71.9	168	7	US-11-087-099-4415	Sequence 4415, Ap
666	23	71.9	169	6	US-10-453-372-838	Sequence 838, App
667	23	71.9	178	6	US-10-453-372-846	Sequence 846, App
668	23	71.9	179	7	US-11-098-686-11402	Sequence 11402, A
669	23	71.9	180	7	US-11-087-099-5210	Sequence 5210, Ap
670	23	71.9	180	7	US-11-087-099-5812	Sequence 5812, Ap
671	23	71.9	180	7	US-11-087-099-6131	Sequence 6131, Ap
672	23	71.9	181	7	US-11-096-568A-14659	Sequence 14659, A
673	23	71.9	182	7	US-11-072-512-3101	Sequence 3101, Ap
674	23	71.9	184	7	US-11-096-568A-14880	Sequence 14880, A
675	23	71.9	185	6	US-10-467-657-144	Sequence 144, App
676	23	71.9	185	6	US-10-467-657-4092	Sequence 4092, Ap
677	23	71.9	185	6	US-10-467-657-7068	Sequence 7068, Ap
678	23	71.9	185	7	US-11-096-568A-15171	Sequence 15171, A
679	23	71.9	187	7	US-11-087-099-717	Sequence 717, App
680	23	71.9	187	7	US-11-096-568A-24121	Sequence 24121, A
681	23	71.9	188	7	US-11-096-568A-4244	Sequence 4244, Ap
682	23	71.9	189	7	US-11-087-099-9544	Sequence 9544, Ap

683	23	71.9	190	7	US-11-096-568A-4337	Sequence 4337, Ap
684	23	71.9	190	7	US-11-096-568A-16124	Sequence 16124, A
685	23	71.9	190	7	US-11-096-568A-26107	Sequence 26107, A
686	23	71.9	192	6	US-10-523-038-7	Sequence 7, Appli
687	23	71.9	193	6	US-10-714-887-360	Sequence 360, App
688	23	71.9	196	7	US-11-096-568A-15354	Sequence 15354, A
689	23	71.9	197	6	US-10-714-887-98	Sequence 98, Appl
690	23	71.9	198	7	US-11-087-099-8329	Sequence 8329, Ap
691	23	71.9	201	7	US-11-082-389-112	Sequence 112, App
692	23	71.9	201	7	US-11-087-099-11366	Sequence 11366, A
693	23	71.9	201	7	US-11-096-568A-4243	Sequence 4243, Ap
694	23	71.9	201	7	US-11-096-568A-15353	Sequence 15353, A
695	23	71.9	203	7	US-11-062-186-70	Sequence 70, Appl
696	23	71.9	203	7	US-11-087-099-5653	Sequence 5653, Ap
697	23	71.9	204	7	US-11-096-568A-18522	Sequence 18522, A
698	23	71.9	204	7	US-11-096-568A-23452	Sequence 23452, A
699	23	71.9	206	7	US-11-062-186-69	Sequence 69, Appl
700	23	71.9	208	7	US-11-062-186-63	Sequence 63, Appl
701	23	71.9	208	7	US-11-096-568A-13190	Sequence 13190, A
702	23	71.9	209	7	US-11-096-568A-23490	Sequence 23490, A
703	23	71.9	211	7	US-11-087-099-2090	Sequence 2090, Ap
704	23	71.9	212	7	US-11-096-568A-13189	Sequence 13189, A
705	23	71.9	213	7	US-11-062-186-67	Sequence 67, Appl
706	23	71.9	213	7	US-11-096-568A-4374	Sequence 4374, Ap
707	23	71.9	214	7	US-11-096-568A-4373	Sequence 4373, Ap
708	23	71.9	214	7	US-11-096-568A-15352	Sequence 15352, A
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710	23	71.9	219	6	US-10-793-626-966	Sequence 966, App
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713	23	71.9	221	7	US-11-051-720-1776	Sequence 1776, Ap
714	23	71.9	221	7	US-11-096-568A-5302	Sequence 5302, Ap
715	23	71.9	221	7	US-11-043-806-574	Sequence 574, App
716	23	71.9	223	7	US-11-240-769-61	Sequence 61, Appl
717	23	71.9	224	7	US-11-062-186-64	Sequence 64, Appl
718	23	71.9	225	7	US-11-096-568A-18881	Sequence 18881, A
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724	23	71.9	231	7	US-11-096-568A-16634	Sequence 16634, A
725	23	71.9	231	7	US-11-096-568A-25618	Sequence 25618, A
726	23	71.9	231	7	US-11-096-568A-25842	Sequence 25842, A
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728	23	71.9	233	7	US-11-096-568A-13188	Sequence 13188, A
729	23	71.9	233	7	US-11-096-568A-18993	Sequence 18993, A
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733	23	71.9	239	7	US-11-096-568A-33251	Sequence 33251, A
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738	23	71.9	245	6	US-10-115-609-2	Sequence 2, Appli
739	23	71.9	247	7	US-11-054-515-2092	Sequence 2092, Ap
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741	23	71.9	247	7	US-11-033-039-877	Sequence 877, App
742	23	71.9	250	7	US-11-054-515-1319	Sequence 1319, Ap
743	23	71.9	250	7	US-11-054-515-1486	Sequence 1486, Ap
744	23	71.9	252	7	US-11-062-186-66	Sequence 66, Appl
745	23	71.9	252	7	US-11-140-416-32	Sequence 32, Appl
746	23	71.9	253	7	US-11-096-568A-5301	Sequence 5301, Ap
747	23	71.9	254	7	US-11-054-515-1350	Sequence 1350, Ap
748	23	71.9	254	7	US-11-087-099-1661	Sequence 1661, Ap
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752	23	71.9	257	7	US-11-054-515-1514	Sequence 1514, Ap
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756	23	71.9	261	6	US-10-537-002-16	Sequence 16, Appl
757	23	71.9	261	6	US-10-537-002-118	Sequence 118, App
758	23	71.9	261	7	US-11-102-240-118	Sequence 118, App
759	23	71.9	261	7	US-11-037-243-78	Sequence 78, Appl
760	23	71.9	261	7	US-11-103-195-118	Sequence 118, App
761	23	71.9	262	7	US-11-096-568A-5179	Sequence 5179, Ap
762	23	71.9	263	7	US-11-082-389-120	Sequence 120, App
763	23	71.9	263	7	US-11-072-512-3517	Sequence 3517, Ap
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766	23	71.9	267	7	US-11-096-568A-19687	Sequence 19687, A
767	23	71.9	268	7	US-11-096-568A-2130	Sequence 2130, Ap
768	23	71.9	269	6	US-10-131-826A-532	Sequence 532, App
769	23	71.9	269	6	US-10-973-115B-532	Sequence 532, App
770	23	71.9	270	6	US-10-485-517-413	Sequence 413, App
771	23	71.9	270	7	US-11-096-568A-12719	Sequence 12719, A
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776	23	71.9	276	7	US-11-096-568A-16633	Sequence 16633, A
777	23	71.9	276	7	US-11-096-568A-25617	Sequence 25617, A
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782	23	71.9	282	7	US-11-096-568A-8188	Sequence 8188, Ap
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793	23	71.9	290	6	US-10-453-372-842	Sequence 842, App
794	23	71.9	290	6	US-10-453-372-848	Sequence 848, App
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797	23	71.9	290	7	US-11-240-769-65	Sequence 65, Appl
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803	23	71.9	293	7	US-11-096-568A-12776	Sequence 12776, A
804	23	71.9	293	7	US-11-096-568A-25840	Sequence 25840, A
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807	23	71.9	295	6	US-10-467-657-2354	Sequence 2354, Ap
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809	23	71.9	295	6	US-10-453-372-840	Sequence 840, App
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813	23	71.9	296	6	US-10-467-657-2860	Sequence 2860, Ap
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819	23	71.9	304	6	US-10-533-811-5	Sequence 5, Appli
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821	23	71.9	305	7	US-11-000-463-863	Sequence 863, App
822	23	71.9	306	7	US-11-087-099-5439	Sequence 5439, Ap
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824	23	71.9	306	7	US-11-087-099-9172	Sequence 9172, Ap
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830	23	71.9	312	6	US-10-718-264-166	Sequence 166, App
831	23	71.9	312	6	US-10-718-264-10	Sequence 10, Appl
832	23	71.9	312	6	US-10-718-264-165	Sequence 165, App
833	23	71.9	312	6	US-10-718-264-166	Sequence 166, App
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835	23	71.9	312	7	US-11-107-219-4	Sequence 4, Appli
836	23	71.9	312	7	US-11-096-568A-2178	Sequence 2178, Ap
837	23	71.9	314	6	US-10-718-264-24	Sequence 24, Appl
838	23	71.9	314	6	US-10-718-264-24	Sequence 24, Appl
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840	23	71.9	314	7	US-11-107-219-3	Sequence 3, Appli
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843	23	71.9	316	7	US-11-096-568A-31551	Sequence 31551, A
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845	23	71.9	317	7	US-11-096-568A-12775	Sequence 12775, A
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853	23	71.9	323	7	US-11-096-568A-31550	Sequence 31550, A
854	23	71.9	324	7	US-11-096-568A-6972	Sequence 6972, Ap
855	23	71.9	325	7	US-11-129-143-88	Sequence 88, Appl
856	23	71.9	325	7	US-11-087-099-7835	Sequence 7835, Ap
857	23	71.9	326	7	US-11-087-099-8724	Sequence 8724, Ap
858	23	71.9	326	7	US-11-096-568A-2177	Sequence 2177, Ap
859	23	71.9	328	7	US-11-072-512-2625	Sequence 2625, Ap
860	23	71.9	328	7	US-11-087-099-6030	Sequence 6030, Ap
861	23	71.9	330	6	US-10-485-517-415	Sequence 415, App
862	23	71.9	331	7	US-11-129-143-87	Sequence 87, Appl
863	23	71.9	331	7	US-11-096-568A-12179	Sequence 12179, A
864	23	71.9	332	6	US-10-873-528-190	Sequence 190, App
865	23	71.9	334	7	US-11-207-626A-22	Sequence 22, Appl
866	23	71.9	334	7	US-11-087-099-8950	Sequence 8950, Ap
867	23	71.9	336	7	US-11-096-568A-14878	Sequence 14878, A
868	23	71.9	336	7	US-11-096-568A-24120	Sequence 24120, A
869	23	71.9	336	7	US-11-096-568A-33249	Sequence 33249, A
870	23	71.9	337	6	US-10-821-234-1004	Sequence 1004, Ap
871	23	71.9	339	7	US-11-096-568A-12178	Sequence 12178, A
872	23	71.9	340	6	US-10-873-528-188	Sequence 188, App
873	23	71.9	341	7	US-11-087-099-7575	Sequence 7575, Ap
874	23	71.9	342	6	US-10-055-877-335	Sequence 335, App
875	23	71.9	342	7	US-11-096-568A-18666	Sequence 18666, A
876	23	71.9	342	7	US-11-096-568A-31300	Sequence 31300, A
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878	23	71.9	347	6	US-10-821-234-1081	Sequence 1081, Ap
879	23	71.9	347	7	US-11-087-099-11612	Sequence 11612, A
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881	23	71.9	350	7	US-11-087-099-4722	Sequence 4722, Ap
882	23	71.9	351	7	US-11-087-099-2245	Sequence 2245, Ap
883	23	71.9	352	7	US-11-096-568A-23159	Sequence 23159, A
884	23	71.9	353	7	US-11-096-568A-12691	Sequence 12691, A
885	23	71.9	356	6	US-10-055-877-184	Sequence 184, App
886	23	71.9	356	6	US-10-055-877-185	Sequence 185, App
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889	23	71.9	358	7	US-11-096-568A-31299	Sequence 31299, A
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891	23	71.9	362	6	US-10-517-939-88	Sequence 88, Appl
892	23	71.9	362	7	US-11-087-099-7071	Sequence 7071, Ap
893	23	71.9	364	7	US-11-096-568A-31867	Sequence 31867, A
894	23	71.9	365	7	US-11-096-568A-22440	Sequence 22440, A
895	23	71.9	366	6	US-10-467-657-1164	Sequence 1164, Ap
896	23	71.9	366	7	US-11-096-568A-29379	Sequence 29379, A
897	23	71.9	366	7	US-11-096-568A-30167	Sequence 30167, A
898	23	71.9	369	7	US-11-096-568A-17040	Sequence 17040, A
899	23	71.9	370	7	US-11-087-099-8655	Sequence 8655, Ap
900	23	71.9	370	7	US-11-096-568A-28963	Sequence 28963, A
901	23	71.9	371	7	US-11-087-099-5960	Sequence 5960, Ap
902	23	71.9	371	7	US-11-096-568A-19392	Sequence 19392, A
903	23	71.9	371	7	US-11-096-568A-27025	Sequence 27025, A
904	23	71.9	371	7	US-11-096-568A-34083	Sequence 34083, A
905	23	71.9	372	7	US-11-096-568A-31549	Sequence 31549, A
906	23	71.9	373	7	US-11-096-568A-12718	Sequence 12718, A
907	23	71.9	373	7	US-11-096-568A-29378	Sequence 29378, A
908	23	71.9	373	7	US-11-096-568A-30166	Sequence 30166, A
909	23	71.9	374	7	US-11-096-568A-27408	Sequence 27408, A
910	23	71.9	375	7	US-11-087-099-8271	Sequence 8271, Ap
911	23	71.9	375	7	US-11-096-568A-12754	Sequence 12754, A
912	23	71.9	375	7	US-11-096-568A-34082	Sequence 34082, A
913	23	71.9	376	7	US-11-213-368-6	Sequence 6, Appli
914	23	71.9	376	7	US-11-213-368-14	Sequence 14, Appl
915	23	71.9	376	7	US-11-238-025-36	Sequence 36, Appl
916	23	71.9	377	7	US-11-096-568A-28962	Sequence 28962, A
917	23	71.9	378	7	US-11-087-099-2807	Sequence 2807, Ap
918	23	71.9	380	7	US-11-087-099-10747	Sequence 10747, A
919	23	71.9	380	7	US-11-096-568A-6971	Sequence 6971, Ap
920	23	71.9	381	7	US-11-096-568A-14664	Sequence 14664, A
921	23	71.9	382	7	US-11-087-099-8325	Sequence 8325, Ap
922	23	71.9	382	7	US-11-096-568A-12612	Sequence 12612, A
923	23	71.9	383	7	US-11-096-568A-12774	Sequence 12774, A
924	23	71.9	385	6	US-10-523-503-8	Sequence 8, Appli
925	23	71.9	387	7	US-11-096-568A-27407	Sequence 27407, A
926	23	71.9	388	7	US-11-072-512-2353	Sequence 2353, Ap
927	23	71.9	388	7	US-11-096-568A-17039	Sequence 17039, A
928	23	71.9	389	7	US-11-060-008-11	Sequence 11, Appl
929	23	71.9	389	7	US-11-096-568A-16089	Sequence 16089, A
930	23	71.9	390	7	US-11-096-568A-16376	Sequence 16376, A
931	23	71.9	392	7	US-11-096-568A-12611	Sequence 12611, A
932	23	71.9	392	7	US-11-096-568A-29673	Sequence 29673, A
933	23	71.9	394	6	US-10-510-386-208	Sequence 208, App
934	23	71.9	395	6	US-10-330-773-98	Sequence 98, Appl
935	23	71.9	396	7	US-11-232-405A-38	Sequence 38, Appl
936	23	71.9	396	7	US-11-096-568A-6970	Sequence 6970, Ap
937	23	71.9	397	7	US-11-087-099-8667	Sequence 8667, Ap
938	23	71.9	398	7	US-11-096-568A-22439	Sequence 22439, A
939	23	71.9	399	7	US-11-096-568A-29672	Sequence 29672, A
940	23	71.9	402	6	US-10-649-591-18	Sequence 18, Appl
941	23	71.9	404	7	US-11-096-568A-31866	Sequence 31866, A
942	23	71.9	405	7	US-11-096-568A-11828	Sequence 11828, A
943	23	71.9	405	7	US-11-096-568A-27406	Sequence 27406, A
944	23	71.9	405	7	US-11-096-568A-31865	Sequence 31865, A
945	23	71.9	408	6	US-10-467-657-8004	Sequence 8004, Ap
946	23	71.9	409	7	US-11-096-568A-22438	Sequence 22438, A
947	23	71.9	410	7	US-11-096-568A-11827	Sequence 11827, A
948	23	71.9	410	7	US-11-096-568A-20785	Sequence 20785, A
949	23	71.9	413	7	US-11-096-568A-26633	Sequence 26633, A
950	23	71.9	414	7	US-11-229-371-45	Sequence 45, Appl
951	23	71.9	414	7	US-11-229-371-89	Sequence 89, Appl
952	23	71.9	414	7	US-11-228-923-45	Sequence 45, Appl
953	23	71.9	414	7	US-11-228-923-89	Sequence 89, Appl
954	23	71.9	414	7	US-11-228-875-45	Sequence 45, Appl
955	23	71.9	414	7	US-11-228-875-89	Sequence 89, Appl
956	23	71.9	414	7	US-11-096-568A-20784	Sequence 20784, A
957	23	71.9	416	7	US-11-096-568A-12717	Sequence 12717, A
958	23	71.9	417	7	US-11-087-099-1146	Sequence 1146, Ap
959	23	71.9	418	7	US-11-109-156-2	Sequence 2, Appli
960	23	71.9	418	7	US-11-099-691-1	Sequence 1, Appli
961	23	71.9	418	7	US-11-096-568A-16380	Sequence 16380, A
962	23	71.9	418	7	US-11-096-568A-22303	Sequence 22303, A
963	23	71.9	420	7	US-11-096-568A-22302	Sequence 22302, A
964	23	71.9	422	7	US-11-082-389-444	Sequence 444, App
965	23	71.9	422	7	US-11-098-686-10563	Sequence 10563, A
966	23	71.9	422	7	US-11-087-099-9441	Sequence 9441, Ap
967	23	71.9	422	7	US-11-096-568A-29377	Sequence 29377, A
968	23	71.9	422	7	US-11-096-568A-30165	Sequence 30165, A
969	23	71.9	423	7	US-11-087-099-9700	Sequence 9700, Ap
970	23	71.9	423	7	US-11-096-568A-19391	Sequence 19391, A
971	23	71.9	424	7	US-11-202-731-35	Sequence 35, Appl
972	23	71.9	425	7	US-11-096-568A-20783	Sequence 20783, A
973	23	71.9	426	7	US-11-087-099-9050	Sequence 9050, Ap
974	23	71.9	427	6	US-10-995-561-816	Sequence 816, App

975	23	71.9	427	6	US-10-995-561-818	Sequence 818, App
976	23	71.9	428	7	US-11-096-568A-13348	Sequence 13348, A
977	23	71.9	431	7	US-11-098-686-10322	Sequence 10322, A
978	23	71.9	433	7	US-11-096-568A-12610	Sequence 12610, A
979	23	71.9	434	7	US-11-087-099-6563	Sequence 6563, Ap
980	23	71.9	437	7	US-11-087-099-2535	Sequence 2535, Ap
981	23	71.9	438	7	US-11-183-136-40	Sequence 40, Appl
982	23	71.9	439	7	US-11-087-099-5043	Sequence 5043, Ap
983	23	71.9	440	7	US-11-087-099-10394	Sequence 10394, A
984	23	71.9	440	7	US-11-087-099-11247	Sequence 11247, A
985	23	71.9	441	7	US-11-087-099-2305	Sequence 2305, Ap
986	23	71.9	444	7	US-11-096-568A-22301	Sequence 22301, A
987	23	71.9	445	7	US-11-087-099-4079	Sequence 4079, Ap
988	23	71.9	445	7	US-11-096-568A-13347	Sequence 13347, A
989	23	71.9	446	7	US-11-087-099-12438	Sequence 12438, A
990	23	71.9	447	6	US-10-467-657-4406	Sequence 4406, Ap
991	23	71.9	448	7	US-11-096-568A-32239	Sequence 32239, A
992	23	71.9	451	7	US-11-087-099-10164	Sequence 10164, A
993	23	71.9	452	6	US-10-995-561-817	Sequence 817, App
994	23	71.9	453	7	US-11-082-389-198	Sequence 198, App
995	23	71.9	453	7	US-11-087-099-6617	Sequence 6617, Ap
996	23	71.9	453	7	US-11-087-099-9141	Sequence 9141, Ap
997	23	71.9	453	7	US-11-087-099-12200	Sequence 12200, A
998	23	71.9	454	7	US-11-087-099-11537	Sequence 11537, A
999	23	71.9	455	7	US-11-087-099-766	Sequence 766, App
1000	23	71.9	456	7	US-11-087-099-11920	Sequence 11920, A

ALIGNMENTS

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RESULT 1
US-10-982-357-9
; Sequence 9, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-9

  Query Match             90.6%;  Score 29;  DB 6;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db          1 TYWMN 5


RESULT 2
US-10-982-357-3
; Sequence 3, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-3

  Query Match             90.6%;  Score 29;  DB 6;  Length 120;
  Best Local Similarity   80.0%;  Pred. No. 1e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db         31 TYWMN 35


RESULT 3
US-09-995-493-62
; Sequence 62, Application US/09995493
; Publication No. US20060035293A1
; GENERAL INFORMATION:
;  APPLICANT: Handfield, Martin
;  APPLICANT:  Hillman, Jeffrey
;  APPLICANT:  Progulske-Fox, Ann
;  TITLE OF INVENTION: Identification of Actinobacillus actinomycetemcomitans Antigens fo
;  TITLE OF INVENTION:  in the Diagnosis, Treatment, and Monitoring of Periodontal Diseas
;  FILE REFERENCE: MBHB01-662
;  CURRENT APPLICATION NUMBER: US/09/995,493
;  CURRENT FILING DATE:  2001-11-28
;  NUMBER OF SEQ ID NOS: 234
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 62
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Actinobacillus actinomycetemcomitans
US-09-995-493-62

  Query Match             90.6%;  Score 29;  DB 5;  Length 214;
  Best Local Similarity   80.0%;  Pred. No. 1.6e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db        109 TYWMN 113


RESULT 4
US-10-467-657-12
; Sequence 12, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 12
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-12

  Query Match             90.6%;  Score 29;  DB 6;  Length 233;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        224 TYWLS 228
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RESULT 5
US-10-467-657-5530
; Sequence 5530, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5530
;   LENGTH: 233
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5530

  Query Match             90.6%;  Score 29;  DB 6;  Length 233;
  Best Local Similarity   80.0%;  Pred. No. 1.7e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        224 TYWLS 228


RESULT 6
US-11-096-568A-32269
; Sequence 32269, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32269
;   LENGTH: 293
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(293)
;   OTHER INFORMATION: Ceres Seq. ID no. 13592551
US-11-096-568A-32269

  Query Match             90.6%;  Score 29;  DB 7;  Length 293;
  Best Local Similarity   80.0%;  Pred. No. 2e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        185 TYWLS 189


RESULT 7
US-11-096-568A-32268
; Sequence 32268, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32268
;   LENGTH: 351
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(351)
;   OTHER INFORMATION: Ceres Seq. ID no. 13592550
US-11-096-568A-32268

  Query Match             90.6%;  Score 29;  DB 7;  Length 351;
  Best Local Similarity   80.0%;  Pred. No. 2.2e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        243 TYWLS 247


RESULT 8
US-11-096-568A-32267
; Sequence 32267, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 32267
;   LENGTH: 378
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(378)
;   OTHER INFORMATION: Ceres Seq. ID no. 13592549
US-11-096-568A-32267

  Query Match             90.6%;  Score 29;  DB 7;  Length 378;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        270 TYWLS 274


RESULT 9
US-11-096-568A-26756
; Sequence 26756, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26756
;   LENGTH: 391
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
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;   LOCATION: (1)..(391)
;   OTHER INFORMATION: Ceres Seq. ID no. 13599723
US-11-096-568A-26756

  Query Match             90.6%;  Score 29;  DB 7;  Length 391;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db         43 TYWMA 47


RESULT 10
US-11-096-568A-18081
; Sequence 18081, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18081
;   LENGTH: 416
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(416)
;   OTHER INFORMATION: Ceres Seq. ID no. 12362603
US-11-096-568A-18081

  Query Match             90.6%;  Score 29;  DB 7;  Length 416;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db         68 TYWMA 72


RESULT 11
US-11-096-568A-26755
; Sequence 26755, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26755
;   LENGTH: 416
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(416)
;   OTHER INFORMATION: Ceres Seq. ID no. 13599722
US-11-096-568A-26755

  Query Match             90.6%;  Score 29;  DB 7;  Length 416;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db         68 TYWMA 72


RESULT 12
US-11-096-568A-26754
; Sequence 26754, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 26754
;   LENGTH: 443
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(443)
;   OTHER INFORMATION: Ceres Seq. ID no. 13599721
US-11-096-568A-26754

  Query Match             90.6%;  Score 29;  DB 7;  Length 443;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db         95 TYWMA 99


RESULT 13
US-11-096-568A-11404
; Sequence 11404, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11404
;   LENGTH: 444
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(444)
;   OTHER INFORMATION: Ceres Seq. ID no. 15219625
US-11-096-568A-11404

  Query Match             90.6%;  Score 29;  DB 7;  Length 444;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db         87 TYWMA 91


RESULT 14
US-11-087-099-1360
; Sequence 1360, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
```

```
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 1360
;   LENGTH: 456
;   TYPE: PRT
;   ORGANISM: Oenococcus oeni MCW
US-11-087-099-1360

  Query Match             90.6%;  Score 29;  DB 7;  Length 456;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         98 TYWLS 102


RESULT 15
US-11-096-568A-18080
; Sequence 18080, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18080
;   LENGTH: 456
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(456)
;   OTHER INFORMATION: Ceres Seq. ID no. 12362602
US-11-096-568A-18080

  Query Match             90.6%;  Score 29;  DB 7;  Length 456;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db        108 TYWMA 112


RESULT 16
US-11-096-568A-18079
; Sequence 18079, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 18079
;   LENGTH: 478
;   TYPE: PRT
;   ORGANISM: Zea mays subsp. mays
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(478)
;   OTHER INFORMATION: Ceres Seq. ID no. 12362601
US-11-096-568A-18079

  Query Match             90.6%;  Score 29;  DB 7;  Length 478;
  Best Local Similarity   80.0%;  Pred. No. 2.8e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db        130 TYWMA 134


RESULT 17
US-11-096-568A-11403
; Sequence 11403, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11403
;   LENGTH: 493
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(493)
;   OTHER INFORMATION: Ceres Seq. ID no. 15219624
US-11-096-568A-11403

  Query Match             90.6%;  Score 29;  DB 7;  Length 493;
  Best Local Similarity   80.0%;  Pred. No. 2.9e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db        136 TYWMA 140


RESULT 18
US-11-096-568A-11402
; Sequence 11402, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11402
;   LENGTH: 522
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(522)
;   OTHER INFORMATION: Ceres Seq. ID no. 15219623
US-11-096-568A-11402

  Query Match             90.6%;  Score 29;  DB 7;  Length 522;
  Best Local Similarity   80.0%;  Pred. No. 3e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              ||||:
Db        165 TYWMA 169


RESULT 19
US-10-850-635-54
; Sequence 54, Application US/10850635
; Publication No. US20050287149A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Keler, Tibor
;  APPLICANT:  Lowy, Israel
;  APPLICANT:  Vitale, Laura
;  APPLICANT:  Blanset, Diane
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST
;  TITLE OF INVENTION:  BACILLUS ANTHRACIS PROTECTIVE ANTIGEN
;  FILE REFERENCE: MXI-305
;  CURRENT APPLICATION NUMBER: US/10/850,635
;  CURRENT FILING DATE:  2004-05-21
;  PRIOR APPLICATION NUMBER: 60/472636
;  PRIOR FILING DATE: 2003-05-21
;  PRIOR APPLICATION NUMBER: 60/512336
;  PRIOR FILING DATE: 2003-10-16
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-850-635-54

  Query Match             87.5%;  Score 28;  DB 6;  Length 5;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db          1 SYWMS 5


RESULT 20
US-11-093-274-35
; Sequence 35, Application US/11093274
; Publication No. US20050266008A1
; GENERAL INFORMATION:
;  APPLICANT: Graziano, Robert
;  APPLICANT:  Cardarelli,  Josephine M.
;  APPLICANT:  Kempe, Thomas
;  APPLICANT:  Cutter, Beth
;  APPLICANT:  Srinivasan, Mohan
;  TITLE OF INVENTION: IRTA-5 ANTIBODIES AND THEIR USES
;  FILE REFERENCE: 04280/1201101-US1
;  CURRENT APPLICATION NUMBER: US/11/093,274
;  CURRENT FILING DATE:  2005-03-28
;  PRIOR APPLICATION NUMBER: 60/557,741
;  PRIOR FILING DATE: 2004-03-29
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
;   LENGTH: 97
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-093-274-35

  Query Match             87.5%;  Score 28;  DB 7;  Length 97;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         30 SYWMS 34


RESULT 21
US-11-054-669-15
; Sequence 15, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
;  FILE REFERENCE: 30219/US/3
;  CURRENT APPLICATION NUMBER: US/11/054,669
;  CURRENT FILING DATE:  2005-02-08
;  PRIOR APPLICATION NUMBER: US 10/194,975
;  PRIOR FILING DATE: 2002-07-12
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-669-15

  Query Match             87.5%;  Score 28;  DB 7;  Length 98;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         31 SYWMS 35


RESULT 22
US-11-084-554-44
; Sequence 44, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-44

  Query Match             87.5%;  Score 28;  DB 7;  Length 98;
  Best Local Similarity   80.0%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         31 SYWMS 35


RESULT 23
US-11-004-590-14
; Sequence 14, Application US/11004590
; Publication No. US20060008883A1
; GENERAL INFORMATION:
;  APPLICANT: Lazar, Gregory Alan
;  APPLICANT:  Desjarlais, John R.
;  APPLICANT:  Hammond, Phillip W.
;  TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
;  TITLE OF INVENTION:  CONTENT AND COMPOSITIONS THEREOF
;  FILE REFERENCE: 185832/US/5
;  CURRENT APPLICATION NUMBER: US/11/004,590
;  CURRENT FILING DATE:  2004-12-03
;  PRIOR APPLICATION NUMBER: US 60/527,167
;  PRIOR FILING DATE: 2003-12-04
;  PRIOR APPLICATION NUMBER: US 60/581,613
;  PRIOR FILING DATE: 2004-06-21
;  PRIOR APPLICATION NUMBER: US 60/601,665
```

; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-590-14

Query Match 87.5%; Score 28; DB 7; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
:||||
Db 31 SYWMS 35

RESULT 24
US-11-136-250-44
; Sequence 44, Application US/11136250
; Publication No. US20060021074A1
; GENERAL INFORMATION:
; APPLICANT: Kellermann, Sirid-Ai
; APPLICANT: Green, Larry L.
; APPLICANT: Korver, Wouter
; TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
; TITLE OF INVENTION: ANTIBODIES THROUGH V GENE MANIPULATION
; FILE REFERENCE: ABGENIX.100A2
; CURRENT APPLICATION NUMBER: US/11/136,250
; CURRENT FILING DATE: 2005-05-23
; PRIOR APPLICATION NUMBER: 11/084,554
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: PCT/US2005/009306
; PRIOR FILING DATE: 2005-03-17
; PRIOR APPLICATION NUMBER: 60/574,661
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: 60/554,372
; PRIOR FILING DATE: 2004-03-19
; NUMBER OF SEQ ID NOS: 266
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-136-250-44

Query Match 87.5%; Score 28; DB 7; Length 98;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
:||||
Db 31 SYWMS 35

RESULT 25
US-10-850-635-12
; Sequence 12, Application US/10850635
; Publication No. US20050287149A1
; GENERAL INFORMATION:
; APPLICANT: Keler, Tibor
; APPLICANT: Lowy, Israel
; APPLICANT: Vitale, Laura
; APPLICANT: Blanset, Diane
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST
; TITLE OF INVENTION: BACILLUS ANTHRACIS PROTECTIVE ANTIGEN
; FILE REFERENCE: MXI-305
; CURRENT APPLICATION NUMBER: US/10/850,635
; CURRENT FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: 60/472636
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 60/512336
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-850-635-12

Query Match 87.5%; Score 28; DB 6; Length 129;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
:||||
Db 31 SYWMS 35

RESULT 26
US-11-137-465-59
; Sequence 59, Application US/11137465
; Publication No. US20050255558A1
; GENERAL INFORMATION:
; APPLICANT: Agarwal, Pankaj
; APPLICANT: Murdoch, Paul R.
; APPLICANT: Rizvi, Safia, K.
; APPLICANT: Smith, Randall, F.
; APPLICANT: Xiang, Zhaoying
; APPLICANT: Kabnick, Karen
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50018
; CURRENT APPLICATION NUMBER: US/11/137,465
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/239,663
; PRIOR FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/US01/09226
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/192,158
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 60/192,668
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: 60/200,166
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-137-465-59

Query Match 87.5%; Score 28; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWM 4
||||
Db 23 TYWM 26

RESULT 27
US-11-087-099-4770
; Sequence 4770, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464

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; SEQ ID NO 4770
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: Bacillus anthracis str. A2012
US-11-087-099-4770

  Query Match            87.5%;  Score 28;  DB 7;  Length 225;
  Best Local Similarity   80.0%;  Pred. No. 2.4e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db         13 TYWIS 17


RESULT 28
US-11-054-515-1889
; Sequence 1889, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1889
;   LENGTH: 241
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1889

  Query Match            87.5%;  Score 28;  DB 7;  Length 241;
  Best Local Similarity   80.0%;  Pred. No. 2.5e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         31 SYWMS 35


RESULT 29
US-11-054-515-1470
; Sequence 1470, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1470
;   LENGTH: 247
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1470

  Query Match            87.5%;  Score 28;  DB 7;  Length 247;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         31 SYWMS 35


RESULT 30
US-11-054-515-1594
; Sequence 1594, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1594
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1594
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```
  Query Match             87.5%;  Score 28;  DB 7;  Length 251;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         31 SYWMS 35


RESULT 31
US-11-054-515-3245
; Sequence 3245, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3245
;   LENGTH: 251
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-3245

  Query Match             87.5%;  Score 28;  DB 7;  Length 251;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         31 SYWMS 35


RESULT 32
US-11-056-825-10
; Sequence 10, Application US/11056825
; Publication No. US20050255109A1
; GENERAL INFORMATION:
;  APPLICANT: Felding-Habermann, Brunhilde
;  APPLICANT:  Janda, Kim D.
;  APPLICANT:  Saven, Alan
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
;  FILE REFERENCE: SCRP-0042
;  CURRENT APPLICATION NUMBER: US/11/056,825
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: US 60/626,726
;  PRIOR FILING DATE: 2004-11-10
;  PRIOR APPLICATION NUMBER: US 60/544,807
;  PRIOR FILING DATE: 2004-02-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
;   LENGTH: 257
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-11-056-825-10

  Query Match             87.5%;  Score 28;  DB 7;  Length 257;
  Best Local Similarity   80.0%;  Pred. No. 2.6e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         33 SYWMS 37


RESULT 33
US-11-096-568A-5086
; Sequence 5086, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 5086
;   LENGTH: 259
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(259)
;   OTHER INFORMATION: Ceres Seq. ID no. 14306954
US-11-096-568A-5086

  Query Match             87.5%;  Score 28;  DB 7;  Length 259;
  Best Local Similarity   80.0%;  Pred. No. 2.7e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db          6 SYWMS 10


RESULT 34
US-11-096-568A-28944
; Sequence 28944, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28944
;   LENGTH: 273
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(273)
;   OTHER INFORMATION: Ceres Seq. ID no. 3094517
US-11-096-568A-28944

  Query Match             87.5%;  Score 28;  DB 7;  Length 273;
```

```
  Best Local Similarity   80.0%;  Pred. No. 2.8e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |:|||
Db         98 TFWMS 102


RESULT 35
US-11-087-099-3415
; Sequence 3415, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 3415
;   LENGTH: 281
;   TYPE: PRT
;   ORGANISM: Gossypium hirsutum
US-11-087-099-3415

  Query Match             87.5%;  Score 28;  DB 7;  Length 281;
  Best Local Similarity   100.0%;  Pred. No. 2.8e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWM 4
              ||||
Db          5 TYWM 8


RESULT 36
US-11-245-053-10
; Sequence 10, Application US/11245053
; Publication No. US20060035334A1
;   GENERAL INFORMATION:
;        APPLICANT: Adams, Camilia W.
;                   Ashkenazi, Avi J.
;                   Chuntharapai, Anan
;                   Kim, Kyung J.
;        TITLE OF INVENTION: Apo-2 Receptor
;        NUMBER OF SEQUENCES: 14
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Genentech, Inc.
;             STREET: 1 DNA Way
;             CITY: South San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94080
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WinPatin (Genentech)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/245,053
;             FILING DATE: 07-Oct-2005
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/10/288,917
;             FILING DATE: 06-Nov-2002
;             APPLICATION NUMBER: 10/052798
;             FILING DATE: 02-NOV-2001
;             APPLICATION NUMBER: 09/079029
;             FILING DATE: 14-MAY-1998
;             APPLICATION NUMBER: 60/074119
;             FILING DATE: 09-FEB-1998
;             APPLICATION NUMBER: 60/046615
;             FILING DATE: 15-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Marschang, Diane L.
;             REGISTRATION NUMBER: 35,600
;             REFERENCE/DOCKET NUMBER: P1101R2D1C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650/225-5416
;             TELEFAX: 650/952-9881
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 312 amino acids
;             TYPE: Amino Acid
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-11-245-053-10

  Query Match             87.5%;  Score 28;  DB 7;  Length 312;
  Best Local Similarity   80.0%;  Pred. No. 3e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              :||||
Db         70 SYWMS 74


RESULT 37
US-11-096-568A-28943
; Sequence 28943, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28943
;   LENGTH: 363
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(363)
;   OTHER INFORMATION: Ceres Seq. ID no. 3094516
US-11-096-568A-28943

  Query Match             87.5%;  Score 28;  DB 7;  Length 363;
  Best Local Similarity   80.0%;  Pred. No. 3.4e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |:|||
Db        188 TFWMS 192


RESULT 38
US/11/185
; Sequence 12, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
;  APPLICANT: Caput, Daniel
;  APPLICANT:  Ferrara, Pascual
;  APPLICANT:  Laurent, Patrick
;  APPLICANT:  Vita, Natalio
;  TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
;  FILE REFERENCE: IVD924 US CNT 1
;  CURRENT APPLICATION NUMBER: US/11/185,230
;  CURRENT FILING DATE:  2005-07-18
;  PRIOR APPLICATION NUMBER: PCT/FR96/01756
;  PRIOR FILING DATE: 1996-11-07
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 378
```

```
;   TYPE: PRT 3
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: variant of SEQ ID NO. 2 in which the sequence VRCVTL is substitut
US/11/185,230-12

  Query Match             87.5%;  Score 28;  DB 7;  Length 378;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        127 TYWIS 131


RESULT 39
US-11-182-384A-12
; Sequence 12, Application US/11182384A
; Publication No. US20060035855A1
; GENERAL INFORMATION:
;  APPLICANT: Caput, Daniel
;  APPLICANT:  Ferrara, Pascual
;  APPLICANT:  Laurent, Patrick
;  APPLICANT:  Vita, Natalio
;  TITLE OF INVENTION: Purified polypeptides having IL-13 receptor activity
;  FILE REFERENCE: IVD924 US DIV 2
;  CURRENT APPLICATION NUMBER: US/11/182,384A
;  CURRENT FILING DATE:  2005-07-15
;  PRIOR APPLICATION NUMBER: 09/077,817
;  PRIOR FILING DATE: 1998-09-14
;  PRIOR APPLICATION NUMBER: PCT/FR96/01756
;  PRIOR FILING DATE: 1996-11-07
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 378
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: SEQ ID NO. 2 substitution 8-C terminal amino acids with VRCTL
US-11-182-384A-12

  Query Match             87.5%;  Score 28;  DB 7;  Length 378;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        127 TYWIS 131


RESULT 40
US-11-183-599A-12
; Sequence 12, Application US/11183599A
; Publication No. US20060035856A1
; GENERAL INFORMATION:
;  APPLICANT: Caput, Daniel
;  APPLICANT:  Ferrara, Pascual
;  APPLICANT:  Laurent, Patrick
;  APPLICANT:  Vita, Natalio
;  TITLE OF INVENTION: Purified polypeptides having IL-13 receptor activity
;  FILE REFERENCE: IVD924 US DIV 1
;  CURRENT APPLICATION NUMBER: US/11/183,599A
;  CURRENT FILING DATE:  2005-07-15
;  PRIOR APPLICATION NUMBER: 09/077,817
;  PRIOR FILING DATE: 1998-09-14
;  PRIOR APPLICATION NUMBER: PCT/FR96/01756
;  PRIOR FILING DATE: 1996-11-07
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 378
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: SEQ ID NO. 2 substitution 8-C terminal amino acids with VRCTL
US-11-183-599A-12

  Query Match             87.5%;  Score 28;  DB 7;  Length 378;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        127 TYWIS 131


RESULT 41
US-10-989-313-4
; Sequence 4, Application US/10989313
; Publication No. US20050277126A1
; GENERAL INFORMATION:
;  APPLICANT: Collins, Mary
;  APPLICANT:  Donaldson, Debra
;  APPLICANT:  Fitz, Lora
;  APPLICANT:  Neben, Tamlyn
;  APPLICANT:  Whitters, Matthew
;  APPLICANT:  Wood, Clive
;  APPLICANT:  Wills-Karp, Marsha
;  APPLICANT:  Genetics Institute, Inc.
;  TITLE OF INVENTION: Cytokine Receptor Chain
;  FILE REFERENCE: GI 5268A
;  CURRENT APPLICATION NUMBER: US/10/989,313
;  CURRENT FILING DATE:  2004-11-15
;  PRIOR APPLICATION NUMBER: US/09/868,123
;  PRIOR FILING DATE: 2002-04-02
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 380
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-989-313-4

  Query Match             87.5%;  Score 28;  DB 6;  Length 380;
  Best Local Similarity   80.0%;  Pred. No. 3.5e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        127 TYWIS 131


RESULT 42
US-11-185-230-2
; Sequence 2, Application US/11185230
; Publication No. US20050282216A1
; GENERAL INFORMATION:
;  APPLICANT: Caput, Daniel
;  APPLICANT:  Ferrara, Pascual
;  APPLICANT:  Laurent, Patrick
;  APPLICANT:  Vita, Natalio
;  TITLE OF INVENTION: Purified Polypeptides Having IL-13 Receptor Activity
;  FILE REFERENCE: IVD924 US CNT 1
;  CURRENT APPLICATION NUMBER: US/11/185,230
;  CURRENT FILING DATE:  2005-07-18
;  PRIOR APPLICATION NUMBER: PCT/FR96/01756
;  PRIOR FILING DATE: 1996-11-07
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 380
;   TYPE: PRT 3
;   ORGANISM: Homo sapiens
;   FEATURE:
US-11-185-230-2
```

Query Match 87.5%; Score 28; DB 7; Length 380;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 127 TYWIS 131

RESULT 43
US-11-182-384A-2
; Sequence 2, Application US/11182384A
; Publication No. US20060035855A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified polypeptides having IL-13 receptor activity
; FILE REFERENCE: IVD924 US DIV 2
; CURRENT APPLICATION NUMBER: US/11/182,384A
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: 09/077,817
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-182-384A-2

Query Match 87.5%; Score 28; DB 7; Length 380;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 127 TYWIS 131

RESULT 44
US-11-183-599A-2
; Sequence 2, Application US/11183599A
; Publication No. US20060035856A1
; GENERAL INFORMATION:
; APPLICANT: Caput, Daniel
; APPLICANT: Ferrara, Pascual
; APPLICANT: Laurent, Patrick
; APPLICANT: Vita, Natalio
; TITLE OF INVENTION: Purified polypeptides having IL-13 receptor activity
; FILE REFERENCE: IVD924 US DIV 1
; CURRENT APPLICATION NUMBER: US/11/183,599A
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: 09/077,817
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: PCT/FR96/01756
; PRIOR FILING DATE: 1996-11-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-183-599A-2

Query Match 87.5%; Score 28; DB 7; Length 380;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|||:|
Db 127 TYWIS 131

RESULT 45
US-11-096-568A-28942
; Sequence 28942, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides E
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28942
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(408)
; OTHER INFORMATION: Ceres Seq. ID no. 3094515
US-11-096-568A-28942

Query Match 87.5%; Score 28; DB 7; Length 408;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|:|||
Db 233 TFWMS 237

RESULT 46
US-11-087-099-6826
; Sequence 6826, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6826
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Capsicum annuum
US-11-087-099-6826

Query Match 87.5%; Score 28; DB 7; Length 438;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYWMS 5
|:|||
Db 428 TFWMS 432

RESULT 47
US-10-878-556A-154
; Sequence 154, Application US/10878556A
; Publication No. US20050266399A1
; GENERAL INFORMATION:
; APPLICANT: Hoffmann La-Roche Inc.
; TITLE OF INVENTION: HCV regulated protein expression
; FILE REFERENCE: 21762
; CURRENT APPLICATION NUMBER: US/10/878,556A
; CURRENT FILING DATE: 2004-06-28
; NUMBER OF SEQ ID NOS: 199

```
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 154
;   LENGTH: 508
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: sw_hum/syfa_human
;   DATABASE ENTRY DATE: 2001-10-16
US-10-878-556A-154

  Query Match             87.5%;  Score 28;  DB 6;  Length 508;
  Best Local Similarity   80.0%;  Pred. No. 4.3e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWMS 5
              |||:|
Db        172 TYWVS 176


RESULT 48
US-11-087-099-2968
; Sequence 2968, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2968
;   LENGTH: 793
;   TYPE: PRT
;   ORGANISM: Neurospora crassa
US-11-087-099-2968

  Query Match             87.5%;  Score 28;  DB 7;  Length 793;
  Best Local Similarity   100.0%;  Pred. No. 6e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWM 4
              ||||
Db        659 TYWM 662


RESULT 49
US-11-098-686-10761
; Sequence 10761, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
;  APPLICANT: Kapur, Vivek and Gebhart, Connie J.
;  TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
;  TITLE OF INVENTION:  FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
;  FILE REFERENCE: 09531-128001
;  CURRENT APPLICATION NUMBER: US/11/098,686
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: PCT/US03/31318
;  PRIOR FILING DATE: 2003-10-01
;  PRIOR APPLICATION NUMBER: US 60/416,395
;  PRIOR FILING DATE: 2002-10-04
;  NUMBER OF SEQ ID NOS: 11433
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10761
;   LENGTH: 992
;   TYPE: PRT
;   ORGANISM: Lawsonia intracellularis
US-11-098-686-10761

  Query Match             87.5%;  Score 28;  DB 7;  Length 992;
  Best Local Similarity   100.0%;  Pred. No. 7e+02;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TYWM 4
              ||||
Db        710 TYWM 713


RESULT 50
US-10-982-357-15
; Sequence 15, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
;   LENGTH: 5
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-15

  Query Match             84.4%;  Score 27;  DB 6;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 1.3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YWMS 5
              ||||
Db          2 YWMS 5


Search completed: March 23, 2006, 02:53:07
Job time : 8.24658 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:40:10 ; Search time 147.877 Seconds
(without alignments)
50.511 Million cell updates/sec

Title: US-10-755-382-24
Perfect score: 90
Sequence: 1 EIHPDSSTINYAPSLKD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	90	100.0	17	2	AAR97317	Aar97317 Humanised
2	90	100.0	17	8	ADM95106	Adm95106 Murine MN
3	90	100.0	17	8	ADM98315	Adm98315 Humanised
4	90	100.0	118	6	ABR42755	Abr42755 Anti-CEA
5	90	100.0	119	2	AAR97336	Aar97336 Humanised
6	90	100.0	119	2	AAR97334	Aar97334 Murine NE
7	90	100.0	119	8	ADM95101	Adm95101 Humanised
8	90	100.0	119	8	ADM95095	Adm95095 Murine MN
9	90	100.0	119	8	ADM98324	Adm98324 Humanised
10	90	100.0	119	8	ADM98318	Adm98318 Murine MN
11	90	100.0	138	6	ABG76489	Abg76489 Heavy cha
12	90	100.0	256	6	ABR42757	Abr42757 Anti-CEA
13	90	100.0	257	6	ABR42758	Abr42758 Anti-CEA
14	90	100.0	261	6	ABR42289	Abr42289 Diabody 6
15	90	100.0	261	6	ABR42754	Abr42754 Anti-CEA
16	90	100.0	261	6	ABR83645	Abr83645 hMN14-scF
17	90	100.0	267	6	ABR42292	Abr42292 Bispecifi
18	90	100.0	267	6	ABR42299	Abr42299 Bispecifi
19	90	100.0	267	6	ABR42296	Abr42296 Bispecifi
20	90	100.0	267	6	ABR42294	Abr42294 Bispecifi
21	90	100.0	358	8	ADU26571	Adu26571 Chimeric
22	90	100.0	363	8	ADU26561	Adu26561 Chimeric
23	90	100.0	364	8	ADU26570	Adu26570 Chimeric
24	90	100.0	370	8	ADU26560	Adu26560 Chimeric
25	90	100.0	415	6	ABR83648	Abr83648 TS1 VH ch
26	90	100.0	443	6	ABG76488	Abg76488 Humanised
27	90	100.0	443	6	ABG74240	Abg74240 Chimaeric
28	90	100.0	468	7	ADE64201	Ade64201 MN14HCF p
29	90	100.0	468	7	ADF60815	Adf60815 hMN-14 he
30	90	100.0	669	9	ADY97271	Ady97271 Exemplary
31	83	92.2	119	8	ADU87733	Adu87733 Heavy cha
32	83	92.2	119	8	ADU87727	Adu87727 Humanized
33	82	91.1	109	2	AAR52046	Aar52046 Heavy cha
34	82	91.1	220	8	ADU86552	Adu86552 Immunoglo
35	79	87.8	17	7	ADD94143	Add94143 Mouse HUI
36	79	87.8	17	8	ADL27483	Adl27483 CDR from
37	79	87.8	17	8	ADR15148	Adr15148 Mouse ant
38	79	87.8	17	8	ADU87717	Adu87717 Anti-CS1
39	79	87.8	17	8	ADU87703	Adu87703 Mouse Luc
40	79	87.8	98	4	AAE06984	Aae06984 Mouse ger
41	79	87.8	98	8	ADQ89269	Adq89269 Mouse imm
42	79	87.8	98	9	AEB09542	Aeb09542 Murine ge
43	79	87.8	113	8	ADN41879	Adn41879 Humanised
44	79	87.8	113	8	ADN41878	Adn41878 Humanised
45	79	87.8	116	3	AAY90820	Aay90820 317G5 hyb
46	79	87.8	119	8	ADR15131	Adr15131 Mouse ant
47	79	87.8	119	8	ADU87692	Adu87692 Mouse Luc
48	79	87.8	119	8	ADU87724	Adu87724 Heavy cha
49	79	87.8	119	8	ADU87731	Adu87731 VH region
50	79	87.8	120	7	ADD94119	Add94119 Mouse HUI
51	79	87.8	121	8	ADU86551	Adu86551 Immunoglo
52	79	87.8	121	8	ADU86550	Adu86550 Immunoglo
53	79	87.8	137	8	ADU87714	Adu87714 Anti-CS1
54	79	87.8	142	9	AEB08073	Aeb08073 HLA-DR sp
55	79	87.8	150	8	ADL27481	Adl27481 Amino aci
56	79	87.8	215	8	ADN41868	Adn41868 Amino aci
57	79	87.8	239	2	AAY17963	Aay17963 Mouse scF
58	79	87.8	243	2	AAR53148	Aar53148 VH and VL
59	79	87.8	251	5	AAU72868	Aau72868 P5-10 sin
60	79	87.8	252	5	AAU72863	Aau72863 P4-14 sin
61	79	87.8	256	5	AAU72864	Aau72864 P4-15 sin
62	79	87.8	258	5	AAU72871	Aau72871 3B10xP4-3
63	79	87.8	468	9	AEB08072	Aeb08072 Murine/hu
64	79	87.8	499	5	AAU72872	Aau72872 3B10xP4-1
65	79	87.8	503	5	AAU72873	Aau72873 3B10xP5-2
66	79	87.8	505	5	AAU72875	Aau72875 Human NKG
67	78	86.7	17	7	ADD94277	Add94277 Mouse HUI
68	78	86.7	117	2	AAR85238	Aar85238 Humanised
69	78	86.7	117	2	AAR85240	Aar85240 Humanised
70	78	86.7	117	2	AAR85235	Aar85235 Murine 20
71	78	86.7	117	2	AAR85241	Aar85241 Humanised
72	78	86.7	117	2	AAR85239	Aar85239 Humanised
73	78	86.7	117	2	AAR85237	Aar85237 Humanised
74	77	85.6	122	2	AAW53172	Aaw53172 Monoclona
75	76	84.4	17	7	ADD94166	Add94166 Mouse HUI
76	75	83.3	17	7	ADD94169	Add94169 Mouse HUI
77	75	83.3	17	7	ADD94168	Add94168 Mouse HUI
78	74	82.2	17	7	ADD94163	Add94163 Mouse HUI
79	74	82.2	17	7	ADD94167	Add94167 Mouse HUI
80	73	81.1	17	7	ADD94165	Add94165 Mouse HUI
81	73	81.1	17	7	ADD94170	Add94170 Mouse HUI
82	73	81.1	17	8	ADP45555	Adp45555 Mouse 11C
83	73	81.1	17	9	ADZ07592	Adz07592 Mouse 3A6
84	73	81.1	221	8	ADP45548	Adp45548 Mouse bin
85	73	81.1	221	9	ADZ07585	Adz07585 Mouse 3A6
86	72	80.0	98	4	AAE06989	Aae06989 Mouse ger
87	72	80.0	98	8	ADQ89274	Adq89274 Mouse imm
88	72	80.0	98	9	AEB09547	Aeb09547 Murine ge
89	71	78.9	17	7	ADD94269	Add94269 Mouse HUI
90	70	77.8	114	2	AAR75430	Aar75430 Human thy
91	69	76.7	17	7	ADD94271	Add94271 Mouse HUI
92	69	76.7	139	3	AAY69403	Aay69403 The heavy
93	69	76.7	139	3	AAY69401	Aay69401 Amino aci
94	69	76.7	140	7	ADD13786	Add13786 Plasmid p
95	69	76.7	237	7	ADD13798	Add13798 Plasmid p
96	68	75.6	17	7	ADD94270	Add94270 Mouse HUI
97	65	72.2	17	8	ADR15149	Adr15149 Mouse ant

98	65	72.2	119	8	ADR15132	Adr15132	Mouse ant
99	63	70.0	17	8	ADR15172	Adr15172	Anti-prot
100	62	68.9	17	7	ADD94164	Add94164	Mouse HUI
101	61	67.8	17	2	AAR62883	Aar62883	Murine an
102	61	67.8	126	2	AAR62879	Aar62879	Murine an
103	61	67.8	126	2	AAR62880	Aar62880	Murine an
104	61	67.8	265	2	AAR52864	Aar52864	Glycophor
105	61	67.8	461	2	AAR44494	Aar44494	Sequence
106	60	66.7	119	2	AAW46960	Aaw46960	Amino aci
107	59	65.6	126	8	ADU04861	Adu04861	TAg25 mon
108	49	54.4	108	7	ADD28091	Add28091	Lymphoma
109	47	52.2	99	2	AAR38160	Aar38160	Sequence
110	47	52.2	125	2	AAR62918	Aar62918	Human cyt
111	47	52.2	125	2	AAR62920	Aar62920	Human cyt
112	46.5	51.7	120	4	AAB62758	Aab62758	Human HIV
113	46	51.1	152	4	AAU47645	Aau47645	Propionib
114	46	51.1	152	6	ABM44164	Abm44164	Propionib
115	45.5	50.6	1116	5	AAE20136	Aae20136	TMV 126kD
116	45.5	50.6	1616	5	AAE20138	Aae20138	TMV 183kD
117	45	50.0	122	2	AAW56518	Aaw56518	H221 anti
118	45	50.0	211	8	ADX71943	Adx71943	Plant ful
119	45	50.0	411	6	ABM68985	Abm68985	Photorhab
120	45	50.0	566	4	ABB61743	Abb61743	Drosophil
121	44.5	49.4	249	8	ADI58076	Adi58076	Reg IV-sp
122	44.5	49.4	250	8	ADI58062	Adi58062	Reg IV-sp
123	44	48.9	114	7	ADM41835	Adm41835	Human ant
124	44	48.9	114	7	ADM41832	Adm41832	Human ant
125	44	48.9	129	6	ABU97043	Abu97043	Recombina
126	44	48.9	245	5	ABP45891	Abp45891	Human BLy
127	44	48.9	245	7	ADG96718	Adg96718	Single ch
128	44	48.9	252	6	ABU97127	Abu97127	Recombina
129	43	47.8	62	4	ABB14891	Abb14891	Human ner
130	43	47.8	116	4	AAM90602	Aam90602	Human imm
131	43	47.8	118	2	AAR79242	Aar79242	Heavy cha
132	43	47.8	120	8	ADH17834	Adh17834	Murine an
133	43	47.8	120	9	ADW11465	Adw11465	Murine an
134	43	47.8	336	8	ADS23589	Ads23589	Bacterial
135	43	47.8	382	6	ABU45726	Abu45726	Protein e
136	43	47.8	389	8	ADJ34920	Adj34920	Xylanase
137	43	47.8	421	2	AAW36010	Aaw36010	Polyamide
138	43	47.8	475	8	ADJ46273	Adj46273	Synechocy
139	43	47.8	580	8	ADX90648	Adx90648	Plant ful
140	43	47.8	1102	4	ABG29358	Abg29358	Novel hum
141	43	47.8	1102	8	ADJ57489	Adj57489	Human pol
142	43	47.8	1342	8	ADJ57463	Adj57463	Breast ca
143	43	47.8	1456	4	ABG29357	Abg29357	Novel hum
144	43	47.8	1456	8	ADJ57490	Adj57490	Human pol
145	42.5	47.2	829	5	ABG93252	Abg93252	C. albica
146	42.5	47.2	2093	5	ABP73828	Abp73828	Candida a
147	42.5	47.2	5245	7	ADI23897	Adi23897	Streptomy
148	42	46.7	47	3	AAB56106	Aab56106	Human sec
149	42	46.7	94	9	ADW97176	Adw97176	Human IL-
150	42	46.7	103	8	ADJ65023	Adj65023	Rat anti-
151	42	46.7	124	8	ADO36355	Ado36355	Intracell
152	42	46.7	124	8	ADQ75228	Adq75228	Immunoglo
153	42	46.7	126	4	AAG62934	Aag62934	Amino aci
154	42	46.7	126	7	ADL91328	Adl91328	VH chain
155	42	46.7	180	6	ADA14367	Ada14367	Mouse spe
156	42	46.7	184	4	AAG74593	Aag74593	Human col
157	42	46.7	248	4	AAG78409	Aag78409	Amino aci
158	42	46.7	265	4	ABG01843	Abg01843	Novel hum
159	42	46.7	296	9	ADW17186	Adw17186	E_grandis
160	42	46.7	366	6	ABU23190	Abu23190	Protein e
161	42	46.7	433	8	ADK16215	Adk16215	Nanoarcha
162	42	46.7	460	8	ADJ65026	Adj65026	Plasmid p
163	42	46.7	516	6	ABM67380	Abm67380	Photorhab
164	42	46.7	521	6	ADA54915	Ada54915	Human pro
165	42	46.7	521	9	ADY19042	Ady19042	PRO polyp
166	42	46.7	582	4	AAG91652	Aag91652	C glutami
167	42	46.7	660	9	ADY18686	Ady18686	PRO polyp
168	42	46.7	811	2	AAW10570	Aaw10570	Bacteriop
169	42	46.7	1855	7	ADK40914	Adk40914	Novel hum
170	42	46.7	1855	8	ADR15637	Adr15637	Kinase 41
171	42	46.7	1871	6	ABR58345	Abr58345	XM_031992
172	42	46.7	1871	8	ABM81185	Abm81185	Tumour-as
173	42	46.7	1884	4	AAB63241	Aab63241	Human bre
174	42	46.7	1884	7	ADJ68477	Adj68477	Human hea
175	42	46.7	1884	8	ADJ66594	Adj66594	RRP5 prot
176	42	46.7	1885	4	AAM78839	Aam78839	Human pro
177	42	46.7	1886	4	AAM79823	Aam79823	Human pro
178	42	46.7	1906	6	ABR58321	Abr58321	BCU0518 p
179	41.5	46.1	117	8	ADP22112	Adp22112	Human ant
180	41.5	46.1	254	5	ABP44833	Abp44833	Human BLy
181	41.5	46.1	254	7	ADG95660	Adg95660	Single ch
182	41.5	46.1	1116	5	AAE18347	Aae18347	TMV 126kD
183	41.5	46.1	1116	5	AAE19946	Aae19946	TMV 126kD
184	41.5	46.1	1616	5	AAE18348	Aae18348	TMV 183kD
185	41.5	46.1	1616	5	AAE19947	Aae19947	TMV 183kD
186	41	45.6	17	8	ADM41601	Adm41601	Interleuk
187	41	45.6	27	8	ADR38444	Adr38444	Human N-t
188	41	45.6	75	8	ADF69304	Adf69304	Human lun
189	41	45.6	77	4	AAE01298	Aae01298	Human gen
190	41	45.6	77	5	ABG63724	Abg63724	Human alb
191	41	45.6	77	8	ADL76989	Adl76989	Albumin f
192	41	45.6	88	2	AAR22576	Aar22576	Heavy cha
193	41	45.6	96	3	AAY56647	Aay56647	Partial p
194	41	45.6	98	9	ADW97156	Adw97156	Human IL-
195	41	45.6	114	3	AAB18880	Aab18880	Amino aci
196	41	45.6	114	3	AAB18864	Aab18864	Amino aci
197	41	45.6	114	3	AAB18860	Aab18860	Amino aci
198	41	45.6	114	3	AAB18878	Aab18878	Amino aci
199	41	45.6	114	3	AAB18870	Aab18870	Amino aci
200	41	45.6	114	3	AAB18876	Aab18876	Amino aci
201	41	45.6	114	3	AAB18858	Aab18858	Amino aci
202	41	45.6	114	3	AAB18874	Aab18874	Amino aci
203	41	45.6	114	3	AAB18856	Aab18856	Amino aci
204	41	45.6	114	3	AAB18862	Aab18862	Amino aci
205	41	45.6	114	3	AAB18866	Aab18866	Amino aci
206	41	45.6	114	3	AAB18872	Aab18872	Amino aci
207	41	45.6	116	2	AAY29452	Aay29452	Human IgG
208	41	45.6	116	3	AAY77755	Aay77755	Human IgG
209	41	45.6	116	3	AAB30312	Aab30312	Human IgG
210	41	45.6	116	6	ABU13789	Abu13789	Human IgG
211	41	45.6	116	6	ABU59502	Abu59502	Human IgG
212	41	45.6	116	7	AAE39085	Aae39085	Human IgG
213	41	45.6	118	4	AAG80213	Aag80213	Human aut
214	41	45.6	120	4	AAE11854	Aae11854	CNA19 ant
215	41	45.6	135	4	AAM24015	Aam24015	Human EST
216	41	45.6	137	8	ADM41551	Adm41551	Anti-inte
217	41	45.6	140	3	AAY56712	Aay56712	Amino aci
218	41	45.6	141	2	AAW56521	Aaw56521	Anti-DNA
219	41	45.6	141	5	ABP62154	Abp62154	Human imm
220	41	45.6	168	7	ABM89453	Abm89453	Rice abio
221	41	45.6	173	7	ABM90211	Abm90211	Rice abio
222	41	45.6	186	1	AAP90616	Aap90616	Fish grow
223	41	45.6	203	1	AAP90617	Aap90617	Fish grow
224	41	45.6	203	2	AAR07248	Aar07248	Fish grow
225	41	45.6	226	8	ADX74585	Adx74585	Plant ful
226	41	45.6	249	5	ABP45946	Abp45946	Human BLy
227	41	45.6	249	7	ADG96773	Adg96773	Single ch
228	41	45.6	270	9	ADY64536	Ady64536	Alocasia
229	41	45.6	277	4	ABG04206	Abg04206	Novel hum
230	41	45.6	320	2	AAY35790	Aay35790	Amino aci
231	41	45.6	336	2	AAY37733	Aay37733	Protein i
232	41	45.6	400	4	ABB66955	Abb66955	Drosophil
233	41	45.6	413	5	ABG96343	Abg96343	Human ova
234	41	45.6	413	7	ADD18926	Add18926	Human dis
235	41	45.6	413	8	ADJ75333	Adj75333	Marker ge
236	41	45.6	413	8	ADN04052	Adn04052	Antipsori
237	41	45.6	413	8	ADO24373	Ado24373	Human PRO
238	41	45.6	413	8	ADQ17919	Adq17919	Human sof
239	41	45.6	413	9	ADY15330	Ady15330	PRO polyp
240	41	45.6	413	9	AEA23464	Aea23464	Human PRO
241	41	45.6	419	6	ABU27357	Abu27357	Protein e
242	41	45.6	452	3	AAY91957	Aay91957	Human cyt
243	41	45.6	463	8	ADM41569	Adm41569	Anti-inte

244	41	45.6	464	2	AAY35231	Aay35231 Protein i
245	41	45.6	464	6	ABU26819	Abu26819 Protein e
246	41	45.6	464	8	ADM41571	Adm41571 Anti-inte
247	41	45.6	467	8	ADM41567	Adm41567 Anti-inte
248	41	45.6	476	2	AAW01818	Aaw01818 Primatise
249	41	45.6	476	2	AAW63761	Aaw63761 Macaque p
250	41	45.6	476	5	AAU11539	Aau11539 Protein s
251	41	45.6	476	6	AAE37360	Aae37360 Monkey 7C
252	41	45.6	483	8	ADS27577	Ads27577 Bacterial
253	41	45.6	498	2	AAW89404	Aaw89404 S. putref
254	41	45.6	499	3	AAB10471	Aab10471 Shewanell
255	41	45.6	525	2	AAR99466	Aar99466 Biosynthe
256	41	45.6	532	2	AAR42457	Aar42457 Enzyme in
257	41	45.6	591	8	ADF70703	Adf70703 Acetic-ac
258	41	45.6	763	4	ABB64640	Abb64640 Drosophil
259	41	45.6	763	8	ADO07919	Ado07919 Fly polyp
260	41	45.6	803	9	ADX06610	Adx06610 Cyclin-de
261	41	45.6	846	8	ABM80253	Abm80253 Tumour-as
262	41	45.6	846	9	ADX06612	Adx06612 Cyclin-de
263	41	45.6	846	9	ADX06614	Adx06614 Cyclin-de
264	41	45.6	1015	9	AEB37420	Aeb37420 L. pneumo
265	41	45.6	1015	9	AEB42344	Aeb42344 L. pneumo
266	40.5	45.0	619	5	AAU72924	Aau72924 Neisseria
267	40.5	45.0	619	6	ABU37974	Abu37974 Protein e
268	40.5	45.0	619	8	ADP08278	Adp08278 Neisseria
269	40	44.4	16	7	ADJ76844	Adj76844 CDR seque
270	40	44.4	16	9	ADZ67014	Adz67014 Murine in
271	40	44.4	17	2	AAR74932	Aar74932 H-CDR-2 o
272	40	44.4	17	8	ADP79364	Adp79364 Thyrotrop
273	40	44.4	17	9	ADZ45395	Adz45395 Murine fa
274	40	44.4	17	9	ADZ45339	Adz45339 Murine fa
275	40	44.4	17	9	ADZ51252	Adz51252 Amino aci
276	40	44.4	17	9	ADZ42126	Adz42126 Mouse ant
277	40	44.4	66	6	ABU56869	Abu56869 BoNT/A Hc
278	40	44.4	96	9	ADW97149	Adw97149 Human IL-
279	40	44.4	114	3	AAB18882	Aab18882 Amino aci
280	40	44.4	114	8	ADO04855	Ado04855 Anti-mous
281	40	44.4	114	8	ADP09934	Adp09934 Anti-mous
282	40	44.4	114	8	ADO25716	Ado25716 Anti-TNF-
283	40	44.4	114	8	ADQ81974	Adq81974 Camelidae
284	40	44.4	114	9	ADZ45337	Adz45337 Murine fa
285	40	44.4	114	9	ADZ51250	Adz51250 Amino aci
286	40	44.4	114	9	ADZ42124	Adz42124 Mouse ant
287	40	44.4	114	9	AEB03736	Aeb03736 Murine an
288	40	44.4	117	7	ADJ76903	Adj76903 Anti-IGF-
289	40	44.4	117	7	ADJ76909	Adj76909 Anti-IGF-
290	40	44.4	117	7	ADJ76917	Adj76917 Anti-IGF-
291	40	44.4	117	7	ADJ76913	Adj76913 Anti-IGF-
292	40	44.4	117	8	ADR38667	Adr38667 Mouse hea
293	40	44.4	117	9	ADZ67083	Adz67083 Human ant
294	40	44.4	117	9	ADZ67087	Adz67087 Human ant
295	40	44.4	117	9	ADZ67073	Adz67073 Murine im
296	40	44.4	117	9	ADZ67079	Adz67079 Human ant
297	40	44.4	118	9	ADZ45393	Adz45393 Murine fa
298	40	44.4	119	2	AAR74940	Aar74940 Immunoglo
299	40	44.4	121	2	AAR88846	Aar88846 Murine an
300	40	44.4	121	8	ADP79362	Adp79362 Thyrotrop
301	40	44.4	122	2	AAW02201	Aaw02201 CDR switc
302	40	44.4	127	7	ADJ76886	Adj76886 Anti-IGF-
303	40	44.4	127	9	ADZ67056	Adz67056 Murine im
304	40	44.4	128	7	ADD28334	Add28334 Human het
305	40	44.4	131	8	ADP79366	Adp79366 Thyrotrop
306	40	44.4	133	2	AAR74960	Aar74960 Anti-idio
307	40	44.4	135	2	AAR74961	Aar74961 Anti-idio
308	40	44.4	135	7	ADJ76911	Adj76911 Anti-IGF-
309	40	44.4	135	7	ADJ76919	Adj76919 Anti-IGF-
310	40	44.4	135	7	ADJ76915	Adj76915 Anti-IGF-
311	40	44.4	135	9	ADZ67089	Adz67089 Human ant
312	40	44.4	135	9	ADZ67081	Adz67081 Human ant
313	40	44.4	135	9	ADZ67085	Adz67085 Human ant
314	40	44.4	171	3	AAG25850	Aag25850 Arabidops
315	40	44.4	185	6	ABU06525	Abu06525 Maize SSI
316	40	44.4	201	3	AAG25837	Aag25837 Arabidops
317	40	44.4	201	3	AAG25849	Aag25849 Arabidops
318	40	44.4	219	3	AAG25836	Aag25836 Arabidops
319	40	44.4	219	3	AAG25848	Aag25848 Arabidops
320	40	44.4	219	3	AAG23520	Aag23520 Arabidops
321	40	44.4	241	8	ADO04862	Ado04862 Anti-mous
322	40	44.4	241	8	ADO25723	Ado25723 Anti-TNF-
323	40	44.4	245	5	ABP45815	Abp45815 Human BLy
324	40	44.4	245	7	ADG96642	Adg96642 Single ch
325	40	44.4	247	8	ADO04863	Ado04863 Anti-mous
326	40	44.4	247	8	ADO25724	Ado25724 Anti-TNF-
327	40	44.4	247	8	ADQ82031	Adq82031 Camelidae
328	40	44.4	249	8	ADO04864	Ado04864 Anti-mous
329	40	44.4	249	8	ADO04869	Ado04869 Anti-mous
330	40	44.4	249	8	ADO25725	Ado25725 Anti-TNF-
331	40	44.4	249	8	ADO25730	Ado25730 Anti-TNF-
332	40	44.4	250	5	ABP45979	Abp45979 Human BLy
333	40	44.4	250	7	ADG96806	Adg96806 Single ch
334	40	44.4	251	8	ADO04876	Ado04876 Anti-mous
335	40	44.4	252	8	ADO04879	Ado04879 Anti-mous
336	40	44.4	252	8	ADP09938	Adp09938 Anti-mous
337	40	44.4	253	8	ADO04866	Ado04866 Anti-mous
338	40	44.4	253	8	ADO25727	Ado25727 Anti-TNF-
339	40	44.4	255	8	ADO04865	Ado04865 Anti-mous
340	40	44.4	255	8	ADO04859	Ado04859 Anti-mous
341	40	44.4	255	8	ADO25720	Ado25720 Anti-TNF-
342	40	44.4	255	8	ADO25726	Ado25726 Anti-TNF-
343	40	44.4	264	5	ABU05638	Abu05638 M. tuberc
344	40	44.4	320	8	ADU17999	Adu17999 Human can
345	40	44.4	322	3	AAG25835	Aag25835 Arabidops
346	40	44.4	325	8	ADR10212	Adr10212 Human pro
347	40	44.4	352	8	ADJ71671	Adj71671 Human NOV
348	40	44.4	360	3	AAG23519	Aag23519 Arabidops
349	40	44.4	361	8	ADT56110	Adt56110 Plant pol
350	40	44.4	367	3	AAG23518	Aag23518 Arabidops
351	40	44.4	370	7	ADC64242	Adc64242 Human hSn
352	40	44.4	384	6	ABU03468	Abu03468 Angiogene
353	40	44.4	384	6	ADA83981	Ada83981 Human BCA
354	40	44.4	384	7	ADD14020	Add14020 Human src
355	40	44.4	384	8	ADJ75494	Adj75494 Marker ge
356	40	44.4	384	8	ADQ80357	Adq80357 Cytosolic
357	40	44.4	384	8	ADP24707	Adp24707 PRO polyp
358	40	44.4	384	9	ADY17091	Ady17091 PRO polyp
359	40	44.4	386	7	ADB80555	Adb80555 Ovarian c
360	40	44.4	386	8	ADJ71673	Adj71673 Human NOV
361	40	44.4	386	8	ADJ71675	Adj71675 Human NOV
362	40	44.4	386	8	ABO84752	Abo84752 Human can
363	40	44.4	386	8	ABM81368	Abm81368 Tumour-as
364	40	44.4	387	8	ADG32242	Adg32242 Mutant B_
365	40	44.4	400	8	ABO84753	Abo84753 Human can
366	40	44.4	400	9	ABM94171	Abm94171 M. xanthu
367	40	44.4	407	8	ADM99717	Adm99717 Human BCA
368	40	44.4	407	8	ADM99714	Adm99714 Human BCA
369	40	44.4	425	4	ABB64296	Abb64296 Drosophil
370	40	44.4	436	3	AAY91026	Aay91026 Apoptobod
371	40	44.4	450	8	ADS18706	Ads18706 Protein s
372	40	44.4	642	5	ABB90825	Abb90825 Herbicida
373	40	44.4	642	8	ADJ38147	Adj38147 Arabidops
374	40	44.4	684	6	ABO07212	Abo07212 Human p53
375	40	44.4	684	8	ADP07455	Adp07455 Human Sno
376	40	44.4	775	8	ADJ49098	Adj49098 Oil-assoc
377	40	44.4	807	8	ADT72097	Adt72097 Amino aci
378	40	44.4	1038	4	ABB71916	Abb71916 Drosophil
379	40	44.4	1710	5	ABP73401	Abp73401 Candida a
380	39.5	43.9	134	3	AAY64684	Aay64684 Human 5'
381	39.5	43.9	134	8	ADU72248	Adu72248 Signal pe
382	39.5	43.9	134	9	ADZ73239	Adz73239 Human inc
383	39.5	43.9	245	5	ABP45853	Abp45853 Human BLy
384	39.5	43.9	245	7	ADG30485	Adg30485 Human GMC
385	39.5	43.9	245	7	ADG96680	Adg96680 Single ch
386	39.5	43.9	247	8	ADR28068	Adr28068 NPB polyp
387	39.5	43.9	313	8	ADN19542	Adn19542 Bacterial
388	39.5	43.9	619	6	ABU37153	Abu37153 Protein e
389	39.5	43.9	668	6	ABP79256	Abp79256 N. gonorr

390	39.5	43.9	684	6	ABU19991	Abu19991 Protein e
391	39.5	43.9	909	8	ADO18826	Ado18826 Human lip
392	39.5	43.9	1116	5	AAE18345	Aae18345 Tobacco m
393	39.5	43.9	1116	5	AAE20137	Aae20137 TMV 126kD
394	39.5	43.9	1616	5	AAE18346	Aae18346 Tobacco m
395	39.5	43.9	1616	5	AAE20139	Aae20139 TMV 183kD
396	39	43.3	16	5	ABP62262	Abp62262 Human imm
397	39	43.3	17	8	ADE85703	Ade85703 Human Eph
398	39	43.3	17	8	ADR43421	Adr43421 CDR with
399	39	43.3	17	8	ADR31566	Adr31566 Murine TE
400	39	43.3	17	8	ADS18673	Ads18673 Peptide s
401	39	43.3	17	9	ADY32283	Ady32283 Human Eph
402	39	43.3	17	9	AEA53616	Aea53616 Novel hum
403	39	43.3	17	9	AEB17139	Aeb17139 EphA2-spe
404	39	43.3	17	9	AEA42939	Aea42939 EphA2 ant
405	39	43.3	17	9	AEC08142	Aec08142 Murine mA
406	39	43.3	38	9	AEB08080	Aeb08080 Chimeric
407	39	43.3	68	4	AAM91606	Aam91606 Human imm
408	39	43.3	96	9	AEA54056	Aea54056 Novel hum
409	39	43.3	100	3	AAY56665	Aay56665 Partial p
410	39	43.3	115	3	AAG00036	Aag00036 Human sec
411	39	43.3	115	7	ADF32517	Adf32517 RVG10 pro
412	39	43.3	117	2	AAR52053	Aar52053 Heavy cha
413	39	43.3	117	4	AAU02506	Aau02506 Anti-adip
414	39	43.3	118	4	AAG62938	Aag62938 Amino aci
415	39	43.3	118	8	ADE85701	Ade85701 Human Eph
416	39	43.3	118	8	ADT61902	Adt61902 Anti-EphA
417	39	43.3	118	9	ADY32219	Ady32219 Human Eph
418	39	43.3	118	9	AEB17137	Aeb17137 EphA2-spe
419	39	43.3	118	9	AEA42937	Aea42937 EphA2 ant
420	39	43.3	119	4	AAG62942	Aag62942 Amino aci
421	39	43.3	124	2	AAW90286	Aaw90286 Human ant
422	39	43.3	124	4	AAU02548	Aau02548 Anti-adip
423	39	43.3	124	6	ABR54879	Abr54879 IgG kappa
424	39	43.3	124	6	ABR54878	Abr54878 IgG kappa
425	39	43.3	124	9	AEB19255	Aeb19255 IgG heavy
426	39	43.3	124	9	AEB19254	Aeb19254 IgG heavy
427	39	43.3	125	2	AAW08504	Aaw08504 C6 human
428	39	43.3	125	9	AEB11688	Aeb11688 Anti-Pseu
429	39	43.3	127	8	ADP03639	Adp03639 Human ant
430	39	43.3	128	7	ADH86110	Adh86110 Enterococ
431	39	43.3	129	4	ABG02056	Abg02056 Novel hum
432	39	43.3	129	7	ADF60502	Adf60502 Human con
433	39	43.3	129	7	ADF59430	Adf59430 Human pol
434	39	43.3	130	4	ABG23720	Abg23720 Novel hum
435	39	43.3	130	9	AEA53260	Aea53260 Novel hum
436	39	43.3	131	2	AAR45608	Aar45608 Monoclona
437	39	43.3	132	5	ABG76523	Abg76523 HCV E1 an
438	39	43.3	133	5	ABG76515	Abg76515 HCV E1 an
439	39	43.3	134	3	AAG13014	Aag13014 Arabidops
440	39	43.3	138	3	AAG03522	Aag03522 Human sec
441	39	43.3	147	3	AAY56730	Aay56730 Amino aci
442	39	43.3	149	2	AAR71338	Aar71338 Deduced s
443	39	43.3	184	3	AAG13012	Aag13012 Arabidops
444	39	43.3	185	7	ADC39950	Adc39950 Yellow gr
445	39	43.3	187	2	AAM49019	Aam49019 Korean ro
446	39	43.3	204	2	AAM49020	Aam49020 Korean ro
447	39	43.3	204	5	ABG31737	Abg31737 Yellow gr
448	39	43.3	204	5	ABG31734	Abg31734 Yellow gr
449	39	43.3	204	7	ADC50041	Adc50041 Orange-sp
450	39	43.3	204	7	ADC39941	Adc39941 Yellow gr
451	39	43.3	211	6	AAE30264	Aae30264 Human LP3
452	39	43.3	213	3	AAG22163	Aag22163 Arabidops
453	39	43.3	222	6	AAE30265	Aae30265 Human LP3
454	39	43.3	222	8	ADP29917	Adp29917 Human sec
455	39	43.3	226	6	AAE30268	Aae30268 Human LP3
456	39	43.3	234	4	AAU43948	Aau43948 Propionib
457	39	43.3	234	6	ABM40467	Abm40467 Propionib
458	39	43.3	234	6	AAE30269	Aae30269 Human LP3
459	39	43.3	241	6	AAE29926	Aae29926 Human LP3
460	39	43.3	246	5	ABP45836	Abp45836 Human BLy
461	39	43.3	246	7	ADG96663	Adg96663 Single ch
462	39	43.3	248	2	AAR20059	Aar20059 Recombina
463	39	43.3	249	8	ADG22313	Adg22313 Cyanophag
464	39	43.3	249	8	ADI58049	Adi58049 Reg IV-sp
465	39	43.3	253	8	ADH71392	Adh71392 Human pro
466	39	43.3	255	2	AAW01200	Aaw01200 Serine pr
467	39	43.3	255	4	AAB50597	Aab50597 Flea seri
468	39	43.3	256	4	AAB62507	Aab62507 Flea seri
469	39	43.3	256	6	AAE29927	Aae29927 Human LP3
470	39	43.3	271	9	ADW47924	Adw47924 Mycobacte
471	39	43.3	278	8	ADP29916	Adp29916 Human sec
472	39	43.3	280	6	ABR42055	Abr42055 Newcastle
473	39	43.3	284	6	AAE30254	Aae30254 Human LP2
474	39	43.3	286	6	AAE30270	Aae30270 Human LP3
475	39	43.3	291	6	AAE30256	Aae30256 Human LP2
476	39	43.3	292	6	AAE30255	Aae30255 Human LP2
477	39	43.3	294	6	AAE30271	Aae30271 Human LP3
478	39	43.3	294	6	ABU33186	Abu33186 Protein e
479	39	43.3	305	7	ADL35981	Adl35981 Human NOV
480	39	43.3	306	6	AAE30252	Aae30252 Human LP2
481	39	43.3	307	5	ABG94638	Abg94638 Human NOV
482	39	43.3	307	8	ADH71402	Adh71402 Human pro
483	39	43.3	309	8	ADH71410	Adh71410 Human pro
484	39	43.3	309	8	ADH71406	Adh71406 Human pro
485	39	43.3	314	6	AAE30253	Aae30253 Human LP2
486	39	43.3	315	8	ADH71394	Adh71394 Human pro
487	39	43.3	319	5	ABG94637	Abg94637 Human NOV
488	39	43.3	319	5	ABG94636	Abg94636 Human NOV
489	39	43.3	319	7	ADL35977	Adl35977 Human NOV
490	39	43.3	319	7	ADL35979	Adl35979 Human NOV
491	39	43.3	319	8	ADH71400	Adh71400 Human pro
492	39	43.3	319	8	ADH71396	Adh71396 Human pro
493	39	43.3	319	8	ADH71404	Adh71404 Human pro
494	39	43.3	320	8	ADH71416	Adh71416 Human pro
495	39	43.3	325	8	ADH71398	Adh71398 Human pro
496	39	43.3	325	8	ADH71390	Adh71390 Human pro
497	39	43.3	334	6	ABU30308	Abu30308 Protein e
498	39	43.3	334	8	ADT05590	Adt05590 Haemophil
499	39	43.3	336	5	AAU84386	Aau84386 Novel hum
500	39	43.3	336	5	ABG94639	Abg94639 Human NOV
501	39	43.3	336	5	ABG96271	Abg96271 Human imm
502	39	43.3	336	6	AAE29924	Aae29924 Human LP2
503	39	43.3	336	6	ABU38874	Abu38874 Protein e
504	39	43.3	336	7	ADL35983	Adl35983 Human NOV
505	39	43.3	336	8	ADH71422	Adh71422 Human pro
506	39	43.3	336	8	ADH71386	Adh71386 Human pro
507	39	43.3	336	8	ADH71420	Adh71420 Human pro
508	39	43.3	336	8	ADH71418	Adh71418 Human pro
509	39	43.3	336	8	ADH71408	Adh71408 Human pro
510	39	43.3	336	8	ADH71412	Adh71412 Human pro
511	39	43.3	336	8	ADH71414	Adh71414 Human pro
512	39	43.3	336	8	ADS24698	Ads24698 Bacterial
513	39	43.3	336	8	ADS22170	Ads22170 Bacterial
514	39	43.3	342	6	ABU22955	Abu22955 Protein e
515	39	43.3	344	8	ADH71388	Adh71388 Human pro
516	39	43.3	351	5	AAU84385	Aau84385 Novel hum
517	39	43.3	353	5	ABP73716	Abp73716 Candida a
518	39	43.3	358	6	ADA35160	Ada35160 Acinetoba
519	39	43.3	359	9	ADX07219	Adx07219 Cyclin-de
520	39	43.3	359	9	AEB71353	Aeb71353 Human mod
521	39	43.3	363	8	ADY12005	Ady12005 Plant ful
522	39	43.3	367	5	ABB57320	Abb57320 Mouse isc
523	39	43.3	367	8	ADJ76316	Adj76316 Marker ge
524	39	43.3	367	8	ADO60056	Ado60056 CRH signa
525	39	43.3	374	7	ABO74631	Abo74631 Pseudomon
526	39	43.3	381	3	AAG22162	Aag22162 Arabidops
527	39	43.3	392	6	AAE38419	Aae38419 Arabidops
528	39	43.3	400	7	ADH86504	Adh86504 Enterococ
529	39	43.3	475	2	AAR20057	Aar20057 Heavy cha
530	39	43.3	496	4	AAG80007	Aag80007 D. melano
531	39	43.3	510	4	AAB46392	Aab46392 H. pylori
532	39	43.3	526	4	ABB58656	Abb58656 Drosophil
533	39	43.3	538	8	ADX90587	Adx90587 Plant ful
534	39	43.3	541	4	AAU35153	Aau35153 Enterococ
535	39	43.3	552	8	ADP98905	Adp98905 C. albica

536	39	43.3	556	6	ABU21343	Abu21343 Protein e
537	39	43.3	615	3	AAG46152	Aag46152 Arabidops
538	39	43.3	626	3	AAY52442	Aay52442 Mycobacte
539	39	43.3	626	4	AAG81100	Aag81100 Mycobacte
540	39	43.3	626	6	ABU34944	Abu34944 Protein e
541	39	43.3	626	6	ABU36405	Abu36405 Protein e
542	39	43.3	626	7	ABO71522	Abo71522 Pseudomon
543	39	43.3	679	3	AAG46151	Aag46151 Arabidops
544	39	43.3	691	3	AAG46150	Aag46150 Arabidops
545	39	43.3	716	4	AAB68956	Aab68956 Arabidops
546	39	43.3	716	8	ADM97329	Adm97329 A thalian
547	39	43.3	728	4	AAB68952	Aab68952 Arabidops
548	39	43.3	728	8	ADM97327	Adm97327 A thalian
549	39	43.3	804	4	ABG28800	Abg28800 Novel hum
550	39	43.3	804	4	ABG29023	Abg29023 Novel hum
551	39	43.3	807	4	ABG28665	Abg28665 Novel hum
552	39	43.3	1066	7	ADG42087	Adg42087 Human SEM
553	39	43.3	1073	4	ABG28599	Abg28599 Novel hum
554	39	43.3	1098	4	AAM25720	Aam25720 Human pro
555	39	43.3	1098	4	ABB11704	Abb11704 Human sem
556	39	43.3	1098	7	ADF60614	Adf60614 Human con
557	39	43.3	1176	2	AAR87973	Aar87973 Nitrite r
558	39	43.3	1303	2	AAY49132	Aay49132 GABA-BR2*
559	39	43.3	1303	5	AAO15098	Aao15098 Human GAB
560	39	43.3	1363	5	ABP73963	Abp73963 Candida a
561	39	43.3	1464	9	AEB86598	Aeb86598 Human cop
562	39	43.3	1513	4	AAU71957	Aau71957 Human bon
563	39	43.3	1812	5	AAE18271	Aae18271 Protein e
564	39	43.3	1812	8	ADN96825	Adn96825 Bugula ne
565	39	43.3	3540	8	ADN96836	Adn96836 Bugula br
566	39	43.3	5509	8	ADN96832	Adn96832 Bugula br
567	39	43.3	6940	8	ADN96829	Adn96829 Bugula br
568	39	43.3	8601	6	AAO29660	Aao29660 Paederus
569	38.5	42.8	16	8	ADQ91400	Adq91400 CDR2 of t
570	38.5	42.8	16	8	ADS52418	Ads52418 Fab targe
571	38.5	42.8	16	9	AEB28743	Aeb28743 Human CDR
572	38.5	42.8	97	7	ADD28115	Add28115 Lymphoma
573	38.5	42.8	98	2	AAY05693	Aay05693 Multiple
574	38.5	42.8	98	5	ABG78223	Abg78223 Human Fv
575	38.5	42.8	98	5	ABG78224	Abg78224 Human Fv
576	38.5	42.8	98	5	ABG77151	Abg77151 Germline
577	38.5	42.8	98	5	ABG91914	Abg91914 Human ant
578	38.5	42.8	98	5	ABG91915	Abg91915 Human ant
579	38.5	42.8	98	6	ABO27101	Abo27101 Human ger
580	38.5	42.8	98	7	ADD28092	Add28092 Lymphoma
581	38.5	42.8	98	7	ADF09937	Adf09937 Antibody
582	38.5	42.8	98	7	ADF10043	Adf10043 VEGF anti
583	38.5	42.8	98	7	ADF10145	Adf10145 Antibody
584	38.5	42.8	98	7	ADJ80317	Adj80317 VH gene l
585	38.5	42.8	98	8	ADR28568	Adr28568 Human ant
586	38.5	42.8	98	9	ADY75322	Ady75322 Protein e
587	38.5	42.8	98	9	AEB13599	Aeb13599 Human var
588	38.5	42.8	98	9	AEC20848	Aec20848 Human var
589	38.5	42.8	109	8	ADS09393	Ads09393 Human c-M
590	38.5	42.8	119	2	AAW62795	Aaw62795 Amino aci
591	38.5	42.8	119	8	ADP13160	Adp13160 Anti-PIPA
592	38.5	42.8	119	8	ADS09380	Ads09380 Human c-M
593	38.5	42.8	121	8	ADS09384	Ads09384 Human c-M
594	38.5	42.8	121	8	ADS09388	Ads09388 Human c-M
595	38.5	42.8	122	4	AAG62962	Aag62962 Amino aci
596	38.5	42.8	124	2	AAW06474	Aaw06474 Human lun
597	38.5	42.8	128	8	ADQ91384	Adq91384 Amino aci
598	38.5	42.8	137	2	AAR33310	Aar33310 MaE15 hea
599	38.5	42.8	137	3	AAY85198	Aay85198 Heavy cha
600	38.5	42.8	159	8	ADX67511	Adx67511 Plant ful
601	38.5	42.8	239	4	AAB46059	Aab46059 Human TF
602	38.5	42.8	240	4	AAB46058	Aab46058 Human TF
603	38.5	42.8	244	4	AAB46060	Aab46060 Human TF
604	38.5	42.8	247	8	ADS09282	Ads09282 Human c-M
605	38.5	42.8	248	8	ADS09259	Ads09259 Human c-M
606	38.5	42.8	248	8	ADS09296	Ads09296 Human c-M
607	38.5	42.8	248	8	ADS09291	Ads09291 Human c-M
608	38.5	42.8	248	8	ADS09269	Ads09269 Human c-M
609	38.5	42.8	248	8	ADS09288	Ads09288 Human c-M
610	38.5	42.8	248	8	ADS09295	Ads09295 Human c-M
611	38.5	42.8	249	8	ADS09292	Ads09292 Human c-M
612	38.5	42.8	249	8	ADS09280	Ads09280 Human c-M
613	38.5	42.8	250	8	ADS09260	Ads09260 Human c-M
614	38.5	42.8	250	8	ADS09267	Ads09267 Human c-M
615	38.5	42.8	250	8	ADS09290	Ads09290 Human c-M
616	38.5	42.8	250	8	ADS09244	Ads09244 Human c-M
617	38.5	42.8	250	8	ADS09298	Ads09298 Human c-M
618	38.5	42.8	251	8	ADS09287	Ads09287 Human c-M
619	38.5	42.8	251	8	ADS09274	Ads09274 Human c-M
620	38.5	42.8	251	8	ADS09286	Ads09286 Human c-M
621	38.5	42.8	251	8	ADS09275	Ads09275 Human c-M
622	38.5	42.8	251	8	ADS09294	Ads09294 Human c-M
623	38.5	42.8	251	8	ADS09268	Ads09268 Human c-M
624	38.5	42.8	251	8	ADS09289	Ads09289 Human c-M
625	38.5	42.8	251	8	ADS09263	Ads09263 Human c-M
626	38.5	42.8	333	8	ADX73870	Adx73870 Plant ful
627	38.5	42.8	377	8	ADX97232	Adx97232 Plant ful
628	38.5	42.8	406	9	ADW18318	Adw18318 Eucalyptu
629	38.5	42.8	425	5	ABB48993	Abb48993 Listeria
630	38.5	42.8	455	8	ADY07200	Ady07200 Plant ful
631	38.5	42.8	455	8	ADY11452	Ady11452 Plant ful
632	38.5	42.8	456	8	ADX66634	Adx66634 Plant ful
633	38.5	42.8	4081	4	ABB62958	Abb62958 Drosophil
634	38	42.2	17	2	AAW89153	Aaw89153 Anti-p53
635	38	42.2	17	8	ADP47196	Adp47196 Human pho
636	38	42.2	17	8	ADP47143	Adp47143 Human pho
637	38	42.2	41	3	AAB27185	Aab27185 SV41 L po
638	38	42.2	99	4	AAO00872	Aao00872 Human pol
639	38	42.2	101	9	ADW97166	Adw97166 Human IL-
640	38	42.2	104	2	AAW89170	Aaw89170 Anti-p53
641	38	42.2	110	5	ABP06700	Abp06700 Human ORF
642	38	42.2	111	6	AAE33330	Aae33330 A5 antibo
643	38	42.2	111	9	ADZ21528	Adz21528 Anti-Muc-
644	38	42.2	114	8	ADS16517	Ads16517 Human ant
645	38	42.2	117	5	ABP52184	Abp52184 Human mon
646	38	42.2	142	2	AAR41285	Aar41285 F105 rear
647	38	42.2	179	8	ADS16619	Ads16619 Human ant
648	38	42.2	207	2	AAR05800	Aar05800 Tilapia (
649	38	42.2	207	2	AAR08122	Aar08122 Tilapia g
650	38	42.2	212	2	AAR06893	Aar06893 Tilapia p
651	38	42.2	212	8	ABO58475	Abo58475 Human gen
652	38	42.2	219	8	ADT57717	Adt57717 Plant pol
653	38	42.2	226	7	ADH85862	Adh85862 Enterococ
654	38	42.2	228	8	ADM48157	Adm48157 Polypepti
655	38	42.2	250	8	ADS09249	Ads09249 Human c-M
656	38	42.2	275	9	ADZ21539	Adz21539 Anti-Muc-
657	38	42.2	280	5	ABB57125	Abb57125 Mouse isc
658	38	42.2	281	6	AAE33335	Aae33335 3D antibo
659	38	42.2	290	8	ADS24406	Ads24406 Bacterial
660	38	42.2	297	4	AAG82770	Aag82770 S. epider
661	38	42.2	299	8	ADU07811	Adu07811 Amino aci
662	38	42.2	302	8	ABO84751	Abo84751 Murine ca
663	38	42.2	306	4	ABG19459	Abg19459 Novel hum
664	38	42.2	317	8	ADS27846	Ads27846 Bacterial
665	38	42.2	336	8	ADQ66304	Adq66304 Novel hum
666	38	42.2	352	7	ADM07184	Adm07184 Aspergill
667	38	42.2	362	7	ADB85180	Adb85180 Rat branc
668	38	42.2	367	8	ABO59909	Abo59909 Human gen
669	38	42.2	377	8	ADS44742	Ads44742 Bacterial
670	38	42.2	386	8	ADJ76254	Adj76254 Marker ge
671	38	42.2	406	2	AAR70981	Aar70981 E. coli a
672	38	42.2	406	6	ABU15090	Abu15090 Protein e
673	38	42.2	410	8	ADT60488	Adt60488 Plant pol
674	38	42.2	412	4	ABU53134	Abu53134 Human tra
675	38	42.2	424	8	ADS41942	Ads41942 Bacterial
676	38	42.2	428	4	AAB96210	Aab96210 Putative
677	38	42.2	428	8	ADN18654	Adn18654 Bacterial
678	38	42.2	428	8	ADS43163	Ads43163 Bacterial
679	38	42.2	437	4	ABB57954	Abb57954 Drosophil
680	38	42.2	447	8	ADQ66378	Adq66378 Novel hum
681	38	42.2	463	4	ABB70018	Abb70018 Drosophil

682	38	42.2	466	4	AAU34428	Aau34428 E. coli c
683	38	42.2	466	6	ABU28481	Abu28481 Protein e
684	38	42.2	466	6	ABU31589	Abu31589 Protein e
685	38	42.2	466	9	AEA41039	Aea41039 Anti-M-CS
686	38	42.2	466	9	AEA41060	Aea41060 Human ant
687	38	42.2	467	9	AEA41058	Aea41058 Human ant
688	38	42.2	467	9	AEA41068	Aea41068 Human ant
689	38	42.2	467	9	AEA41067	Aea41067 Human ant
690	38	42.2	470	9	AEA41070	Aea41070 Human ant
691	38	42.2	478	2	AAW01820	Aaw01820 Primatise
692	38	42.2	478	2	AAW63763	Aaw63763 Macaque p
693	38	42.2	478	5	AAU11644	Aau11644 Protein s
694	38	42.2	478	6	AAE37362	Aae37362 Monkey 7B
695	38	42.2	479	8	ADX92371	Adx92371 Plant ful
696	38	42.2	480	2	AAR42867	Aar42867 Platelet
697	38	42.2	480	4	AAB94410	Aab94410 Human pro
698	38	42.2	481	7	ABO65805	Abo65805 Klebsiell
699	38	42.2	498	8	ADX87495	Adx87495 Plant ful
700	38	42.2	518	8	ADX89667	Adx89667 Plant ful
701	38	42.2	532	8	ADX71357	Adx71357 Plant ful
702	38	42.2	549	6	ABM71064	Abm71064 Staphyloc
703	38	42.2	557	7	ADJ70983	Adj70983 Human hea
704	38	42.2	561	8	ADX66359	Adx66359 Plant ful
705	38	42.2	567	2	AAR12517	Aar12517 Maize nit
706	38	42.2	574	5	ABG94250	Abg94250 Human IgE
707	38	42.2	574	5	ABG80562	Abg80562 Human IgE
708	38	42.2	574	6	ABP96592	Abp96592 Human IgE
709	38	42.2	574	7	ADE97368	Ade97368 Human imm
710	38	42.2	577	8	ADY22720	Ady22720 Plant ful
711	38	42.2	595	8	ADU07813	Adu07813 Amino aci
712	38	42.2	625	8	ADR10287	Adr10287 Human pro
713	38	42.2	679	4	ABB58212	Abb58212 Drosophil
714	38	42.2	755	4	AAB93735	Aab93735 Human pro
715	38	42.2	755	8	ADP56673	Adp56673 Human pro
716	38	42.2	764	8	ADX91667	Adx91667 Plant ful
717	38	42.2	863	4	AAG82458	Aag82458 S. epider
718	38	42.2	876	5	ABP39098	Abp39098 Staphyloc
719	38	42.2	876	8	ADS07310	Ads07310 Staphyloc
720	38	42.2	958	3	AAY51120	Aay51120 Human SAR
721	38	42.2	958	8	ADL83102	Adl83102 Human PRO
722	38	42.2	1044	8	ADS44283	Ads44283 Bacterial
723	38	42.2	1162	7	ABO84018	Abo84018 Pseudomon
724	38	42.2	1207	4	AAY72643	Aay72643 Mouse gly
725	38	42.2	1207	6	AAE33542	Aae33542 Human nov
726	38	42.2	1212	6	AAE33541	Aae33541 Human nov
727	38	42.2	1222	4	AAY72642	Aay72642 Human gly
728	38	42.2	1222	6	ABU11849	Abu11849 Human sec
729	38	42.2	1431	5	AAM47675	Aam47675 Rat Hyalu
730	38	42.2	1431	6	ABG72498	Abg72498 Rat 175kD
731	38	42.2	2516	2	AAW01875	Aaw01875 Neuronal
732	38	42.2	2516	2	AAW01884	Aaw01884 Invertebr
733	38	42.2	2516	4	ABB61076	Abb61076 Drosophil
734	38	42.2	2516	5	ABJ17935	Abj17935 Drosophil
735	38	42.2	3129	3	AAB07427	Aab07427 Amino aci
736	38	42.2	3129	9	ADZ67207	Adz67207 Fusarium
737	37.5	41.7	16	6	ABP96289	Abp96289 Anti-hTNF
738	37.5	41.7	16	7	ADJ32092	Adj32092 Human int
739	37.5	41.7	16	7	ADJ32090	Adj32090 Human int
740	37.5	41.7	16	7	ADJ32096	Adj32096 Human int
741	37.5	41.7	16	9	ADV21361	Adv21361 Human ant
742	37.5	41.7	16	9	ADV21345	Adv21345 Human ant
743	37.5	41.7	16	9	ADX98337	Adx98337 Human ant
744	37.5	41.7	80	2	AAW62794	Aaw62794 Amino aci
745	37.5	41.7	97	2	AAY05694	Aay05694 Multiple
746	37.5	41.7	97	5	ABG78212	Abg78212 Human Fv
747	37.5	41.7	97	5	ABG91903	Abg91903 Human ant
748	37.5	41.7	97	6	ABO27107	Abo27107 Human ger
749	37.5	41.7	97	7	ADB75646	Adb75646 Human pro
750	37.5	41.7	97	7	ADD28104	Add28104 Lymphoma
751	37.5	41.7	97	7	ADF10048	Adf10048 VEGF anti
752	37.5	41.7	97	7	ADF10150	Adf10150 Antibody
753	37.5	41.7	97	7	ADF09942	Adf09942 Antibody
754	37.5	41.7	97	7	ADJ80323	Adj80323 VH gene l
755	37.5	41.7	97	9	ADY75328	Ady75328 Protein e
756	37.5	41.7	97	9	AEB13604	Aeb13604 Human var
757	37.5	41.7	114	3	AAB01949	Aab01949 Anti-Id1
758	37.5	41.7	114	3	AAB01950	Aab01950 Anti-Id1
759	37.5	41.7	114	3	AAB01953	Aab01953 Anti-Id1
760	37.5	41.7	114	3	AAB01959	Aab01959 High affi
761	37.5	41.7	114	3	AAB01952	Aab01952 Anti-Id1
762	37.5	41.7	114	3	AAB01955	Aab01955 Strepativ
763	37.5	41.7	114	3	AAB01951	Aab01951 Anti-Id1
764	37.5	41.7	114	3	AAB01956	Aab01956 Strepativ
765	37.5	41.7	114	3	AAB01948	Aab01948 Wild-type
766	37.5	41.7	114	3	AAB01954	Aab01954 Anti-Id1
767	37.5	41.7	114	7	ADG70086	Adg70086 Diversifi
768	37.5	41.7	114	7	ADG70013	Adg70013 Diversifi
769	37.5	41.7	115	9	ADW91686	Adw91686 Human LDC
770	37.5	41.7	116	2	AAR66324	Aar66324 Human imm
771	37.5	41.7	117	4	AAM60904	Aam60904 Human bra
772	37.5	41.7	117	4	ABG55317	Abg55317 Human liv
773	37.5	41.7	117	5	ABG43454	Abg43454 Human pep
774	37.5	41.7	118	6	ADA89246	Ada89246 Human ant
775	37.5	41.7	118	9	ADX98419	Adx98419 Human ant
776	37.5	41.7	119	9	ADV21357	Adv21357 Human ant
777	37.5	41.7	120	2	AAR66343	Aar66343 Human imm
778	37.5	41.7	122	7	ADK17418	Adk17418 Anti-huma
779	37.5	41.7	122	8	ADG42840	Adg42840 scFv Ab12
780	37.5	41.7	123	2	AAW03757	Aaw03757 Anti-rhes
781	37.5	41.7	124	9	ADZ41991	Adz41991 Ig H chai
782	37.5	41.7	125	6	ADA89266	Ada89266 Human ant
783	37.5	41.7	125	6	ADA89274	Ada89274 Human ant
784	37.5	41.7	126	9	ADV21341	Adv21341 Human ant
785	37.5	41.7	126	9	ADZ41994	Adz41994 Ig H chai
786	37.5	41.7	126	9	ADZ41997	Adz41997 Ig H chai
787	37.5	41.7	126	9	ADZ41993	Adz41993 Ig H chai
788	37.5	41.7	130	9	ADX02063	Adx02063 SARS coro
789	37.5	41.7	130	9	ADX02187	Adx02187 SARS coro
790	37.5	41.7	139	3	AAY99556	Aay99556 Human LH1
791	37.5	41.7	139	6	ABR42859	Abr42859 Tumour-sp
792	37.5	41.7	139	7	ABW02445	Abw02445 Human mon
793	37.5	41.7	139	9	ADX98271	Adx98271 Human ant
794	37.5	41.7	142	6	ABP96287	Abp96287 Anti-hTNF
795	37.5	41.7	154	6	ABP96293	Abp96293 Human ant
796	37.5	41.7	172	4	AAU41613	Aau41613 Propionib
797	37.5	41.7	172	6	ABM38132	Abm38132 Propionib
798	37.5	41.7	190	2	AAY34304	Aay34304 IgM antib
799	37.5	41.7	202	2	AAY34303	Aay34303 IgM antib
800	37.5	41.7	205	2	AAY34299	Aay34299 IgM antib
801	37.5	41.7	218	7	ADG70090	Adg70090 Diversifi
802	37.5	41.7	223	7	ADJ32112	Adj32112 Human int
803	37.5	41.7	224	7	ADG70088	Adg70088 Diversifi
804	37.5	41.7	229	7	ADJ32128	Adj32128 Human int
805	37.5	41.7	230	7	ADJ32118	Adj32118 Human int
806	37.5	41.7	241	4	AAB46061	Aab46061 Human TF
807	37.5	41.7	241	9	ADV21480	Adv21480 Mature fo
808	37.5	41.7	244	2	AAY21883	Aay21883 Amino aci
809	37.5	41.7	248	9	ADV21478	Adv21478 Mature fo
810	37.5	41.7	249	5	ABP45310	Abp45310 Human BLy
811	37.5	41.7	249	5	ABP44946	Abp44946 Human BLy
812	37.5	41.7	249	7	ADG96137	Adg96137 Single ch
813	37.5	41.7	249	7	ADG95773	Adg95773 Single ch
814	37.5	41.7	250	5	ABP45402	Abp45402 Human BLy
815	37.5	41.7	250	7	ADG96229	Adg96229 Single ch
816	37.5	41.7	253	5	ABP45322	Abp45322 Human BLy
817	37.5	41.7	253	7	ADG96149	Adg96149 Single ch
818	37.5	41.7	254	5	ABP45648	Abp45648 Human BLy
819	37.5	41.7	254	7	ADG96475	Adg96475 Single ch
820	37.5	41.7	260	9	ADX01964	Adx01964 SARS coro
821	37.5	41.7	260	9	ADX02026	Adx02026 SARS coro
822	37.5	41.7	404	6	ABU58175	Abu58175 Rice stre
823	37.5	41.7	431	8	ADO80299	Ado80299 Halobacte
824	37.5	41.7	431	8	ADS29670	Ads29670 Bacterial
825	37.5	41.7	450	6	ABP96294	Abp96294 4A5-3.1.1
826	37.5	41.7	453	6	ABP96295	Abp96295 4A5-3.1.1
827	37.5	41.7	472	2	AAR93166	Aar93166 Anti-rhes

828	37.5	41.7	494	9	ADV21531	Adv21531	Mature fo
829	37.5	41.7	494	9	ADV21521	Adv21521	Mature fo
830	37.5	41.7	496	9	ADV21501	Adv21501	Mature fo
831	37.5	41.7	496	9	ADV21537	Adv21537	Mature fo
832	37.5	41.7	496	9	ADV21511	Adv21511	Mature fo
833	37.5	41.7	497	9	ADV21541	Adv21541	Mature fo
834	37.5	41.7	501	9	ADV21519	Adv21519	Mature fo
835	37.5	41.7	501	9	ADV21529	Adv21529	Mature fo
836	37.5	41.7	503	9	ADV21509	Adv21509	Mature fo
837	37.5	41.7	503	9	ADV21499	Adv21499	Mature fo
838	37.5	41.7	537	3	AAY96290	Aay96290	Human IGF
839	37.5	41.7	717	6	ABU30061	Abu30061	Protein e
840	37.5	41.7	718	7	ADC95607	Adc95607	E. faeciu
841	37.5	41.7	910	7	ABM88319	Abm88319	Rice abio
842	37.5	41.7	1022	8	ADL61320	Adl61320	Human pro
843	37.5	41.7	1022	8	ADQ88210	Adq88210	Human 127
844	37.5	41.7	1022	8	ABO85032	Abo85032	Human can
845	37.5	41.7	1022	8	ADR67030	Adr67030	Human can
846	37.5	41.7	1022	9	ADZ13375	Adz13375	Human can
847	37.5	41.7	1041	7	ADG76329	Adg76329	Human Inc
848	37.5	41.7	1041	9	ADZ13363	Adz13363	Human can
849	37.5	41.7	1045	4	ABG28188	Abg28188	Novel hum
850	37.5	41.7	1051	9	ADZ13367	Adz13367	Human can
851	37.5	41.7	1056	4	ABG06612	Abg06612	Novel hum
852	37.5	41.7	1062	9	ADZ13373	Adz13373	Human can
853	37.5	41.7	1065	8	ABO85030	Abo85030	Murine ca
854	37.5	41.7	1065	8	ADR67025	Adr67025	Mouse can
855	37.5	41.7	1065	9	ADZ13358	Adz13358	Murine ca
856	37.5	41.7	1081	9	ADZ13361	Adz13361	Human can
857	37.5	41.7	1093	5	ABB08201	Abb08201	Human lip
858	37.5	41.7	1175	7	ADE54798	Ade54798	Human Pro
859	37.5	41.7	1175	7	ADE54796	Ade54796	Rat Prote
860	37.5	41.7	1175	7	ADD48413	Add48413	Human Pro
861	37.5	41.7	1175	7	ADD48411	Add48411	Rat Prote
862	37.5	41.7	1175	8	ABO85031	Abo85031	Human can
863	37.5	41.7	1175	8	ADR67028	Adr67028	Human can
864	37.5	41.7	1958	4	ABB61606	Abb61606	Drosophil
865	37	41.1	17	2	AAY05056	Aay05056	Tumour an
866	37	41.1	17	3	AAY79427	Aay79427	Tie2 rece
867	37	41.1	17	4	AAB61282	Aab61282	Anti-TANG
868	37	41.1	17	6	ABU11248	Abu11248	Human TAN
869	37	41.1	17	7	ADC82830	Adc82830	CDR regio
870	37	41.1	17	8	ADI61984	Adi61984	Human TS-
871	37	41.1	17	8	ADR03402	Adr03402	Humanised
872	37	41.1	17	8	ADR03405	Adr03405	Humanised
873	37	41.1	17	8	ADR03398	Adr03398	Humanised
874	37	41.1	17	8	ADS18665	Ads18665	Peptide s
875	37	41.1	17	9	AEA45757	Aea45757	Apolipopr
876	37	41.1	17	9	AEA45754	Aea45754	Apolipopr
877	37	41.1	17	9	AEB70889	Aeb70889	Toll-like
878	37	41.1	63	2	AAR76972	Aar76972	HSV-neutr
879	37	41.1	72	5	ABP01231	Abp01231	Human ORF
880	37	41.1	98	2	AAR34279	Aar34279	Human TNF
881	37	41.1	98	2	AAR54800	Aar54800	SpA-react
882	37	41.1	98	3	AAB40130	Aab40130	Anti-hIL1
883	37	41.1	98	3	AAB40134	Aab40134	Anti-hIL1
884	37	41.1	98	5	ABG78235	Abg78235	Human Fv
885	37	41.1	98	5	ABG78207	Abg78207	Human Fv
886	37	41.1	98	5	ABG78236	Abg78236	Human Fv
887	37	41.1	98	5	ABG91898	Abg91898	Human ant
888	37	41.1	98	5	ABG91926	Abg91926	Human ant
889	37	41.1	98	5	ABG91927	Abg91927	Human ant
890	37	41.1	98	6	ABO27095	Abo27095	Human ger
891	37	41.1	98	7	ADD28062	Add28062	Lymphoma
892	37	41.1	98	7	ADF10054	Adf10054	VEGF anti
893	37	41.1	98	7	ADF10034	Adf10034	VEGF anti
894	37	41.1	98	7	ADF10157	Adf10157	Antibody
895	37	41.1	98	7	ADF09926	Adf09926	Antibody
896	37	41.1	98	7	ADF09949	Adf09949	Antibody
897	37	41.1	98	7	ADF10136	Adf10136	Antibody
898	37	41.1	98	7	ADJ80329	Adj80329	VH gene l
899	37	41.1	98	7	ADJ80308	Adj80308	VH gene l
900	37	41.1	98	9	ADY75334	Ady75334	Protein e
901	37	41.1	98	9	ADY75313	Ady75313	Protein e
902	37	41.1	98	9	AEB13610	Aeb13610	Human var
903	37	41.1	103	4	AAG80949	Aag80949	Human nGP
904	37	41.1	103	5	ABG93767	Abg93767	Human G p
905	37	41.1	109	8	ADP22390	Adp22390	Human ant
906	37	41.1	110	2	AAR34280	Aar34280	Human hea
907	37	41.1	111	2	AAR34282	Aar34282	Human hea
908	37	41.1	113	9	ADZ42027	Adz42027	Ig H chai
909	37	41.1	114	7	ADP03975	Adp03975	Murine-ex
910	37	41.1	114	8	ADS16562	Ads16562	Human ant
911	37	41.1	115	8	ADI61978	Adi61978	Human TS-
912	37	41.1	116	4	AAU02604	Aau02604	Anti-adip
913	37	41.1	116	9	AEA41083	Aea41083	Germline
914	37	41.1	117	2	AAR66336	Aar66336	Human imm
915	37	41.1	117	9	AEB70887	Aeb70887	Toll-like
916	37	41.1	118	9	ADZ42021	Adz42021	Ig H chai
917	37	41.1	118	9	AEB46913	Aeb46913	Human var
918	37	41.1	119	3	AAY79424	Aay79424	Tie2 rece
919	37	41.1	119	7	ADP03976	Adp03976	Murine-ex
920	37	41.1	119	9	ADZ42025	Adz42025	Ig H chai
921	37	41.1	119	9	ADZ42022	Adz42022	Ig H chai
922	37	41.1	119	9	ADZ42023	Adz42023	Ig H chai
923	37	41.1	119	9	ADZ42026	Adz42026	Ig H chai
924	37	41.1	119	9	ADZ42028	Adz42028	Ig H chai
925	37	41.1	120	6	AAE37731	Aae37731	Mouse CD4
926	37	41.1	120	9	ADW13533	Adw13533	Anti-anti
927	37	41.1	120	9	ADZ42029	Adz42029	Ig H chai
928	37	41.1	123	8	ADO36393	Ado36393	Intracell
929	37	41.1	124	7	ADJ80429	Adj80429	Hybrid hu
930	37	41.1	126	2	AAW13534	Aaw13534	Anti-mela
931	37	41.1	128	9	AEB39974	Aeb39974	L. pneumo
932	37	41.1	129	4	AAG75727	Aag75727	Human col
933	37	41.1	129	4	AAG93631	Aag93631	Human ant
934	37	41.1	129	6	ABO27438	Abo27438	Anti-Rh(D
935	37	41.1	132	9	AEB36582	Aeb36582	L. pneumo
936	37	41.1	134	4	AAO00837	Aao00837	Human pol
937	37	41.1	134	5	ABP08416	Abp08416	Human ORF
938	37	41.1	136	9	ADZ57715	Adz57715	Germline
939	37	41.1	141	3	AAY43873	Aay43873	Heavy cha
940	37	41.1	152	5	ABB48232	Abb48232	Listeria
941	37	41.1	160	3	AAG14263	Aag14263	Arabidops
942	37	41.1	160	3	AAG13556	Aag13556	Arabidops
943	37	41.1	164	4	AAB76618	Aab76618	Corynebac
944	37	41.1	166	3	AAG13555	Aag13555	Arabidops
945	37	41.1	167	3	AAG13554	Aag13554	Arabidops
946	37	41.1	170	7	ABO63986	Abo63986	Klebsiell
947	37	41.1	171	7	ABO67069	Abo67069	Klebsiell
948	37	41.1	188	6	ABP57450	Abp57450	Mycobacte
949	37	41.1	211	6	ABU18552	Abu18552	Protein e
950	37	41.1	213	3	AAG15701	Aag15701	Arabidops
951	37	41.1	214	3	AAG27664	Aag27664	Arabidops
952	37	41.1	220	4	ABB58471	Abb58471	Drosophil
953	37	41.1	222	5	ABP10538	Abp10538	Human ORF
954	37	41.1	228	3	AAG14262	Aag14262	Arabidops
955	37	41.1	228	9	ADX18563	Adx18563	VEGF-spec
956	37	41.1	228	9	AEA13918	Aea13918	VEGF rela
957	37	41.1	228	9	AEA13948	Aea13948	VEGF rela
958	37	41.1	229	2	AAY27341	Aay27341	Group B S
959	37	41.1	232	9	ADW13531	Adw13531	Anti-anti
960	37	41.1	239	7	ADF06446	Adf06446	Bacterial
961	37	41.1	241	9	AEB46931	Aeb46931	Human CD1
962	37	41.1	242	3	AAY83291	Aay83291	Borrelia
963	37	41.1	243	5	ABP46091	Abp46091	Human BLy
964	37	41.1	243	7	ADG96918	Adg96918	Single ch
965	37	41.1	247	7	ABO76170	Abo76170	Pseudomon
966	37	41.1	248	5	ABP46077	Abp46077	Human BLy
967	37	41.1	248	7	ADG96904	Adg96904	Single ch
968	37	41.1	249	4	AAB68087	Aab68087	An anti-a
969	37	41.1	250	8	ADI61980	Adi61980	Human scF
970	37	41.1	253	5	ABP45407	Abp45407	Human BLy
971	37	41.1	253	5	ABP45661	Abp45661	Human BLy
972	37	41.1	253	7	ADG96488	Adg96488	Single ch
973	37	41.1	253	7	ADG96234	Adg96234	Single ch

974	37	41.1	254	2	AAW49693	Aaw49693 Human ScF
975	37	41.1	261	3	AAG15700	Aag15700 Arabidops
976	37	41.1	263	3	AAG15699	Aag15699 Arabidops
977	37	41.1	263	8	ADN73215	Adn73215 Thale cre
978	37	41.1	264	5	ABU05745	Abu05745 M. tuberc
979	37	41.1	269	4	AAG66730	Aag66730 Pinellia
980	37	41.1	269	8	ADX74191	Adx74191 Plant ful
981	37	41.1	271	9	ADW47925	Adw47925 Mycobacte
982	37	41.1	291	3	AAG27663	Aag27663 Arabidops
983	37	41.1	295	6	ADA33905	Ada33905 Acinetoba
984	37	41.1	304	3	AAG27662	Aag27662 Arabidops
985	37	41.1	304	8	ADY09002	Ady09002 Plant ful
986	37	41.1	305	2	AAR54839	Aar54839 Antiviral
987	37	41.1	305	2	AAR80106	Aar80106 P. insula
988	37	41.1	307	3	AAY28421	Aay28421 Rice bran
989	37	41.1	317	2	AAW14321	Aaw14321 T. neopol
990	37	41.1	323	7	ADF71441	Adf71441 Maize pan
991	37	41.1	323	9	ADZ39236	Adz39236 Corn pant
992	37	41.1	325	7	ADF71439	Adf71439 Maize pan
993	37	41.1	325	9	ADZ39234	Adz39234 Corn pant
994	37	41.1	331	6	AAE37727	Aae37727 Chemokine
995	37	41.1	331	6	AAE37733	Aae37733 Chemokine
996	37	41.1	339	6	AAE37728	Aae37728 Chemokine
997	37	41.1	347	3	AAG43023	Aag43023 Arabidops
998	37	41.1	347	3	AAG13494	Aag13494 Arabidops
999	37	41.1	347	8	ADN20237	Adn20237 Bacterial
1000	37	41.1	348	3	AAG13493	Aag13493 Arabidops

ALIGNMENTS

RESULT 1
AAR97317
ID AAR97317 standard; peptide; 17 AA.
XX
AC AAR97317;
XX
DT 15-OCT-1996 (first entry)
XX
DE Humanised monoclonal antibody heavy chain CDR.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Mus musculus.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Claim 5; Page 39; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. This sequence is a murine derived CDR region which corresponds
CC to CDR 2 in the heavy chain of the humanised MAb. See AAR97313-97333
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 90; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
|||||||||||||||||
Db 1 EIHPDSSTINYAPSLKD 17

RESULT 2
ADM95106
ID ADM95106 standard; peptide; 17 AA.
XX
AC ADM95106;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 MAb heavy chain variable region CDR2.
XX
KW non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW complementarity determining region; pancreatic cancer; breast cancer;
KW ovarian cancer.
XX
OS Mus sp.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-364813/34.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Claim 6; SEQ ID NO 24; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the CDR2 of
CC the murine MN-14 antibody heavy chain variable region and used to
CC generate the humanised/chimeric antibody of the invention.
XX
SQ Sequence 17 AA;

Query Match 100.0%; Score 90; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db          1 EIHPDSSTINYAPSLKD 17
```

RESULT 3
ADM98315
ID ADM98315 standard; peptide; 17 AA.
XX
AC ADM98315;
XX
DT 15-JUL-2004 (first entry)
XX
DE Humanised murine MN-14 antibody heavy chain variable region CDR2 peptide.
XX
KW carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; humanised;
KW murine; mouse; antibody; MN-14; non-medullary thyroid carcinoma;
KW medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW hepatocellular carcinoma; breast cancer; lung cancer;
KW antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW apoptosis.
XX
OS Mus sp.
OS Synthetic.
XX
PN WO2004032857-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031801.
XX
PR 08-OCT-2002; 2002US-0416531P.
PR 11-OCT-2002; 2002WO-US032307.
PR 02-MAY-2003; 2003US-0467161P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-340797/31.
XX
PT Treating non-medullary or medullary thyroid carcinoma, involves
PT administering to subject, either concurrently or sequentially, anti-
PT carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS Claim 8; Page 76; 122pp; English.
XX
CC This invention relates to methods for treating cancers that express
CC carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC antibodies that can be used following administration of an agent that
CC will increase antibody effector functions or following administration of
CC an amount of interferon effective to upregulate CEA expression in tumour
CC cells. The present invention describes the anti-CEA antibody as a class
CC III humanised murine monoclonal antibody that retains specificity for CEA
CC binding and is preferably an MN-14 antibody or fragment thereof.
CC Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC composition useful for the treatment of non-medullary or medullary
CC thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC carcinoma, as well as breast or lung cancer. Furthermore, it can
CC stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC cell growth and angiogenesis. This peptide sequence is a CDR region of
CC the humanised murine MN-14 antibody of the invention.
XX
SQ Sequence 17 AA;

```
  Query Match            100.0%;  Score 90;  DB 8;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db          1 EIHPDSSTINYAPSLKD 17
```

RESULT 4
ABR42755
ID ABR42755 standard; protein; 118 AA.
XX
AC ABR42755;
XX
DT 26-AUG-2003 (first entry)
XX
DE Anti-CEA humanized monoclonal antibody hMN-14 VH region.
XX
KW Humanized; monoclonal antibody; antibody; hMN-14;
KW carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003033654-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032718.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
PR 08-JAN-2002; 2002US-0345641P.
PR 22-AUG-2002; 2002US-0404919P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg DM;
XX
DR WPI; 2003-513460/48.
XX
PT New multivalent, monospecific binding protein comprising two or more
PT binding sites having affinity for the same single target antigen, where
PT each binding site is associated with scFv fragments, useful for
PT diagnosing or treating tumor.
XX
PS Disclosure; Fig 12; 62pp; English.
XX
CC The present sequence is the protein sequence of the heavy chain variable
CC region of anti-carcinoembryonic antigen (CEA) humanized monoclonal
CC antibody hMN-14. scFv constructs comprising the hMN-14 VH and Vkappa
CC regions are used in novel multivalent, monospecific binding proteins
CC (diabody, triabody and tetrabody) of the invention (see also ABR42754,
CC ABR42757 and ABR42758). Claimed binding proteins are specific for a
CC tumour-associated antigen, and are used in the diagnosis and treatment of
CC a tumour, carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma,
CC lymphoma or myeloma, or a cancer selected from acute lymphoblastic
CC leukaemia, acute myelogenous leukaemia, biliary, breast, cervical,
CC chronic lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC prostate and bladder
XX
SQ Sequence 118 AA;

```
  Query Match            100.0%;  Score 90;  DB 6;  Length 118;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66
```

RESULT 5
AAR97336
ID AAR97336 standard; protein; 119 AA.
XX

```
AC   AAR97336;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Humanised antibody variable heavy chain (MN14HuVH).
XX
KW   Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW   complementary determining region; anti-carcinoembryonic antigen; CEA;
KW   diagnosis; imaging; therapy; immune response.
XX
OS   Mus musculus.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    31. .35
FT                   /label= CDR 1.
FT   Binding-site    50. .66
FT                   /label= CDR 2.
FT   Binding-site    99. .108
FT                   /label= CDR 3.
XX
PN   WO9611013-A1.
XX
PD   18-APR-1996.
XX
PF   28-SEP-1995;   95WO-US011964.
XX
PR   05-OCT-1994;   94US-00318157.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Hansen HJ,  Armour KL;
XX
DR   WPI; 1996-209653/21.
DR   N-PSDB; AAT29012.
XX
PT   New humanised anti-CEA monoclonal antibody - having engrafted murine
PT   CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS   Disclosure; Fig 7; 62pp; English.
XX
CC   New humanised monoclonal antibodies (MAbs) comprising the complementary
CC   determining regions (CDRs) of a parental murine class III anti-
CC   carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC   heterologous antibody which can be derived from any species including
CC   human, retain the anti-CEA binding specificity of the parental murine MAb
CC   but are less immunogenic in a human subject than the parental MAb. The
CC   humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC   -producing cancers and patients receiving the humanised antibodies and
CC   conjugates show improved therapeutic results, decreased immune responses
CC   and decreased immune-mediated adverse effects compared to the parent
CC   antibody. See AAR97313-97333 for the CDR sequence and framework regions
CC   of the humanised MAbs
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 90;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 6
AAR97334
ID   AAR97334 standard; protein; 119 AA.
XX
AC   AAR97334;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Murine NEWM MN-14 variable region heavy chain.
XX
KW   Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW   complementary determining region; anti-carcinoembryonic antigen; CEA;
KW   diagnosis; imaging; therapy; immune response.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    31. .35
FT                   /label= CDR 1.
FT   Binding-site    50. .66
FT                   /label= CDR 2.
FT   Binding-site    99. .108
FT                   /label= CDR 3.
XX
PN   WO9611013-A1.
XX
PD   18-APR-1996.
XX
PF   28-SEP-1995;   95WO-US011964.
XX
PR   05-OCT-1994;   94US-00318157.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Hansen HJ,  Armour KL;
XX
DR   WPI; 1996-209653/21.
DR   N-PSDB; AAT29010.
XX
PT   New humanised anti-CEA monoclonal antibody - having engrafted murine
PT   CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS   Example 5; Fig 1; 62pp; English.
XX
CC   New humanised monoclonal antibodies (MAbs) comprising the complementary
CC   determining regions (CDRs) of a parental murine class III anti-
CC   carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC   heterologous antibody which can be derived from any species including
CC   human, retain the anti-CEA binding specificity of the parental murine MAb
CC   but are less immunogenic in a human subject than the parental MAb. The
CC   humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC   -producing cancers and patients receiving the humanised antibodies and
CC   conjugates show improved therapeutic results, decreased immune responses
CC   and decreased immune-mediated adverse effects compared to the parent
CC   antibody. See AAR97313-97333 for the CDR sequence and framework regions
CC   of the humanised MAbs
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 90;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 7
ADM95101
ID   ADM95101 standard; protein; 119 AA.
XX
AC   ADM95101;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 MAb heavy chain variable region coding sequence.
XX
KW   non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW   complementarity determining region; pancreatic cancer; breast cancer;
KW   ovarian cancer.
```

XX
OS Mus sp.
OS Homo sapiens.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-364813/34.
DR N-PSDB; ADM95099.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Claim 14; Fig 16B; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the humanised
CC murine MN-14 antibody heavy chain variable region.
XX
SQ Sequence 119 AA;

Query Match 100.0%; Score 90; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||||||||||||||||||
Db 50 EIHPDSSTINYAPSLKD 66

RESULT 8
ADM95095
ID ADM95095 standard; protein; 119 AA.
XX
AC ADM95095;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 MAb heavy chain variable region.
XX
KW non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW complementarity determining region; pancreatic cancer; breast cancer;
KW ovarian cancer.
XX
OS Mus sp.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-364813/34.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Disclosure; Fig 11A-B; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the murine MN-
CC 14 antibody heavy chain variable region.
XX
SQ Sequence 119 AA;

Query Match 100.0%; Score 90; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||||||||||||||||||
Db 50 EIHPDSSTINYAPSLKD 66

RESULT 9
ADM98324
ID ADM98324 standard; protein; 119 AA.
XX
AC ADM98324;
XX
DT 15-JUL-2004 (first entry)
XX
DE Humanised murine MN-14 antibody heavy chain variable region protein.
XX
KW carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW antibody; MN-14; non-medullary thyroid carcinoma;
KW medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW hepatocellular carcinoma; breast cancer; lung cancer;
KW antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW apoptosis; humanised.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 33. .34
FT /note= "Encoded by TGGGATAGCAGTACGATTAACTATGCGATG"
FT Misc-difference 53. .62
FT /note= "Encoded by CCACCG"
XX
PN WO2004032857-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031801.
XX
PR 08-OCT-2002; 2002US-0416531P.
PR 11-OCT-2002; 2002WO-US032307.
PR 02-MAY-2003; 2003US-0467161P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;

```
XX
DR   WPI; 2004-340797/31.
DR   N-PSDB; ADM98323.
XX
PT   Treating non-medullary or medullary thyroid carcinoma, involves
PT   administering to subject, either concurrently or sequentially, anti-
PT   carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS   Disclosure; Fig 23b; 122pp; English.
XX
CC   This invention relates to methods for treating cancers that express
CC   carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC   therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC   antibodies that can be used following administration of an agent that
CC   will increase antibody effector functions or following administration of
CC   an amount of interferon effective to upregulate CEA expression in tumour
CC   cells. The present invention describes the anti-CEA antibody as a class
CC   III humanised murine monoclonal antibody that retains specificity for CEA
CC   binding and is preferably an MN-14 antibody or fragment thereof.
CC   Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC   composition useful for the treatment of non-medullary or medullary
CC   thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC   carcinoma, as well as breast or lung cancer. Furthermore, it can
CC   stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC   mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC   cell growth and angiogenesis. This polypeptide sequence is the humanised
CC   murine MN-14 antibody heavy chain variable region protein of the
CC   invention.
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 90;  DB 8;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 10
ADM98318
ID   ADM98318 standard; protein; 119 AA.
XX
AC   ADM98318;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Murine MN-14 antibody heavy chain variable region protein.
XX
KW   carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW   antibody; MN-14; non-medullary thyroid carcinoma;
KW   medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW   hepatocellular carcinoma; breast cancer; lung cancer;
KW   antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW   apoptosis.
XX
OS   Mus sp.
XX
PN   WO2004032857-A2.
XX
PD   22-APR-2004.
XX
PF   08-OCT-2003; 2003WO-US031801.
XX
PR   08-OCT-2002; 2002US-0416531P.
PR   11-OCT-2002; 2002WO-US032307.
PR   02-MAY-2003; 2003US-0467161P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-340797/31.
DR   N-PSDB; ADM98317.
XX
PT   Treating non-medullary or medullary thyroid carcinoma, involves
PT   administering to subject, either concurrently or sequentially, anti-
PT   carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS   Disclosure; Fig 11; 122pp; English.
XX
CC   This invention relates to methods for treating cancers that express
CC   carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC   therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC   antibodies that can be used following administration of an agent that
CC   will increase antibody effector functions or following administration of
CC   an amount of interferon effective to upregulate CEA expression in tumour
CC   cells. The present invention describes the anti-CEA antibody as a class
CC   III humanised murine monoclonal antibody that retains specificity for CEA
CC   binding and is preferably an MN-14 antibody or fragment thereof.
CC   Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC   composition useful for the treatment of non-medullary or medullary
CC   thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC   carcinoma, as well as breast or lung cancer. Furthermore, it can
CC   stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC   mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC   cell growth and angiogenesis. This polypeptide sequence is murine MN-14
CC   antibody heavy chain variable region protein of the invention.
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 90;  DB 8;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 11
ABG76489
ID   ABG76489 standard; protein; 138 AA.
XX
AC   ABG76489;
XX
DT   13-MAY-2003  (first entry)
XX
DE   Heavy chain variable, VH, region of antibody hMN14.
XX
KW   CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW   colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW   human; zeta signalling chain; CD8alpha hinge; humanised antibody;
KW   heavy chain variable region; VH.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .19
FT                   /label= Signal_peptide
FT   Protein         20. .138
FT                   /label= Mature_VH_of_hMN14
XX
PN   US2002165360-A1.
XX
PD   07-NOV-2002.
XX
PF   10-DEC-2001; 2001US-00006771.
XX
PR   30-NOV-2000; 2000US-0250087P.
PR   30-NOV-2000; 2000US-0250090P.
XX
```

```
PA   (JUNG/) JUNGHANS R P.
XX
PI   Junghans RP;
XX
DR   WPI; 2003-298705/29.
DR   N-PSDB; ABX13169.
XX
PT   New chimeric molecule from humanized antibody against carcinoembryonic
PT   antigen and having signaling molecules of T cells and other effector
PT   cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS   Disclosure; Page 9; 20pp; English.
XX
CC   The invention relates to a chimaeric molecule comprising the
CC   carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC   as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC   chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC   which the cysteine residues have been mutated, with the IgTCR molecule
CC   occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC   appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC   NK (not defined) or other effector cells are useful in treating patients
CC   with cancers expressing the CEA antigen, together with other or with
CC   heterologous constructs to engage additional stimulatory and functional
CC   properties of the effector cells to enhance the anti-tumour therapeutic
CC   efficacy. The cancer disorder includes colorectal, breast and lung
CC   cancers. The present sequence represents the heavy chain variable, VH,
CC   region of antibody hMN14. The VH protein is humanised (complementarity
CC   determining region-grafted) and has a leader peptide
XX
SQ   Sequence 138 AA;

  Query Match             100.0%;  Score 90;  DB 6;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         69 EIHPDSSTINYAPSLKD 85


RESULT 12
ABR42757
ID   ABR42757 standard; protein; 256 AA.
XX
AC   ABR42757;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-0.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-0;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; triabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .256
FT                   /label= hMN-14-0
FT   Region          142. .250
FT                   /label= hMN-14Vkappa
FT   Region          251. .256
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
DR   N-PSDB; ACC58722.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 39; Fig 13; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-0, which is
CC   designed to form an hMN-14 triabody. The hMN-14-0 polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa without a peptide linker. The use of the zero linker enables the
CC   secreted polypeptide to form a triabody, forming 3 binding sites for CEA.
CC   The polypeptide also includes a pelB signal peptide, which precedes the
CC   VH moiety to facilitate synthesis of the polypeptide in the periplasmic
CC   space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific triabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 256 AA;

  Query Match             100.0%;  Score 90;  DB 6;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 13
ABR42758
ID   ABR42758 standard; protein; 257 AA.
XX
AC   ABR42758;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-1G.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-1G;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; tetrabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
```

```
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .257
FT                   /label= hMN-14-0
FT   Region          142
FT                   /label= 1G_linker
FT   Region          143. .251
FT                   /label= hMN-14Vkappa
FT   Region          252. .257
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 48; Fig 14; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-1G, which is
CC   designed to form an hMN-14 tetrabody. The hMN-14-1G polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa via a single glycine residues. Use of the 1G linker enables some
CC   of the the secreted polypeptide to form a tetrabody with 4 binding sites
CC   for CEA. The polypeptide also includes a pelB signal peptide, which
CC   precedes the VH moiety to facilitate synthesis of the polypeptide in the
CC   periplasmic space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific tetrabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 257 AA;

  Query Match             100.0%;  Score 90;  DB 6;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 14
ABR42289
ID   ABR42289 standard; protein; 261 AA.
XX
AC   ABR42289;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Diabody 679-scFv-L5 polypeptide (VH-I3Q/C101S mutant).
XX
KW   Diabody; antibody; 679-scFv-L5; histamine-succinyl-glycyl; HSG;
KW   affinity enhancement system; tumour; targeting; mutant; mutein.
XX
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB signal peptide"
FT   Misc-difference 3
FT                   /note= "wild-type Ile substituted by Gln"
FT   Protein         23. .268
FT                   /label= 679-scFv-L5
FT   Region          23. .142
FT                   /label= 679VH(I3Q/C101S)
FT   Misc-difference 101
FT                   /note= "wild-type Cys substituted by Ser"
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .260
FT                   /label= 679Vk
FT   Region          261. .268
FT                   /label= 6His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57803.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Disclosure; Fig 28; 87pp; English.
XX
CC   The present sequence is the protein sequence of a 679 mutant diabody in
CC   which antibody 679 VH has a Gln for Ile amino acid substitution at
CC   position 3 and a Ser for Gln amino acid substitution at position 101.
CC   Murine monoclonal antibody 679 binds with high affinity to molecules
CC   containing the moiety histamine-succinyl-glycyl (HSG). The present
CC   polypeptide comprises: 679 VH(I3Q) linked to 679 Vk via a peptide linker
CC   (enables the secreted polypeptide to dimerise into a diabody, forming 2
CC   sites for HSG); a pelB leader signal peptide (facilitates transport of
CC   the polypeptide into the periplasmic space of Escherichia coli); and 6
CC   His residues (allows purification by IMAC). The 679 diabody was expressed
CC   in E. coli at a level of 10 ug/l of culture, compared with 1 ug/l for the
CC   non-mutant polypeptide. The invention provides a bispecific diabody
CC   comprising an HSG binding site and a carcinoembryonic antigen (CEA)
CC   binding site. The HSG antigen binding site may comprise the VH and Vk
CC   polypeptides of 679 MAb. These diabodies are produced via recombinant DNA
CC   technology and create a novel affinity enhancement system that shows
```

```
CC   specific affinity for HSG and CEA. They pre-target CEA positive tumours
CC   for subsequent specific delivery of therapeutic radioisotopes carried by
CC   HSG-carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 261 AA;

  Query Match            100.0%;  Score 90;  DB 6;  Length 261;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 15
ABR42754
ID   ABR42754 standard; protein; 261 AA.
XX
AC   ABR42754;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-scFv-L5.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-scFv-15;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .261
FT                   /label= hMN-14-scFv-L5
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .255
FT                   /label= hMN-14Vkappa
FT   Region          256. .261
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
DR   N-PSDB; ACC58721.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 31; Fig 11; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-scFv-L5, which was
CC   designed to form an hMN-14 diabody. The hMN-14-scFv-L5 polypeptide
CC   comprises the C-terminal end of anti-carcinoembryonic antigen (CEA)
CC   humanized monoclonal antibody hMN-14 VH linked to the N-terminal part of
CC   hMN-14 Vkappa by a peptide linker that enables the secreted polypeptide
CC   to dimerize into a diabody, forming 2 binding sites for CEA. The
CC   polypeptide also includes a pelB signal peptide, which precedes the VH
CC   moiety to facilitate synthesis of the polypeptide in the periplasmic
CC   space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. In the claimed monospecific diabody, each scFv comprises
CC   the present sequence. The diabody is an example of claimed multivalent
CC   binding proteins specific for a tumour-associated antigen. The binding
CC   proteins are used in the diagnosis and treatment of a tumour, carcinoma,
CC   melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma or myeloma,
CC   or a cancer selected from acute lymphoblastic leukaemia, acute
CC   myelogenous leukaemia, biliary, breast, cervical, chronic lymphocytic
CC   leukaemia, chronic myelogenous leukaemia, colorectal, endometrial,
CC   oesophageal, gastric, head and neck, Hodgkin's lymphoma, lung, medullary
CC   thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic, prostate and
CC   bladder
XX
SQ   Sequence 261 AA;

  Query Match            100.0%;  Score 90;  DB 6;  Length 261;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 16
ABR83645
ID   ABR83645 standard; protein; 261 AA.
XX
AC   ABR83645;
XX
DT   16-OCT-2003  (first entry)
XX
DE   hMN14-scFv-L5 amino acid sequence.
XX
KW   Multispecific binding protein; multivalent; target antigen; cytostatic;
KW   immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW   immunotherapy; autoimmune disease; infectious disease;
KW   cardiovascular disease; inflammatory disease.
XX
OS   Escherichia coli.
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003057829-A2.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-US038985.
XX
PR   26-DEC-2001; 2001US-0342103P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg D;
XX
DR   WPI; 2003-607997/57.
DR   N-PSDB; ACF57430.
XX
PT   Novel multivalent, multi-specific binding protein useful for treating
PT   cancer, has first binding site having affinity towards hapten group and
PT   second and third binding sites each having affinity towards target
PT   antigen.
XX
```

```
PS   Claim 11; Fig 6; 43pp; English.
XX
CC   The present invention describes a multivalent, multi-specific binding
CC   protein (I) comprising a first binding site having an affinity towards a
CC   hapten group and a second and a third binding sites each having affinity
CC   towards a target antigen, which may be the same or a different target
CC   antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC   and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC   useful for delivering a diagnostic agent, a therapeutic agent, or its
CC   combination to a target, which involves administering (I) to a subject,
CC   waiting for a sufficient amount of time for an amount of the non-binding
CC   protein to clear the subject's blood stream, and administering to the
CC   subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC   agent, or its combination, that binds to a binding site of the binding
CC   protein. (I) is also useful for detecting or treating a human disorder,
CC   preferably cancer, autoimmune diseases, infectious diseases,
CC   cardiovascular diseases and inflammatory diseases. The present sequence
CC   represents a hMN14-scFv-L5 amino acid sequence, which is used in the
CC   exemplification of the present invention
XX
SQ   Sequence 261 AA;

  Query Match             100.0%;  Score 90;  DB 6;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 17
ABR42292
ID   ABR42292 standard; protein; 267 AA.
XX
AC   ABR42292;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .267
FT                   /label= BSI_polypeptide#1
FT   Region          24. .141
FT                   /label= hMN14_VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .259
FT                   /label= 679_Vk
FT   Region          262. .267
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57806.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 31; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of a
CC   novel bispecific diabody comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen. The bispecific diabody can be produced using
CC   recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC   a novel affinity enhancement system that shows specific affinity for HSG
CC   and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC   subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC   carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             100.0%;  Score 90;  DB 6;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 18
ABR42299
ID   ABR42299 standard; protein; 267 AA.
XX
AC   ABR42299;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS1.5H polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BS1.5H_polypeptide#2
FT   Region          24. .142
FT                   /label= hMN14_VH
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
```

```
FT                  /label= h679_Vk
FT   Region         257. .262
FT                  /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57813.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 38; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of novel
CC   bispecific diabody BS1.5H comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). A humanised version of its VH and Vk sequences
CC   have been used in BS1.5H. Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC   using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC   provides a novel affinity enhancement system that shows specific affinity
CC   for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC   tumours for subsequent specific delivery of therapeutic radioisotopes
CC   carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC   disease, cardiovascular diseases and inflammatory diseases can be
CC   detected or treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             100.0%;  Score 90;  DB 6;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 19
ABR42296
ID   ABR42296 standard; protein; 267 AA.
XX
AC   ABR42296;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS2 polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .267
FT                   /label= BS2_polypeptide#2
FT   Region          24. .141
FT                   /label= hMN14-VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .259
FT                   /label= 679_Vk
FT   Region          262. .267
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57810.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 35; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of novel
CC   bispecific diabody BS2 comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC   using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC   provides a novel affinity enhancement system that shows specific affinity
CC   for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC   tumours for subsequent specific delivery of therapeutic radioisotopes
CC   carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC   disease, cardiovascular diseases and inflammatory diseases can be
CC   detected or treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             100.0%;  Score 90;  DB 6;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 20
ABR42294
ID   ABR42294 standard; protein; 267 AA.
XX
AC   ABR42294;
XX
DT   11-AUG-2003  (first entry)
XX
```

```
DE   Bispecific diabody BS1.5 polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .267
FT                   /label= BS1.5_polypeptide#2
FT   Region          24. .141
FT                   /label= hMN14_VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .259
FT                   /label= 679_Vk(I3Q)
FT   Region          261. .267
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57808.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 33; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of a
CC   novel bispecific diabody comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen. The bispecific diabody can be produced using
CC   recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC   a novel affinity enhancement system that shows specific affinity for HSG
CC   and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC   subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC   carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             100.0%;  Score 90;  DB 6;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 21
ADU26571
ID   ADU26571 standard; protein; 358 AA.
XX
AC   ADU26571;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric hBS14 polypeptide 2.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26573.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 2; SEQ ID NO 12; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
CC   activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC   site of inflammation (caused by infectious agent). (I) is useful in
CC   antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
```

```
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric hBS14 polypeptide 2 containing heavy and light chain variable
CC   regions.
XX
SQ   Sequence 358 AA;

  Query Match             100.0%;  Score 90;  DB 8;  Length 358;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db        164 EIHPDSSTINYAPSLKD 180


RESULT 22
ADU26561
ID   ADU26561 standard; protein; 363 AA.
XX
AC   ADU26561;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric BS14hp polypeptide 2.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .6
FT                   /note= "signal peptide"
FT   Protein         7. .363
FT                   /note= "mature protein"
FT   Region          30. .40
FT                   /note= "CDR1hMN14Vk"
FT   Region          56. .62
FT                   /note= "CDR2hMN14Vk"
FT   Region          95. .102
FT                   /note= "CDR3hMN14Vk"
FT   Region          114. .119
FT                   /note= "linker region"
FT   Region          150. .154
FT                   /note= "CDR1hMN14Vh"
FT   Region          169. .185
FT                   /note= "CDR2hMN14Vh"
FT   Region          218. .227
FT                   /note= "CDR3hMN14Vh"
FT   Region          238. .242
FT                   /note= "linker region"
FT   Region          266. .282
FT                   /note= "CDR1h679Vk"
FT   Region          298. .304
FT                   /note= "CDR2h679Vk"
FT   Region          337. .344
FT                   /note= "CDR3h679Vk"
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26569.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 1; SEQ ID NO 2; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
CC   activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC   site of inflammation (caused by infectious agent). (I) is useful in
CC   antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric BS14HP polypeptide 2 containing heavy and light chain variable
CC   regions. The encoded polypeptide is designated alpha-factor-hMN-14Vk-
CC   GGGGS-hMN-14Vh-LEGGGS-h679Vk-6-His where the hMN14 is from a humanized
CC   antibody that binds specifically to the carcinoembryonic antigen and the
CC   h679 is a monoclonal antibody that binds the tri-peptide moiety histamine
CC   -succinyl-glycyl (HSG).
XX
SQ   Sequence 363 AA;

  Query Match             100.0%;  Score 90;  DB 8;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db        169 EIHPDSSTINYAPSLKD 185


RESULT 23
ADU26570
ID   ADU26570 standard; protein; 364 AA.
XX
AC   ADU26570;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric hBS14 polypeptide 1.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
```

```
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26572.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 2; SEQ ID NO 11; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
CC   activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC   site of inflammation (caused by infectious agent). (I) is useful in
CC   antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric hBS14 polypeptide 1 containing heavy and light chain variable
CC   regions.
XX
SQ   Sequence 364 AA;

  Query Match             100.0%;  Score 90;  DB 8;  Length 364;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db        288 EIHPDSSTINYAPSLKD 304


RESULT 24
ADU26560
ID   ADU26560 standard; protein; 370 AA.
XX
AC   ADU26560;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric  BS14HP polypeptide 1.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .7
FT                   /note= "signal peptide"
FT   Protein         8. .370
FT                   /note= "mature protein"
FT   Region          38. .42
FT                   /note= "CDR1h679Vh"
FT   Region          57. .68
FT                   /note= "CDR2h679Vh"
FT   Region          106. .115
FT                   /note= "CDR3h679Vh"
FT   Region          127. .131
FT                   /note= "linker region"
FT   Region          155. .165
FT                   /note= "CDR1hMN14Vk"
FT   Region          181. .187
FT                   /note= "CDR2hMN14Vk"
FT   Region          220. .227
FT                   /note= "CDR3hMN14Vk"
FT   Region          239. .244
FT                   /note= "linker region"
FT   Region          275. .279
FT                   /note= "CDR1hMN14Vh"
FT   Region          294. .310
FT                   /note= "CDR2hMN14Vh"
FT   Region          343. .352
FT                   /note= "CDR3hMN14Vh"
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26568.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
```

PT bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT chains having immunoglobulin variable domains, to form complex having
PT three antigen binding sites.
XX
PS Example 1; SEQ ID NO 1; 148pp; English.
XX
CC The invention relates to a polyvalent protein complex (PPC) (I),
CC comprising a first and second polypeptide chains having immunoglobulin
CC variable domains, where the first and second polypeptide chains form a
CC complex having three antigen binding sites, and where each binding site
CC comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC useful in pretargeting method of treating or diagnosing, or treating and
CC diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC also useful for diagnosing a non-neoplastic disease or disorder where the
CC disease or disorder is caused by a fungus, a virus, a bacterium, a
CC mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC infarction, ischemic heart disease, atherosclerotic plaques, graft
CC rejection, Alzheimer's disease or inflammation caused by accretion of
CC activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC site of inflammation (caused by infectious agent). (I) is useful in
CC antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC molecule, and immunostaining technique. This sequence corresponds to the
CC chimeric BS14HP polypeptide 1 containing heavy and light chain variable
CC regions. The encoded polypeptide is designated alpha-factor-h679Vh-GGGGS-
CC hMN-14Vk-LEGGGS-hMN-14Vh-6-His where the hMN14 is from a humanized
CC antibody that binds specifically to the carcinoembryonic antigen and the
CC h679 is a monoclonal antibody that binds the tri-peptide moiety histamine
CC -succinyl-glycyl (HSG).
XX
SQ Sequence 370 AA;

Query Match 100.0%; Score 90; DB 8; Length 370;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||||||||||||||||||
Db 294 EIHPDSSTINYAPSLKD 310

RESULT 25
ABR83648
ID ABR83648 standard; protein; 415 AA.
XX
AC ABR83648;
XX
DT 16-OCT-2003 (first entry)
XX
DE TS1 VH chain amino acid sequence.
XX
KW Multispecific binding protein; multivalent; target antigen; cytostatic;
KW immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW immunotherapy; autoimmune disease; infectious disease;
KW cardiovascular disease; inflammatory disease.
XX
OS Escherichia coli.
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003057829-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US038985.
XX
PR 26-DEC-2001; 2001US-0342103P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg D;
XX
DR WPI; 2003-607997/57.
DR N-PSDB; ACF57433.
XX
PT Novel multivalent, multi-specific binding protein useful for treating
PT cancer, has first binding site having affinity towards hapten group and
PT second and third binding sites each having affinity towards target
PT antigen.
XX
PS Claim 48; Fig 8A-B; 43pp; English.
XX
CC The present invention describes a multivalent, multi-specific binding
CC protein (I) comprising a first binding site having an affinity towards a
CC hapten group and a second and a third binding sites each having affinity
CC towards a target antigen, which may be the same or a different target
CC antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC useful for delivering a diagnostic agent, a therapeutic agent, or its
CC combination to a target, which involves administering (I) to a subject,
CC waiting for a sufficient amount of time for an amount of the non-binding
CC protein to clear the subject's blood stream, and administering to the
CC subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC agent, or its combination, that binds to a binding site of the binding
CC protein. (I) is also useful for detecting or treating a human disorder,
CC preferably cancer, autoimmune diseases, infectious diseases,
CC cardiovascular diseases and inflammatory diseases. The present sequence
CC represents the TS1 VH chain amino acid sequence, which is used in the
CC exemplification of the present invention
XX
SQ Sequence 415 AA;

Query Match 100.0%; Score 90; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||||||||||||||||||
Db 73 EIHPDSSTINYAPSLKD 89

RESULT 26
ABG76488
ID ABG76488 standard; protein; 443 AA.
XX
AC ABG76488;
XX
DT 13-MAY-2003 (first entry)
XX
DE Humanised anti-CEA antibody, hMN14.
XX
KW CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW human; zeta signalling chain; CD8alpha hinge; humanised antibody.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
PN US2002165360-A1.
XX
PD 07-NOV-2002.
XX
PF 10-DEC-2001; 2001US-00006771.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250090P.
XX
PA (JUNG/) JUNGHANS R P.
XX
PI Junghans RP;
XX
DR WPI; 2003-298705/29.
DR N-PSDB; ABX13168.

```
XX
PT   New chimeric molecule from humanized antibody against carcinoembryonic
PT   antigen and having signaling molecules of T cells and other effector
PT   cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS   Disclosure; Page 7-8; 20pp; English.
XX
CC   The invention relates to a chimaeric molecule comprising the
CC   carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC   as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC   chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC   which the cysteine residues have been mutated, with the IgTCR molecule
CC   occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC   appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC   NK (not defined) or other effector cells are useful in treating patients
CC   with cancers expressing the CEA antigen, together with other or with
CC   heterologous constructs to engage additional stimulatory and functional
CC   properties of the effector cells to enhance the anti-tumour therapeutic
CC   efficacy. The cancer disorder includes colorectal, breast and lung
CC   cancers. The present sequence represents the chimaeric molecule of the
CC   invention
XX
SQ   Sequence 443 AA;

  Query Match             100.0%;  Score 90;  DB 6;  Length 443;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db        191 EIHPDSSTINYAPSLKD 207


RESULT 27
ABG74240
ID   ABG74240 standard; protein; 443 AA.
XX
AC   ABG74240;
XX
DT   23-OCT-2003  (revised)
DT   22-APR-2003  (first entry)
XX
DE   Chimaeric hMN14/T-cell receptor.
XX
KW   Retroviral vector; T-cell receptor; hMN14; antibody; IgTCR; receptor;
KW   cytostatic; dermatological; neuroprotective; immunostimulant; GD3;
KW   ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4; 3E11;
KW   prostate-specific membrane antigen; zeta signalling chain; human; cancer;
KW   melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer;
KW   mouse; CD8alpha hinge.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
XX
PN   US2002132983-A1.
XX
PD   19-SEP-2002.
XX
PF   10-DEC-2001; 2001US-00006773.
XX
PR   30-NOV-2000; 2000US-0250087P.
PR   30-NOV-2000; 2000US-0250089P.
XX
PA   (JUNG/) JUNGHANS R P.
XX
PI   Junghans RP;
XX
DR   WPI; 2003-208946/20.
DR   N-PSDB; ABX16565.
XX
PT   New chimeric molecule useful in treating patients with disorders, such as
PT   melanoma, neuroendocrine disorders, prostate and small cell lung cancer
PT   comprises GD3 and/or PSMA binding domains of antibody.
XX
PS   Disclosure; Page 7-8; 35pp; English.
XX
CC   The invention relates to a chimaeric molecule comprising the GD3
CC   (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC   variable gene sequences, or the PSMA (prostate-specific membrane antigen)
CC   binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC   sequences, the zeta signalling chain of the T cell receptor and an
CC   intervening CD8alpha hinge in which cysteine residues have been mutated.
CC   The chimaeric molecules expressed in T cells or NK cells or other
CC   effector cells are useful in treating patients with cancers expressing
CC   the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC   and/or together with each other or with heterologous constructs to engage
CC   additional stimulatory and functional properties of the effector cells to
CC   enhance the antitumour therapeutic efficacy (claimed). They are
CC   particularly useful in disorders including melanoma, neuroendocrine
CC   tumours and prostate and small cell lung cancer. The present sequence is
CC   a hMN14 antibody (specific to CEA antigen) in a fusion protein with the
CC   modified CD8alpha hinge and the T-cell receptor zeta chain (IgTCR)
CC   encoded by a retroviral vector. The hMN14 antibody coding region is
CC   replaced with the MB3.6, 3D8, 4D4 or 3E11 genes of the invention.
CC   (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ   Sequence 443 AA;

  Query Match             100.0%;  Score 90;  DB 6;  Length 443;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db        191 EIHPDSSTINYAPSLKD 207


RESULT 28
ADE64201
ID   ADE64201 standard; protein; 468 AA.
XX
AC   ADE64201;
XX
DT   29-JAN-2004  (first entry)
XX
DE   MN14HCF protein related to a novel antibody library.
XX
KW   antibody library; retroviral vector; antibody light chain;
KW   antibody heavy chain; human therapy; multiplicity of infection; MOI;
KW   plasmid; GATEWAY vector; MN14HCF.
XX
OS   Unidentified.
XX
PN   WO2003083077-A2.
XX
PD   09-OCT-2003.
XX
PF   28-MAR-2003; 2003WO-US009662.
XX
PR   28-MAR-2002; 2002US-0368808P.
PR   10-APR-2002; 2002US-0371299P.
PR   28-MAR-2003; 2003US-00371299.
XX
PA   (GALA-) GALA DESIGN INC.
XX
PI   Bremel RD,  Eakle K,  Imboden M;
XX
DR   WPI; 2003-804051/75.
DR   N-PSDB; ADE64206.
XX
PT   New antibody library comprising cells comprising at least one integrated
PT   retroviral vector expressing an antibody light or heavy chain, useful in
PT   preparing a composition for diagnosing or treating disorders.
XX
PS   Disclosure; Fig 6; 57pp; English.
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XX
CC   This invention relates to a new antibody library which comprises at least
CC   100 cells, each of which comprises at least one integrated retroviral
CC   vector expressing an antibody light or heavy chain. Antibodies are of
CC   increasing importance in human therapy, assay procedures and diagnostic
CC   methods and a need exists for efficient methods of generating and
CC   screening antibody libraries containing large numbers of antibodies. The
CC   antibody library of the invention addresses this need, with the
CC   additional advantage of strict control over multiplicity of infection
CC   (MOI), and is useful in preparing a composition for diagnosing or
CC   treating a wide variety of disorders. The present sequence is the amino
CC   acid sequence of the MN14HCF protein, which was encoded by the Gateway
CC   retroviral vectors used in the exemplification of the invention.
XX
SQ   Sequence 468 AA;

  Query Match             100.0%;  Score 90;  DB 7;  Length 468;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         69 EIHPDSSTINYAPSLKD 85


RESULT 29
ADF60815
ID   ADF60815 standard; protein; 468 AA.
XX
AC   ADF60815;
XX
DT   12-FEB-2004  (first entry)
XX
DE   hMN-14 heavy chain amino acid sequence.
XX
KW   Immunomodulatory; antidiabetic; immunosuppressive; cardiovascular;
KW   neuroprotective; nootropic; fungicide; virucide; antimalarial;
KW   antihelmintic; antiparasitic; haemostatic; muscular; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; cytostatic; mutant;
KW   bispecific antibody; immunoglobulin G; IgG; scFvs; Fvs; CH2 domain;
KW   immune; autoimmune; disease; organ graft rejection; cardiovascular;
KW   neurological; Alzheimer's disease; graft vs host disease;
KW   systemic lupus erythematosus; diabetes mellitus.
XX
OS   Homo sapiens.
XX
PN   WO2003074569-A2.
XX
PD   12-SEP-2003.
XX
PF   03-MAR-2003; 2003WO-GB000871.
XX
PR   01-MAR-2002; 2002US-0361037P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (MCCA/) MCCALL J D.
XX
PI   Qu Z,  Hansen H,  Goldenberg DM;
XX
DR   WPI; 2003-902725/82.
DR   N-PSDB; ADF60814.
XX
PT   Mutant bispecific antibody which is rapidly cleared from a patient's
PT   body, useful as a pretargeting agent in methods for diagnosing or
PT   treating diseases, such as autoimmune disease, and disease caused by
PT   infectious agents.
XX
PS   Example; Fig 1; 68pp; English.
XX
CC   The invention relates to a mutant bispecific antibody (mbAb1) comprising
CC   at least a human hinge constant region from immunoglobulin G (IgG), two
CC   single chain variable fragments (scFvs), and two variable fragments
CC   (Fvs), where the constant region contains one or more amino acid
CC   mutations in the heavy chain 2 (CH2) domain. The methods and antibody of
CC   the invention are used to diagnose or treat an immune dysregulation
CC   disease, an autoimmune disease, organ graft rejection, cardiovascular
CC   disease, neurological disease (Alzheimer's disease) or graft vs. host
CC   disease. The methods are also useful for treating a disease caused by a
CC   fungus, virus, parasite, or bacterium. The methods may also be used for
CC   intraoperative or endoscopic diagnosis to identify diseased tissue. The
CC   autoimmune diseases that may be diagnosed or treated include acute or
CC   chronic idiopathic thrombocytopenic purpura, dermatomyositis, Sydenham's
CC   chorea, myasthenia gravis, systemic lupus erythematosus, lupus nephritis,
CC   rheumatic fever, polyglandular syndromes and diabetes mellitus. The
CC   current sequence represents the hMN-14 heavy chain amino acid sequence.
XX
SQ   Sequence 468 AA;

  Query Match             100.0%;  Score 90;  DB 7;  Length 468;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         69 EIHPDSSTINYAPSLKD 85


RESULT 30
ADY97271
ID   ADY97271 standard; protein; 669 AA.
XX
AC   ADY97271;
XX
DT   16-JUN-2005  (first entry)
XX
DE   Exemplary antibody fusion protein SEQ ID NO:3.
XX
KW   antibody engineering; fusion protein; cytostatic; antimicrobial;
KW   virucide; antibacterial; cancer; infection.
XX
OS   Synthetic.
XX
PN   US2005069552-A1.
XX
PD   31-MAR-2005.
XX
PF   28-JUL-2004; 2004US-00900928.
XX
PR   28-JUL-2003; 2003US-0490569P.
XX
PA   (BLEC/) BLECK G T.
PA   (YORK/) YORK D.
PA   (COLL/) COLLINS I.
XX
PI   Bleck GT,  York D,  Collins I;
XX
DR   WPI; 2005-261600/27.
DR   N-PSDB; ADY97269.
XX
PT   Composition useful as cancer vaccine, comprises polypeptide having
PT   antibody heavy chain fused to antibody light chain, or multivalent
PT   antibody having two polypeptides with antibody heavy chain fused to
PT   antibody light chain.
XX
PS   Disclosure; SEQ ID NO 3; 101pp; English.
XX
CC   The invention describes a composition (I) comprising: (a) a polypeptide
CC   comprising at least one antibody heavy chain fused to at least one
CC   antibody light chain; or (b) a multivalent antibody comprising at least
CC   two polypeptides, where each of the polypeptides comprises at least one
CC   antibody heavy chain fused to at least one antibody light chain. Also
CC   described: (1) a composition (II) comprising a nucleic acid comprising at
CC   least one antibody heavy chain gene and at least one antibody light chain
CC   gene, where the nucleic acid encodes a polypeptide comprising at least
CC   one antibody heavy chain fused to at least one antibody light chain; (2)
CC   a method (M1) of binding an antigen, involves providing a polypeptide
```

CC comprising at least one antibody heavy chain fused to at least one
CC antibody light chain, and contacting the polypeptide with a sample having
CC an antigen under conditions such that the polypeptide binds to the
CC antigen; (3) a method (M2), which involves providing a vector comprising
CC a bicistronic expression construct comprising genes encoding an antibody
CC heavy chain gene and an antibody light chain gene, and altering the
CC nucleic acid sequence of a splice acceptor sequence or a splice donor
CC sequence in the antibody light chain gene or the antibody heavy chain
CC gene under conditions such that splicing is prevented at the splice
CC acceptor sequence or donor sequence; (4) a nucleic acid sequence produced
CC by (M2); (5) a vector (III) comprising a modified antibody heavy or light
CC gene, where modification eliminates a splice donor or acceptor sequence
CC in antibody heavy or light chain gene; and (6) a host cell comprising
CC (III). (I) is useful in in vitro binding assays for identifying antigens
CC in a mixture or determining the presence or absence of expression of a
CC particular protein. (I) is also useful as vaccine for treating cancer and
CC infections caused by pathogens e.g. virus or bacteria. The present
CC sequence represents an exemplary antibody fusion protein from the present
CC invention.
XX
SQ Sequence 669 AA;

Query Match 100.0%; Score 90; DB 9; Length 669;
Best Local Similarity 100.0%; Pred. No. 7.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
|||||||||||||||||
Db 50 EIHPDSSTINYAPSLKD 66

RESULT 31
ADU87733
ID ADU87733 standard; protein; 119 AA.
XX
AC ADU87733;
XX
DT 10-FEB-2005 (first entry)
XX
DE Heavy chain variable region of humanized Luc63.
XX
KW Antibody; CS1; SLAM family member 7; SLAMF7; immunoglobulin;
KW pharmaceutical; antibody-dependent cellular cytotoxicity;
KW FcgammaR receptor; cell proliferation; leukocyte; cancer;
KW multiple myeloma; multiple myeloma-related bone disorder; plasmacytoma;
KW macroglobulinemia; amyloidosis; chronic lymphocytic leukemia;
KW autoimmune disease; inflammatory bowel disease;
KW systemic lupus erythematosus; cytostatic; immunosuppressive;
KW antiinflammatory; gastrointestinal-gen.; dermatological; luc63;
KW heavy chain variable region; humanized antibody.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004100898-A2.
XX
PD 25-NOV-2004.
XX
PF 10-MAY-2004; 2004WO-US014866.
XX
PR 08-MAY-2003; 2003US-0469211P.
PR 29-MAR-2004; 2004US-0557620P.
PR 29-MAR-2004; 2004US-0557621P.
PR 29-MAR-2004; 2004US-0557622P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Williams M, Tso YJ, Landolfi NF;
XX
DR WPI; 2004-821790/81.
XX
PT New anti-CS1 antibodies, useful for diagnosing, preventing or treating
PT cancer, myeloma, autoimmune disorder, inflammatory bowel disease, or
PT systemic lupus erythematosus.
XX
PS Example 5; SEQ ID NO 47; 151pp; English.
XX
CC The invention relates to an antibody or its antigen-binding fragment,
CC which binds to CS1 (also known as SLAM family member 7, SLAMF7) and
CC inhibits immunoglobulin secretion, where the antibody binds to
CC substantially the same epitope as an antibody comprising an amino acid
CC sequence of any one of SEQ ID NOS: 3-26, the antibody comprises an amino
CC acid sequence of SEQ ID NOS: 27-44, and where the heavy chain variable
CC region comprises a complementarity determining region (CDR) of SEQ ID NO:
CC 33. Also disclosed are (i) a heavy chain CDR of an antibody comprising an
CC amino acid sequence of SEQ ID NOS: 9-11, 15-17, 21-23, 29-33, (ii) a
CC light chain CDR of an antibody comprising an amino acid sequence of SEQ
CC ID NOS: 12-14, 18-20, 24-26, 34-370, (iii) a pharmaceutical composition
CC comprising a pharmaceutical carrier and the antibody described above,
CC (iv) a method of inhibiting proliferation of CS1 expressing cells, (v)
CC inhibiting immunoglobulin secretion, and (vi) increasing antibody-
CC dependent cellular cytotoxicity (ADCC) activity of the antibody described
CC above, where the antibody has decreased levels of fucose or is mutated to
CC increase antibody affinity for a FcgammaR receptor. The antibody of the
CC invention inhibits the proliferation of leukocytes or cancer cells. The
CC antibody triggers cytotoxic effects on cells expressing CS1 or enhances
CC cytotoxicity mediated by immune cells, or triggers ADCC-mediated
CC cytotoxicity of cells expressing CS1. The antibody binds to substantially
CC the same epitope as the antibody produced by a hybridoma cell line having
CC ATCC accession number PTA-5091 or a Luc63 antibody. The antibody is
CC produced by a hybridoma cell line having ATCC accession number PTA-5091
CC or by a hybridoma cell line expressing Luc63 antibody. The antibody is a
CC monoclonal antibody, e.g. a chimeric antibody, a humanized antibody, or a
CC fully human antibody. The antibody is conjugated with a cytotoxic agent.
CC The antibody comprises a heavy chain variable region comprising amino
CC acid sequences of SEQ ID NOS: 3, 5, 7, or 27, and a light chain variable
CC region comprising amino acid sequences of SEQ ID NOS: 4, 6, 8, or 28. The
CC antibody, compositions, and methods are useful for diagnosing, preventing
CC or treating plasma cell cancer, e.g. myeloma, multiple myeloma, myeloma
CC of bone, extramedullary plasmacytoma, macroglobulinemia (including
CC Waldenstrom's macroglobulinemia), heavy-chain disease, primary
CC amyloidosis or monoclonal gammopathy of unknown significance, non-plasma
CC cell cancer (chronic lymphocytic leukemia), autoimmune disorder,
CC inflammatory bowel disease (IBD), or systemic lupus erythematosus (SLE).
CC This sequence represents humanized mouse Luc63 heavy chain variable
CC region (HuLuc63 VH).
XX
SQ Sequence 119 AA;

Query Match 92.2%; Score 83; DB 8; Length 119;
Best Local Similarity 94.1%; Pred. No. 1.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:||||||||||||||
Db 50 EINPDSSTINYAPSLKD 66

RESULT 32
ADU87727
ID ADU87727 standard; protein; 119 AA.
XX
AC ADU87727;
XX
DT 10-FEB-2005 (first entry)
XX
DE Humanized Luc63 heavy chain variable region.
XX
KW Antibody; CS1; SLAM family member 7; SLAMF7; immunoglobulin;
KW pharmaceutical; antibody-dependent cellular cytotoxicity;
KW FcgammaR receptor; cell proliferation; leukocyte; cancer;
KW multiple myeloma; multiple myeloma-related bone disorder; plasmacytoma;
KW macroglobulinemia; amyloidosis; chronic lymphocytic leukemia;
KW autoimmune disease; inflammatory bowel disease;
KW systemic lupus erythematosus; cytostatic; immunosuppressive;

KW antiinflammatory; gastrointestinal-gen.; dermatological; luc63;
KW heavy chain variable region; humanized antibody.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004100898-A2.
XX
PD 25-NOV-2004.
XX
PF 10-MAY-2004; 2004WO-US014866.
XX
PR 08-MAY-2003; 2003US-0469211P.
PR 29-MAR-2004; 2004US-0557620P.
PR 29-MAR-2004; 2004US-0557621P.
PR 29-MAR-2004; 2004US-0557622P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Williams M, Tso YJ, Landolfi NF;
XX
DR WPI; 2004-821790/81.
XX
PT New anti-CS1 antibodies, useful for diagnosing, preventing or treating
PT cancer, myeloma, autoimmune disorder, inflammatory bowel disease, or
PT systemic lupus erythematosus.
XX
PS Claim 19; SEQ ID NO 41; 151pp; English.
XX
CC The invention relates to an antibody or its antigen-binding fragment,
CC which binds to CS1 (also known as SLAM family member 7, SLAMF7) and
CC inhibits immunoglobulin secretion, where the antibody binds to
CC substantially the same epitope as an antibody comprising an amino acid
CC sequence of any one of SEQ ID NOS: 3-26, the antibody comprises an amino
CC acid sequence of SEQ ID NOS: 27-44, and where the heavy chain variable
CC region comprises a complementarity determining region (CDR) of SEQ ID NO:
CC 33. Also disclosed are (i) a heavy chain CDR of an antibody comprising an
CC amino acid sequence of SEQ ID NOS: 9-11, 15-17, 21-23, 29-33, (ii) a
CC light chain CDR of an antibody comprising an amino acid sequence of SEQ
CC ID NOS: 12-14, 18-20, 24-26, 34-370, (iii) a pharmaceutical composition
CC comprising a pharmaceutical carrier and the antibody described above,
CC (iv) a method of inhibiting proliferation of CS1 expressing cells, (v)
CC inhibiting immunoglobulin secretion, and (vi) increasing antibody-
CC dependent cellular cytotoxicity (ADCC) activity of the antibody described
CC above, where the antibody has decreased levels of fucose or is mutated to
CC increase antibody affinity for a FcgammaR receptor. The antibody of the
CC invention inhibits the proliferation of leukocytes or cancer cells. The
CC antibody triggers cytotoxic effects on cells expressing CS1 or enhances
CC cytotoxicity mediated by immune cells, or triggers ADCC-mediated
CC cytotoxicity of cells expressing CS1. The antibody binds to substantially
CC the same epitope as the antibody produced by a hybridoma cell line having
CC ATCC accession number PTA-5091 or a Luc63 antibody. The antibody is
CC produced by a hybridoma cell line having ATCC accession number PTA-5091
CC or by a hybridoma cell line expressing Luc63 antibody. The antibody is a
CC monoclonal antibody, e.g. a chimeric antibody, a humanized antibody, or a
CC fully human antibody. The antibody is conjugated with a cytotoxic agent.
CC The antibody comprises a heavy chain variable region comprising amino
CC acid sequences of SEQ ID NOS: 3, 5, 7, or 27, and a light chain variable
CC region comprising amino acid sequences of SEQ ID NOS: 4, 6, 8, or 28. The
CC antibody, compositions, and methods are useful for diagnosing, preventing
CC or treating plasma cell cancer, e.g. myeloma, multiple myeloma, myeloma
CC of bone, extramedullary plasmacytoma, macroglobulinemia (including
CC Waldenstrom's macroglobulinemia), heavy-chain disease, primary
CC amyloidosis or monoclonal gammopathy of unknown significance, non-plasma
CC cell cancer (chronic lymphocytic leukemia), autoimmune disorder,
CC inflammatory bowel disease (IBD), or systemic lupus erythematosus (SLE).
CC This sequence represents humanized mouse Luc63 heavy chain variable
CC region (HuLuc63 VH).
XX
SQ Sequence 119 AA;

Query Match 92.2%; Score 83; DB 8; Length 119;
Best Local Similarity 94.1%; Pred. No. 1.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:|||||||||||||||
Db 50 EINPDSSTINYAPSLKD 66

RESULT 33
AAR52046
ID AAR52046 standard; protein; 109 AA.
XX
AC AAR52046;
XX
DT 27-SEP-1996 (first entry)
XX
DE Heavy chain variable region of murine antibody 2fbj.
XX
KW antibody; humanised; murine; human; heavy chain; light; variable;
KW framework region; complementarity determining region; reshaping;
KW modelling; surface residue; modify.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Region 1. .30
FT /label= framework_region_1
FT /note= "FR 1"
FT Region 31. .35
FT /label= complementarity_determining_region_1
FT /note= "CDR 1"
FT Region 36. .49
FT /label= FR_2
FT Region 50. .59
FT /label= CDR_2
FT Region 60. .98
FT /label= FR_3
FT Region 99. .107
FT /label= CDR_3
XX
PN EP592106-A1.
XX
PD 13-APR-1994.
XX
PF 07-SEP-1993; 93EP-00307051.
XX
PR 09-SEP-1992; 92US-00942245.
XX
PA (IMMU-) IMMUNOGEN INC.
XX
PI Pedersen JT, Searle SMJ, Rees AR, Roguska MA, Guild BC;
XX
DR WPI; 1994-120230/15.
XX
PT Method of resurfacing of rodent antibodies to produce humanised antibody
PT forms - for producing non human antibodies with improved therapeutic
PT efficiency by presenting human surface on V-region.
XX
PS Example 1; Fig 3B; 230pp; English.
XX
CC The present sequence is that of the heavy chain variable (LC VR) region
CC of murine antibody 2fbj. This sequence was aligned with 11 other known
CC antibody LC VRs and a set of framework positions of surface exposed amino
CC acid residues was determined. This information can be used in a method to
CC determine how to modify a rodent antibody or fragment by resurfacing in
CC order to produce a humanised rodent antibody. Residues (determined from
CC alignment) at positions 118, 120, 122, 126, 127, 128, 130, 131, 132, 136,
CC 143, 145, 160, 161, 162, 183, 184, 186, 187, 195, 196, 197, 208, 209,
CC 210, 212 (numbered from the N-terminal of the complete heavy chain) are
CC accessible residues. None of the entire combinations of surface residues
CC in the murine sequences were found in the human sequences and vice versa.
CC However the residues in individual positions appear to be conserved
XX

```
SQ   Sequence 109 AA;

  Query Match             91.1%;  Score 82;  DB 2;  Length 109;
  Best Local Similarity   88.2%;  Pred. No. 2e-05;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||| |||| |||||
Db         50 EIHPDSGTINYTPSLKD 66


RESULT 34
ADU86552
ID   ADU86552 standard; protein; 220 AA.
XX
AC   ADU86552;
XX
DT   10-FEB-2005  (first entry)
XX
DE   Immunoglobulin variable domain protein seqid 41.
XX
KW   antiinflammatory; antibacterial; virucide; cytostatic; antipsoriatic;
KW   antidiabetic; vasotropic; vaccine; protein purification; protein folding;
KW   diagnosis; inflammation; immune disorder; allergic hypersensitivity;
KW   infection; autoimmune disease; asthma; psoriasis;
KW   insulin dependent diabetes; multiple sclerosis; rheumatoid arthritis;
KW   systemic lupus erythematosus; myasthenia gravis; hematological disease;
KW   neoplasm; immunoglobulin; variable region.
XX
OS   Homo sapiens.
XX
PN   WO2004101790-A1.
XX
PD   25-NOV-2004.
XX
PF   14-MAY-2004; 2004WO-GB002102.
XX
PR   14-MAY-2003; 2003US-0470340P.
PR   17-MAR-2004; 2004US-0554021P.
XX
PA   (DOMA-) DOMANTIS LTD.
XX
PI   Jespers LS,  Jones PC,  Famm KHJ,  Winter GP;
XX
DR   WPI; 2004-821888/81.
XX
PT   Recovering a polypeptide that unfolds reversibly from a repertoire of
PT   polypeptides for treating e.g., cancer, by unfolding a portion of the
PT   displayed polypeptides and refolding a portion of the unfolded
PT   polypeptides.
XX
PS   Disclosure; SEQ ID NO 41; 222pp; English.
XX
CC   The invention describes a method of recovering a polypeptide that unfolds
CC   reversibly from a repertoire of polypeptides that unfolds reversibly and
CC   has a common selectable characteristic that distinguishes folded
CC   polypeptides from unfolded or misfolded polypeptides. The method
CC   comprises: providing a polypeptide display system comprising the
CC   repertoire of displayed polypeptides; unfolding at least a portion of the
CC   displayed polypeptides; refolding at least a portion of the unfolded
CC   polypeptides; and recovering at least one polypeptide that unfolds
CC   reversibly and has the selectable characteristic from the refolded
CC   portion. The method is useful in recovering a polypeptide that unfolds
CC   reversibly from a repertoire of polypeptides that unfolds reversibly. The
CC   library or repertoire is useful for selecting a polypeptide comprising an
CC   antibody variable domain that unfolds reversibly or a polypeptide that
CC   refolds reversibly and comprising an antibody format. The polypeptide is
CC   useful in the manufacture of a medicament for diagnosing, treating or
CC   preventing a disease or medical condition mediated by a cytokine,
CC   cytokine receptor, enzyme, enzyme co-factor or DNA binding protein, such
CC   as an inflammatory state, allergic hypersensitivity, cancer, bacterial or
CC   viral infection or an autoimmune disorder, e.g., asthma, psoriasis, Type
CC   I diabetes, multiple sclerosis, rheumatoid arthritis, systemic lupus
CC   erythematosus, Crohn's disease, myasthenia gravis, leukemia or solid
CC   tumor. This is the amino acid sequence of an immunoglobulin variable
CC   region associated with the protein purification method of the invention.
XX
SQ   Sequence 220 AA;

  Query Match             91.1%;  Score 82;  DB 8;  Length 220;
  Best Local Similarity   88.2%;  Pred. No. 4.5e-05;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||| |||| |||||
Db         50 EIHPDSGTINYTPSLKD 66


RESULT 35
ADD94143
ID   ADD94143 standard; peptide; 17 AA.
XX
AC   ADD94143;
XX
DT   29-JAN-2004  (first entry)
XX
DE   Mouse HUIV26 heavy chain CDR2 partial amino acid sequence SeqID28.
XX
KW   grafted antibody; complementarity determining region; CDR; light CDR;
KW   heavy CDR; cryptic collagen epitope; solid tumour;
KW   new blood vessel growth; angiogenesis; tumour growth; cytostatic;
KW   collagen agonist; collagen antagonist; cancer metastasis;
KW   anti-cryptic collagen; antibody; HUIV26; variable region heavy chain;
KW   mouse; murine.
XX
OS   Mus musculus.
XX
PN   WO2003046204-A2.
XX
PD   05-JUN-2003.
XX
PF   26-NOV-2002; 2002WO-US038147.
XX
PR   26-NOV-2001; 2001US-00995529.
PR   06-DEC-2001; 2001US-00011250.
XX
PA   (CELL-) CELL MATRIX INC.
XX
PI   Watking JD,  Huse WD,  Tang Y,  Broek D,  Brooks PC;
XX
DR   WPI; 2003-513649/48.
DR   N-PSDB; ADD94142.
XX
PT   New cryptic collagen antibody with one or more complementarity
PT   determining regions, useful for diagnosing and treating disorders
PT   associated with angiogenesis, tumor growth and/or cancer metastasis.
XX
PS   Claim 1; SEQ ID NO 28; 232pp; English.
XX
CC   This invention relates to a novel grafted antibody or its functional
CC   fragment comprising one or more complementarity determining regions
CC   (CDRs) of a defined light CDR and a heavy CDR with at least one amino
CC   acid (aa) substitution where the antibody has specific binding activity
CC   for a cryptic collagen epitope. The growth of all solid tumours requires
CC   new blood vessel growth, angiogenesis, inhibition of which is an approach
CC   to limiting tumour growth. The invention may allow development of
CC   therapeutics with a cytostatic activity as a collagen agonist or
CC   antagonist. The invention is useful for diagnosing and treating disorders
CC   associated with angiogenesis, tumour growth and/or cancer metastasis. The
CC   present sequence is the partial amino acid sequence of a mouse anti-
CC   cryptic collagen site antibody HUIV26 variable region heavy chain CDR
CC   which is related to the invention.
XX
SQ   Sequence 17 AA;

  Query Match             87.8%;  Score 79;  DB 7;  Length 17;
```

```
  Best Local Similarity   88.2%;  Pred. No. 7.7e-06;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db          1 EINPDSSTINYTPSLKD 17


RESULT 36
ADL27483
ID   ADL27483 standard; peptide; 17 AA.
XX
AC   ADL27483;
XX
DT   20-MAY-2004  (first entry)
XX
DE   CDR from the heavy chain of antibody EGP16D8-1-2.
XX
KW   glycoprotein; EGP6D8-1-1; EGP13F6-1-2; EGP13C6-1-1;
KW   Ebola virus infection; antibody; heavy chain;
KW   Complementarity determining region; CDR.
XX
OS   Mus sp.
XX
PN   WO2004018649-A2.
XX
PD   04-MAR-2004.
XX
PF   21-AUG-2003; 2003WO-US027450.
XX
PR   23-AUG-2002; 2002US-00226795.
XX
PA   (USSA ) US ARMY MEDICAL RES INST INFECTIOUS DISE.
XX
PI   Hart MK,  Wilson JA;
XX
DR   WPI; 2004-226835/21.
XX
PT   New isolated monoclonal antibody that binds Ebola virus GP, which
PT   monoclonal antibody comprises a heavy chain variable region, useful for
PT   treating or ameliorating Ebola virus infection.
XX
PS   Claim 31; Page 64; 68pp; English.
XX
CC   The specification describes monoclonal antibodies that bind Ebola virus
CC   glycoprotein. The antibodies are EGP6D8-1-1, EGP13F6-1-2, and EGP13C6-1-
CC   1. The monoclonal antibodies of the invention are useful for treating or
CC   ameliorating an Ebola virus infection. The antibodies were found to be
CC   effective when administered 2 days after challenge, after significant
CC   viral replication had occurred. ADL27482-ADL27484 represents
CC   complementarity determining regions (CDRs) from the heavy chain of a
CC   monoclonal antibody of the invention.
XX
SQ   Sequence 17 AA;

  Query Match             87.8%;  Score 79;  DB 8;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 7.7e-06;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db          1 EINPDSSTINYTPSLKD 17


RESULT 37
ADR15148
ID   ADR15148 standard; peptide; 17 AA.
XX
AC   ADR15148;
XX
DT   21-OCT-2004  (first entry)
XX
DE   Mouse anti-protein C inhibitor antibody peptide #8.
XX
KW   anti-protein C inhibitor antibody; anti-PCI antibody;
KW   activated protein C; aPC; sepsis; disseminated intravascular coagulation;
KW   arterial thrombosis; protein C inhibitor; mouse; murine.
XX
OS   Mus musculus.
XX
PN   WO2004065418-A1.
XX
PD   05-AUG-2004.
XX
PF   20-JAN-2004; 2004WO-JP000429.
XX
PR   20-JAN-2003; 2003JP-00011529.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Koga T,  Kimura N,  Yoshino T,  Ono K;
XX
DR   WPI; 2004-593430/57.
XX
PT   New anti-protein C inhibitor (PCI) antibody, inhibiting PCI with respect
PT   to activation protein C (apc) activity, and apc production by
PT   thrombin/thrombomodulin composite, useful for treating sepsis, arterial
PT   thrombosis.
XX
PS   Disclosure; SEQ ID NO 29; 105pp; Japanese.
XX
CC   The invention comprises anti-protein C inhibitor (PCI) antibody. The anti
CC   -PCI antibody of the invention is useful for treating or preventing a
CC   disease which develops and/or progresses due to reduced activated protein
CC   C (aPC) activity. Such diseases include: sepsis, disseminated
CC   intravascular coagulation, and arterial thrombosis. The present amino
CC   acid sequence represents a mouse anti-protein C inhibitor antibody
CC   peptide.
XX
SQ   Sequence 17 AA;

  Query Match             87.8%;  Score 79;  DB 8;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 7.7e-06;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db          1 EINPDSSTINYTPSLKD 17


RESULT 38
ADU87717
ID   ADU87717 standard; peptide; 17 AA.
XX
AC   ADU87717;
XX
DT   10-FEB-2005  (first entry)
XX
DE   Anti-CS1 mouse Luc63 heavy chain variable region, CDR3.
XX
KW   Antibody; CS1; SLAM family member 7; SLAMF7; immunoglobulin;
KW   pharmaceutical; antibody-dependent cellular cytotoxicity;
KW   FcgammaR receptor; cell proliferation; leukocyte; cancer;
KW   multiple myeloma; multiple myeloma-related bone disorder; plasmacytoma;
KW   macroglobulinemia; amyloidosis; chronic lymphocytic leukemia;
KW   autoimmune disease; inflammatory bowel disease;
KW   systemic lupus erythematosus; cytostatic; immunosuppressive;
KW   antiinflammatory; gastrointestinal-gen.; dermatological; luc63;
KW   heavy chain variable region; complementarity determining region; CDR.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 12
FT                   /note= "Wild-type Thr mutated to Ala in the humanization
FT                   of the CS1 antibody"
```

XX
PN WO2004100898-A2.
XX
PD 25-NOV-2004.
XX
PF 10-MAY-2004; 2004WO-US014866.
XX
PR 08-MAY-2003; 2003US-0469211P.
PR 29-MAR-2004; 2004US-0557620P.
PR 29-MAR-2004; 2004US-0557621P.
PR 29-MAR-2004; 2004US-0557622P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Williams M, Tso YJ, Landolfi NF;
XX
DR WPI; 2004-821790/81.
XX
PT New anti-CS1 antibodies, useful for diagnosing, preventing or treating
PT cancer, myeloma, autoimmune disorder, inflammatory bowel disease, or
PT systemic lupus erythematosus.
XX
PS Claim 19; SEQ ID NO 31; 151pp; English.
XX
CC The invention relates to an antibody or its antigen-binding fragment,
CC which binds to CS1 (also known as SLAM family member 7, SLAMF7) and
CC inhibits immunoglobulin secretion, where the antibody binds to
CC substantially the same epitope as an antibody comprising an amino acid
CC sequence of any one of SEQ ID NOS: 3-26, the antibody comprises an amino
CC acid sequence of SEQ ID NOS: 27-44, and where the heavy chain variable
CC region comprises a complementarity determining region (CDR) of SEQ ID NO:
CC 33. Also disclosed are (i) a heavy chain CDR of an antibody comprising an
CC amino acid sequence of SEQ ID NOS: 9-11, 15-17, 21-23, 29-33, (ii) a
CC light chain CDR of an antibody comprising an amino acid sequence of SEQ
CC ID NOS: 12-14, 18-20, 24-26, 34-370, (iii) a pharmaceutical composition
CC comprising a pharmaceutical carrier and the antibody described above,
CC (iv) a method of inhibiting proliferation of CS1 expressing cells, (v)
CC inhibiting immunoglobulin secretion, and (vi) increasing antibody-
CC dependent cellular cytotoxicity (ADCC) activity of the antibody described
CC above, where the antibody has decreased levels of fucose or is mutated to
CC increase antibody affinity for a FcgammaR receptor. The antibody of the
CC invention inhibits the proliferation of leukocytes or cancer cells. The
CC antibody triggers cytotoxic effects on cells expressing CS1 or enhances
CC cytotoxicity mediated by immune cells, or triggers ADCC-mediated
CC cytotoxicity of cells expressing CS1. The antibody binds to substantially
CC the same epitope as the antibody produced by a hybridoma cell line having
CC ATCC accession number PTA-5091 or a Luc63 antibody. The antibody is
CC produced by a hybridoma cell line having ATCC accession number PTA-5091
CC or by a hybridoma cell line expressing Luc63 antibody. The antibody is a
CC monoclonal antibody, e.g. a chimeric antibody, a humanized antibody, or a
CC fully human antibody. The antibody is conjugated with a cytotoxic agent.
CC The antibody comprises a heavy chain variable region comprising amino
CC acid sequences of SEQ ID NOS: 3, 5, 7, or 27, and a light chain variable
CC region comprising amino acid sequences of SEQ ID NOS: 4, 6, 8, or 28. The
CC antibody, compositions, and methods are useful for diagnosing, preventing
CC or treating plasma cell cancer, e.g. myeloma, multiple myeloma, myeloma
CC of bone, extramedullary plasmacytoma, macroglobulinemia (including
CC Waldenstrom's macroglobulinemia), heavy-chain disease, primary
CC amyloidosis or monoclonal gammopathy of unknown significance, non-plasma
CC cell cancer (chronic lymphocytic leukemia), autoimmune disorder,
CC inflammatory bowel disease (IBD), or systemic lupus erythematosus (SLE).
CC This sequence represents a CDR from an anti-CS1 antibody.
XX
SQ Sequence 17 AA;

Query Match 87.8%; Score 79; DB 8; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:||||||| |||||
Db 1 EINPDSSTINYTPSLKD 17

RESULT 39
ADU87703
ID ADU87703 standard; peptide; 17 AA.
XX
AC ADU87703;
XX
DT 10-FEB-2005 (first entry)
XX
DE Mouse Luc63 heavy chain variable region, CDR2.
XX
KW Antibody; CS1; SLAM family member 7; SLAMF7; immunoglobulin;
KW pharmaceutical; antibody-dependent cellular cytotoxicity;
KW FcgammaR receptor; cell proliferation; leukocyte; cancer;
KW multiple myeloma; multiple myeloma-related bone disorder; plasmacytoma;
KW macroglobulinemia; amyloidosis; chronic lymphocytic leukemia;
KW autoimmune disease; inflammatory bowel disease;
KW systemic lupus erythematosus; cytostatic; immunosuppressive;
KW antiinflammatory; gastrointestinal-gen.; dermatological; luc90;
KW light chain variable region; complementarity determining region; CDR.
XX
OS Mus sp.
XX
PN WO2004100898-A2.
XX
PD 25-NOV-2004.
XX
PF 10-MAY-2004; 2004WO-US014866.
XX
PR 08-MAY-2003; 2003US-0469211P.
PR 29-MAR-2004; 2004US-0557620P.
PR 29-MAR-2004; 2004US-0557621P.
PR 29-MAR-2004; 2004US-0557622P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Williams M, Tso YJ, Landolfi NF;
XX
DR WPI; 2004-821790/81.
XX
PT New anti-CS1 antibodies, useful for diagnosing, preventing or treating
PT cancer, myeloma, autoimmune disorder, inflammatory bowel disease, or
PT systemic lupus erythematosus.
XX
PS Claim 12; SEQ ID NO 16; 151pp; English.
XX
CC The invention relates to an antibody or its antigen-binding fragment,
CC which binds to CS1 (also known as SLAM family member 7, SLAMF7) and
CC inhibits immunoglobulin secretion, where the antibody binds to
CC substantially the same epitope as an antibody comprising an amino acid
CC sequence of any one of SEQ ID NOS: 3-26, the antibody comprises an amino
CC acid sequence of SEQ ID NOS: 27-44, and where the heavy chain variable
CC region comprises a complementarity determining region (CDR) of SEQ ID NO:
CC 33. Also disclosed are (i) a heavy chain CDR of an antibody comprising an
CC amino acid sequence of SEQ ID NOS: 9-11, 15-17, 21-23, 29-33, (ii) a
CC light chain CDR of an antibody comprising an amino acid sequence of SEQ
CC ID NOS: 12-14, 18-20, 24-26, 34-370, (iii) a pharmaceutical composition
CC comprising a pharmaceutical carrier and the antibody described above,
CC (iv) a method of inhibiting proliferation of CS1 expressing cells, (v)
CC inhibiting immunoglobulin secretion, and (vi) increasing antibody-
CC dependent cellular cytotoxicity (ADCC) activity of the antibody described
CC above, where the antibody has decreased levels of fucose or is mutated to
CC increase antibody affinity for a FcgammaR receptor. The antibody of the
CC invention inhibits the proliferation of leukocytes or cancer cells. The
CC antibody triggers cytotoxic effects on cells expressing CS1 or enhances
CC cytotoxicity mediated by immune cells, or triggers ADCC-mediated
CC cytotoxicity of cells expressing CS1. The antibody binds to substantially
CC the same epitope as the antibody produced by a hybridoma cell line having
CC ATCC accession number PTA-5091 or a Luc63 antibody. The antibody is
CC produced by a hybridoma cell line having ATCC accession number PTA-5091
CC or by a hybridoma cell line expressing Luc63 antibody. The antibody is a
CC monoclonal antibody, e.g. a chimeric antibody, a humanized antibody, or a
CC fully human antibody. The antibody is conjugated with a cytotoxic agent.

CC The antibody comprises a heavy chain variable region comprising amino
CC acid sequences of SEQ ID NOS: 3, 5, 7, or 27, and a light chain variable
CC region comprising amino acid sequences of SEQ ID NOS: 4, 6, 8, or 28. The
CC antibody, compositions, and methods are useful for diagnosing, preventing
CC or treating plasma cell cancer, e.g. myeloma, multiple myeloma, myeloma
CC of bone, extramedullary plasmacytoma, macroglobulinemia (including
CC Waldenstrom's macroglobulinemia), heavy-chain disease, primary
CC amyloidosis or monoclonal gammopathy of unknown significance, non-plasma
CC cell cancer (chronic lymphocytic leukemia), autoimmune disorder,
CC inflammatory bowel disease (IBD), or systemic lupus erythematosus (SLE).
CC This sequence represents a CDR from a CS1 antibody.
XX
SQ Sequence 17 AA;

Query Match 87.8%; Score 79; DB 8; Length 17;
Best Local Similarity 88.2%; Pred. No. 7.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:|||||||| |||||
Db 1 EINPDSSTINYTPSLKD 17

RESULT 40
AAE06984
ID AAE06984 standard; protein; 98 AA.
XX
AC AAE06984;
XX
DT 16-OCT-2001 (first entry)
XX
DE Mouse germline heavy chain variable (VH) region, V-H_441/V441.
XX
KW Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
KW neuroprotective; immunosuppressive; human immunodeficiency virus;
KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
KW multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
KW fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS;
KW inflammatory glomerulopathy; vascular intervention;
KW neointimal hyperplasia; VH; heavy chain variable region.
XX
OS Mus sp.
XX
PN WO200157226-A1.
XX
PD 09-AUG-2001.
XX
PF 02-FEB-2001; 2001WO-US003537.
XX
PR 03-FEB-2000; 2000US-00497625.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Larosa GJ, Horvath C, Newman W, Jones ST, O'brien S, O'keefe T;
XX
DR WPI; 2001-488888/53.
XX
PT Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated
PT disorder in a patient, comprises a binding specificity for CCR2, and a
PT non-human antigen binding region and human immunoglobulin.
XX
PS Disclosure; Page 157; 183pp; English.
XX
CC The patent discloses a humanised antibody or its antigen-binding
CC fragment, having binding specificity for CC-chemokine receptor 2 (CCR2),
CC comprising an antigen binding region of non-human origin and at least a
CC portion of an immunoglobulin of human origin. The humanised antibodies
CC are useful for inhibiting the interaction of a cell expressing CCR2. They
CC are useful for inhibiting or treating HIV infection. The proteins of the
CC invention are useful for inhibiting leukocyte trafficking, for treating
CC CCR2-mediated disorders such as inflammatory disorder, autoimmune
CC disorders such as rheumatoid arthritis and multiple sclerosis,
CC atherogenesis and atherosclerosis, and for inhibiting restenosis. They
CC are useful in therapy or diagnosis, and in the manufacture of a
CC medicament for treating CCR-2 mediated disease. They are also useful for
CC treating allergy, anaphylaxis, malignancy, chronic and acute
CC inflammation, histamine and IgE- mediated allergic reaction, shock,
CC stenosis, allograft rejection, fibrotic disease, asthma, inflammatory
CC glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis
CC associated with vascular intervention, including angioplasty and/or stent
CC placement in a mammal. Humanised antibodies are also useful for
CC inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting
CC neointimal hyperplasia of a vessel in a mammal, preferably associated
CC with vascular intervention. The present sequence is mouse germline heavy
CC chain variable (VH) region, V-H_441/V441
XX
SQ Sequence 98 AA;

Query Match 87.8%; Score 79; DB 4; Length 98;
Best Local Similarity 88.2%; Pred. No. 5.6e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:|||||||| |||||
Db 50 EINPDSSTINYTPSLKD 66

RESULT 41
ADQ89269
ID ADQ89269 standard; protein; 98 AA.
XX
AC ADQ89269;
XX
DT 21-OCT-2004 (first entry)
XX
DE Mouse immunoglobulin protein #29.
XX
KW Mouse; immunoglobulin; heavy chain; light chain; CC-chemokine receptor 2;
KW CCR2; inflammatory disease; autoimmune disorder; graft rejection;
KW HIV infection; atherosclerosis; antiinflammatory; immunosuppressive;
KW anti-HIV; virucide; antiarteriosclerotic.
XX
OS Mus musculus.
XX
PN US2004151721-A1.
XX
PD 05-AUG-2004.
XX
PF 10-DEC-2003; 2003US-00733563.
XX
PR 19-OCT-2001; 2001US-0350166P.
PR 26-JUN-2002; 2002US-0392364P.
PR 17-OCT-2002; 2002US-00272899.
XX
PA (OKEE/) O'KEEFE T.
PA (PONA/) PONATH P.
XX
PI O'keefe T, Ponath P;
XX
DR WPI; 2004-580175/56.
XX
PT New humanized immunoglobulin CC-chemokine receptor 2 (CCR2) antagonists,
PT useful for diagnosing and/or treating inflammatory or autoimmune
PT diseases, and HIV infection.
XX
PS Example 2; SEQ ID NO 47; 128pp; English.
XX
CC The invention relates to humanised immunoglobulin heavy and light chains
CC which have specificity for the CC-chemokine receptor 2 (CCR2) and an
CC immunoglobulin or its antigen binding fragment comprising the chains. The
CC humanised immunoglobulin or its antigen binding fragment preferably
CC comprises two heavy chains and two light chains. The humanised
CC immunoglobulin and its heavy and light chains are useful for the
CC diagnosis, prevention and/or treatment of diseases or conditions

CC associated with aberrant expression or activity of the CCR2 polypeptide, CC such as inflammatory diseases, autoimmune disorders, graft rejection, HIV CC infection and atherosclerosis. This sequence represents a mouse CC immunoglobulin protein of the invention.
XX
SQ Sequence 98 AA;

Query Match 87.8%; Score 79; DB 8; Length 98;
Best Local Similarity 88.2%; Pred. No. 5.6e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:|||||||| |||||
Db 50 EINPDSSTINYTPSLKD 66

RESULT 42
AEB09542
ID AEB09542 standard; protein; 98 AA.
XX
AC AEB09542;
XX
DT 08-SEP-2005 (first entry)
XX
DE Murine germline heavy chain variable region SEQ ID NO 46.
XX
KW antiinflammatory; immunosuppressive; anti-HIV; antiarteriosclerotic;
KW antibody engineering; therapeutic; diagnosis; inflammation;
KW autoimmune disease; immune disorder; graft rejection; HIV infection;
KW infection; atherosclerosis; cardiovascular disease; metabolic disorder;
KW heavy chain variable region.
XX
OS Mus musculus.
XX
PN WO2005060368-A2.
XX
PD 07-JUL-2005.
XX
PF 10-DEC-2003; 2003WO-US039599.
XX
PR 10-DEC-2003; 2003WO-US039599.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Okeefe T, Ponath P;
XX
DR WPI; 2005-488561/49.
XX
PT New humanized immunoglobulin or its antigen binding portion having
PT binding specificity for CC-chemokine receptor 2 and having a heavy chain
PT and light chain, for treating inflammatory diseases, HIV, and autoimmune
PT diseases.
XX
PS Disclosure; SEQ ID NO 47; 192pp; English.
XX
CC The invention describes a humanized immunoglobulin (I) or its antigen
CC binding portion having binding specificity for CC-chemokine receptor 2
CC (CCR2) and having a heavy chain and a light chain, where the heavy chain
CC comprises a fully defined 117 and 330 amino acid (SEQ ID NO: 17 and 110)
CC sequence, given in specification or its portion, and the light chain
CC comprises a fully defined 112 amino acid (SEQ ID NO: 12) sequence given
CC in specification. Also described are: a humanized immunoglobulin heavy
CC chain, or its antigen binding fragment, having binding specificity for
CC CCR2 and comprising the amino acid sequence of (SEQ ID NO: 17) and the
CC amino acid of (SEQ ID NO: 110), or its portion; and a humanized
CC immunoglobulin light chain, or its antigen binding fragment, having
CC binding specificity for CCR2 and comprising the amino acid sequence of
CC (SEQ ID NO: 12) and the fully defined 107 amino acid (SEQ ID NO: 112)
CC sequence, given in specification. The following are disclosed: isolated
CC nucleic acid molecules comprising nucleic acid sequence encoding (I); a
CC construct comprising nucleic acid molecule encoding (I); and host cell
CC comprising the nucleic acid molecule. (I) Is useful as a therapeutic
CC agent for controlling lymphocyte homing the mucosal lymphoid tissue thus
CC reducing inflammatory response, for use in the treatment of diseases
CC associated with leukocyte infiltration of tissue, e.g. in the treatment
CC of inflammatory diseases, autoimmune diseases, graft rejection, HIV
CC infection and monocyte-mediated disorders such as atherosclerosis. (I) Is
CC useful for detecting and/or measuring the level of CCR2 in a sample (e.g.
CC tissues or body fluids such as inflammatory exudates, blood, serum, bowel
CC fluid), and for modulating binding function and/or leukocyte trafficking
CC modulated by CCR2. This sequence represents a murine germline heavy chain
CC variable region used in a comparison with a murine 1D9 antibody heavy
CC chain variable region fragment in the creation of a humanized anti-CCR2-
CC antibody.
XX
SQ Sequence 98 AA;

Query Match 87.8%; Score 79; DB 9; Length 98;
Best Local Similarity 88.2%; Pred. No. 5.6e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:|||||||| |||||
Db 50 EINPDSSTINYTPSLKD 66

RESULT 43
ADN41879
ID ADN41879 standard; protein; 113 AA.
XX
AC ADN41879;
XX
DT 15-JUL-2004 (first entry)
XX
DE Humanised heavy chain variable domain of antibody 2286.
XX
KW Alzheimer's disease; amyloid beta peptide; Down's syndrome; antibody;
KW antibody 2286.
XX
OS Mus sp.
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004032868-A2.
XX
PD 22-APR-2004.
XX
PF 09-OCT-2003; 2003WO-US032080.
XX
PR 09-OCT-2002; 2002US-0417232P.
PR 13-FEB-2003; 2003US-0447611P.
PR 22-APR-2003; 2003US-0464754P.
PR 20-JUN-2003; 2003US-0480353P.
XX
PA (RINA-) RINAT NEUROSCIENCE CORP.
XX
PI Rosenthal A, Levkowitz G;
XX
DR WPI; 2004-340802/31.
XX
PT Treating or preventing diseases associated with expression of amyloid-
PT beta peptide, e.g. Alzheimer's disease or Down's syndrome, comprises
PT administering an amount of an antibody directed against amyloid-beta
PT peptide.
XX
PS Example 4; Page 63; 89pp; English.
XX
CC The specification describes a method for treating Alzheimer's disease.
CC The method comprises administering to a subject a pharmaceutical
CC composition comprising an antibody that binds preferentially to amino
CC acids 28-40 of beta-amyloid peptide (1-40). The method is useful for
CC diagnosing, treating or preventing diseases associated with expression of
CC amyloid-beta peptide, such as Alzheimer's disease or Down's syndrome. The
CC present sequence represents the humanised heavy chain variable domain
CC (germline framework VH4) of the monoclonal antibody 2286. This antibody
CC represents an antibody of the invention.

```
XX
SQ   Sequence 113 AA;

  Query Match             87.8%;  Score 79;  DB 8;  Length 113;
  Best Local Similarity   88.2%;  Pred. No. 6.6e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         50 EINPDSSTINYTPSLKD 66


RESULT 44
ADN41878
ID   ADN41878 standard; protein; 113 AA.
XX
AC   ADN41878;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised heavy chain variable domain of antibody 2286.
XX
KW   Alzheimer's disease; amyloid beta peptide; Down's syndrome; antibody;
KW   antibody 2286.
XX
OS   Mus sp.
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2004032868-A2.
XX
PD   22-APR-2004.
XX
PF   09-OCT-2003; 2003WO-US032080.
XX
PR   09-OCT-2002; 2002US-0417232P.
PR   13-FEB-2003; 2003US-0447611P.
PR   22-APR-2003; 2003US-0464754P.
PR   20-JUN-2003; 2003US-0480353P.
XX
PA   (RINA-) RINAT NEUROSCIENCE CORP.
XX
PI   Rosenthal A,  Levkowitz G;
XX
DR   WPI; 2004-340802/31.
XX
PT   Treating or preventing diseases associated with expression of amyloid-
PT   beta peptide, e.g. Alzheimer's disease or Down's syndrome, comprises
PT   administering an amount of an antibody directed against amyloid-beta
PT   peptide.
XX
PS   Example 4; Page 63; 89pp; English.
XX
CC   The specification describes a method for treating Alzheimer's disease.
CC   The method comprises administering to a subject a pharmaceutical
CC   composition comprising an antibody that binds preferentially to amino
CC   acids 28-40 of beta-amyloid peptide (1-40). The method is useful for
CC   diagnosing, treating or preventing diseases associated with expression of
CC   amyloid-beta peptide, such as Alzheimer's disease or Down's syndrome. The
CC   present sequence represents the humanised heavy chain variable domain
CC   (germline framework VH3) of the monoclonal antibody 2286. This antibody
CC   represents an antibody of the invention.
XX
SQ   Sequence 113 AA;

  Query Match             87.8%;  Score 79;  DB 8;  Length 113;
  Best Local Similarity   88.2%;  Pred. No. 6.6e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         50 EINPDSSTINYTPSLKD 66


RESULT 45
AAY90820
ID   AAY90820 standard; protein; 116 AA.
XX
AC   AAY90820;
XX
DT   29-AUG-2000  (first entry)
XX
DE   317G5 hybridoma VH domain SEQ ID NO:18.
XX
KW   Antigen binding site; immunoglobulin; cancer antigen; immunological;
KW   antibody; tumour; human; mucin; cancer; cytostatic; hybridoma;
KW   specific binding assay; affinity purification; drug targeting;
KW   toxin targeting; imaging; genetic; therapeutic.
XX
OS   Homo sapiens.
XX
PN   US6054561-A.
XX
PD   25-APR-2000.
XX
PF   07-JUN-1995;   95US-00483749.
XX
PR   08-FEB-1984;   84US-00577976.
PR   11-JAN-1985;   85US-00690750.
PR   21-MAR-1986;   86US-00842476.
PR   08-MAY-1988;   88US-00190778.
PR   11-AUG-1994;   94US-00288981.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Ring DB;
XX
DR   WPI; 2000-338508/29.
DR   N-PSDB; AAA38904.
XX
PT   Monoclonal antibody capable of binding to human breast cancer antigen
PT   useful for affinity purification, drug or toxin targeting, imaging, and
PT   treating cancer.
XX
PS   Disclosure; Fig 9; 57pp; English.
XX
CC   The present invention describes a monoclonal antibody (MAb) (I) that
CC   binds to a human breast cancer antigen that is also bound by MAb 454C11
CC   and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also
CC   described is a hybridoma that produces (I). (I) is useful in specific
CC   binding assays, affinity purification, drug or toxin targeting, imaging,
CC   and genetic or immunological therapeutics for various cancers. The
CC   present sequence represents a VH domain derived from a 317G5 hybridoma,
CC   which is used in the exemplification of the present invention
XX
SQ   Sequence 116 AA;

  Query Match             87.8%;  Score 79;  DB 3;  Length 116;
  Best Local Similarity   88.2%;  Pred. No. 6.8e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         50 EINPDSSTINYTPSLKD 66


RESULT 46
ADR15131
ID   ADR15131 standard; protein; 119 AA.
XX
AC   ADR15131;
XX
DT   21-OCT-2004  (first entry)
XX
DE   Mouse anti-protein C inhibitor antibody #5.
XX
```

KW anti-protein C inhibitor antibody; anti-PCI antibody;
KW activated protein C; aPC; sepsis; disseminated intravascular coagulation;
KW arterial thrombosis; protein C inhibitor; mouse; murine.
XX
OS Mus musculus.
XX
PN WO2004065418-A1.
XX
PD 05-AUG-2004.
XX
PF 20-JAN-2004; 2004WO-JP000429.
XX
PR 20-JAN-2003; 2003JP-00011529.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Koga T, Kimura N, Yoshino T, Ono K;
XX
DR WPI; 2004-593430/57.
XX
PT New anti-protein C inhibitor (PCI) antibody, inhibiting PCI with respect
PT to activation protein C (apc) activity, and apc production by
PT thrombin/thrombomodulin composite, useful for treating sepsis, arterial
PT thrombosis.
XX
PS Disclosure; SEQ ID NO 12; 105pp; Japanese.
XX
CC The invention comprises anti-protein C inhibitor (PCI) antibody. The anti
CC -PCI antibody of the invention is useful for treating or preventing a
CC disease which develops and/or progresses due to reduced activated protein
CC C (aPC) activity. Such diseases include: sepsis, disseminated
CC intravascular coagulation, and arterial thrombosis. The present amino
CC acid sequence represents a mouse anti-protein C inhibitor antibody.
XX
SQ Sequence 119 AA;

Query Match 87.8%; Score 79; DB 8; Length 119;
Best Local Similarity 88.2%; Pred. No. 7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:|||||||| |||||
Db 50 EINPDSSTINYTPSLKD 66

RESULT 47
ADU87692
ID ADU87692 standard; protein; 119 AA.
XX
AC ADU87692;
XX
DT 10-FEB-2005 (first entry)
XX
DE Mouse Luc63 heavy chain variable region.
XX
KW Antibody; CS1; SLAM family member 7; SLAMF7; immunoglobulin;
KW pharmaceutical; antibody-dependent cellular cytotoxicity;
KW FcgammaR receptor; cell proliferation; leukocyte; cancer;
KW multiple myeloma; multiple myeloma-related bone disorder; plasmacytoma;
KW macroglobulinemia; amyloidosis; chronic lymphocytic leukemia;
KW autoimmune disease; inflammatory bowel disease;
KW systemic lupus erythematosus; cytostatic; immunosuppressive;
KW antiinflammatory; gastrointestinal-gen.; dermatological; luc63;
KW heavy chain variable region.
XX
OS Mus sp.
XX
PN WO2004100898-A2.
XX
PD 25-NOV-2004.
XX
PF 10-MAY-2004; 2004WO-US014866.
XX
PR 08-MAY-2003; 2003US-0469211P.
PR 29-MAR-2004; 2004US-0557620P.
PR 29-MAR-2004; 2004US-0557621P.
PR 29-MAR-2004; 2004US-0557622P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Williams M, Tso YJ, Landolfi NF;
XX
DR WPI; 2004-821790/81.
XX
PT New anti-CS1 antibodies, useful for diagnosing, preventing or treating
PT cancer, myeloma, autoimmune disorder, inflammatory bowel disease, or
PT systemic lupus erythematosus.
XX
PS Claim 12; SEQ ID NO 5; 151pp; English.
XX
CC The invention relates to an antibody or its antigen-binding fragment,
CC which binds to CS1 (also known as SLAM family member 7, SLAMF7) and
CC inhibits immunoglobulin secretion, where the antibody binds to
CC substantially the same epitope as an antibody comprising an amino acid
CC sequence of any one of SEQ ID NOS: 3-26, the antibody comprises an amino
CC acid sequence of SEQ ID NOS: 27-44, and where the heavy chain variable
CC region comprises a complementarity determining region (CDR) of SEQ ID NO:
CC 33. Also disclosed are (i) a heavy chain CDR of an antibody comprising an
CC amino acid sequence of SEQ ID NOS: 9-11, 15-17, 21-23, 29-33, (ii) a
CC light chain CDR of an antibody comprising an amino acid sequence of SEQ
CC ID NOS: 12-14, 18-20, 24-26, 34-370, (iii) a pharmaceutical composition
CC comprising a pharmaceutical carrier and the antibody described above,
CC (iv) a method of inhibiting proliferation of CS1 expressing cells, (v)
CC inhibiting immunoglobulin secretion, and (vi) increasing antibody-
CC dependent cellular cytotoxicity (ADCC) activity of the antibody described
CC above, where the antibody has decreased levels of fucose or is mutated to
CC increase antibody affinity for a FcgammaR receptor. The antibody of the
CC invention inhibits the proliferation of leukocytes or cancer cells. The
CC antibody triggers cytotoxic effects on cells expressing CS1 or enhances
CC cytotoxicity mediated by immune cells, or triggers ADCC-mediated
CC cytotoxicity of cells expressing CS1. The antibody binds to substantially
CC the same epitope as the antibody produced by a hybridoma cell line having
CC ATCC accession number PTA-5091 or a Luc63 antibody. The antibody is
CC produced by a hybridoma cell line having ATCC accession number PTA-5091
CC or by a hybridoma cell line expressing Luc63 antibody. The antibody is a
CC monoclonal antibody, e.g. a chimeric antibody, a humanized antibody, or a
CC fully human antibody. The antibody is conjugated with a cytotoxic agent.
CC The antibody comprises a heavy chain variable region comprising amino
CC acid sequences of SEQ ID NOS: 3, 5, 7, or 27, and a light chain variable
CC region comprising amino acid sequences of SEQ ID NOS: 4, 6, 8, or 28. The
CC antibody, compositions, and methods are useful for diagnosing, preventing
CC or treating plasma cell cancer, e.g. myeloma, multiple myeloma, myeloma
CC of bone, extramedullary plasmacytoma, macroglobulinemia (including
CC Waldenstrom's macroglobulinemia), heavy-chain disease, primary
CC amyloidosis or monoclonal gammopathy of unknown significance, non-plasma
CC cell cancer (chronic lymphocytic leukemia), autoimmune disorder,
CC inflammatory bowel disease (IBD), or systemic lupus erythematosus (SLE).
CC This sequence represents a CS1 antibody.
XX
SQ Sequence 119 AA;

Query Match 87.8%; Score 79; DB 8; Length 119;
Best Local Similarity 88.2%; Pred. No. 7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:|||||||| |||||
Db 50 EINPDSSTINYTPSLKD 66

RESULT 48
ADU87724
ID ADU87724 standard; protein; 119 AA.
XX
AC ADU87724;
XX

DT 10-FEB-2005 (first entry)
XX
DE Heavy chain variable region of mouse Luc63.
XX
KW Antibody; CS1; SLAM family member 7; SLAMF7; immunoglobulin;
KW pharmaceutical; antibody-dependent cellular cytotoxicity;
KW FcgammaR receptor; cell proliferation; leukocyte; cancer;
KW multiple myeloma; multiple myeloma-related bone disorder; plasmacytoma;
KW macroglobulinemia; amyloidosis; chronic lymphocytic leukemia;
KW autoimmune disease; inflammatory bowel disease;
KW systemic lupus erythematosus; cytostatic; immunosuppressive;
KW antiinflammatory; gastrointestinal-gen.; dermatological; luc63;
KW heavy chain variable region.
XX
OS Mus sp.
XX
PN WO2004100898-A2.
XX
PD 25-NOV-2004.
XX
PF 10-MAY-2004; 2004WO-US014866.
XX
PR 08-MAY-2003; 2003US-0469211P.
PR 29-MAR-2004; 2004US-0557620P.
PR 29-MAR-2004; 2004US-0557621P.
PR 29-MAR-2004; 2004US-0557622P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Williams M, Tso YJ, Landolfi NF;
XX
DR WPI; 2004-821790/81.
XX
PT New anti-CS1 antibodies, useful for diagnosing, preventing or treating
PT cancer, myeloma, autoimmune disorder, inflammatory bowel disease, or
PT systemic lupus erythematosus.
XX
PS Claim 19; Page 102; 151pp; English.
XX
CC The invention relates to an antibody or its antigen-binding fragment,
CC which binds to CS1 (also known as SLAM family member 7, SLAMF7) and
CC inhibits immunoglobulin secretion, where the antibody binds to
CC substantially the same epitope as an antibody comprising an amino acid
CC sequence of any one of SEQ ID NOS: 3-26, the antibody comprises an amino
CC acid sequence of SEQ ID NOS: 27-44, and where the heavy chain variable
CC region comprises a complementarity determining region (CDR) of SEQ ID NO:
CC 33. Also disclosed are (i) a heavy chain CDR of an antibody comprising an
CC amino acid sequence of SEQ ID NOS: 9-11, 15-17, 21-23, 29-33, (ii) a
CC light chain CDR of an antibody comprising an amino acid sequence of SEQ
CC ID NOS: 12-14, 18-20, 24-26, 34-370, (iii) a pharmaceutical composition
CC comprising a pharmaceutical carrier and the antibody described above,
CC (iv) a method of inhibiting proliferation of CS1 expressing cells, (v)
CC inhibiting immunoglobulin secretion, and (vi) increasing antibody-
CC dependent cellular cytotoxicity (ADCC) activity of the antibody described
CC above, where the antibody has decreased levels of fucose or is mutated to
CC increase antibody affinity for a FcgammaR receptor. The antibody of the
CC invention inhibits the proliferation of leukocytes or cancer cells. The
CC antibody triggers cytotoxic effects on cells expressing CS1 or enhances
CC cytotoxicity mediated by immune cells, or triggers ADCC-mediated
CC cytotoxicity of cells expressing CS1. The antibody binds to substantially
CC the same epitope as the antibody produced by a hybridoma cell line having
CC ATCC accession number PTA-5091 or a Luc63 antibody. The antibody is
CC produced by a hybridoma cell line having ATCC accession number PTA-5091
CC or by a hybridoma cell line expressing Luc63 antibody. The antibody is a
CC monoclonal antibody, e.g. a chimeric antibody, a humanized antibody, or a
CC fully human antibody. The antibody is conjugated with a cytotoxic agent.
CC The antibody comprises a heavy chain variable region comprising amino
CC acid sequences of SEQ ID NOS: 3, 5, 7, or 27, and a light chain variable
CC region comprising amino acid sequences of SEQ ID NOS: 4, 6, 8, or 28. The
CC antibody, compositions, and methods are useful for diagnosing, preventing
CC or treating plasma cell cancer, e.g. myeloma, multiple myeloma, myeloma
CC of bone, extramedullary plasmacytoma, macroglobulinemia (including
CC Waldenstrom's macroglobulinemia), heavy-chain disease, primary
CC amyloidosis or monoclonal gammopathy of unknown significance, non-plasma
CC cell cancer (chronic lymphocytic leukemia), autoimmune disorder,
CC inflammatory bowel disease (IBD), or systemic lupus erythematosus (SLE).
CC This sequence represents the heavy chain variable region of mouse Luc63
CC (MuLuc63 VH). Note: The present sequence given as SEQ ID No:37 given on
CC page 102 differs from another sequence also given as SEQ ID No:37 on page
CC 101 of the specification.
XX
SQ Sequence 119 AA;

Query Match 87.8%; Score 79; DB 8; Length 119;
Best Local Similarity 88.2%; Pred. No. 7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:|||||||| |||||
Db 50 EINPDSSTINYTPSLKD 66

RESULT 49
ADU87731
ID ADU87731 standard; protein; 119 AA.
XX
AC ADU87731;
XX
DT 10-FEB-2005 (first entry)
XX
DE VH region of mouse Luc63.
XX
KW Antibody; CS1; SLAM family member 7; SLAMF7; immunoglobulin;
KW pharmaceutical; antibody-dependent cellular cytotoxicity;
KW FcgammaR receptor; cell proliferation; leukocyte; cancer;
KW multiple myeloma; multiple myeloma-related bone disorder; plasmacytoma;
KW macroglobulinemia; amyloidosis; chronic lymphocytic leukemia;
KW autoimmune disease; inflammatory bowel disease;
KW systemic lupus erythematosus; cytostatic; immunosuppressive;
KW antiinflammatory; gastrointestinal-gen.; dermatological; luc63;
KW heavy chain variable region.
XX
OS Mus sp.
XX
PN WO2004100898-A2.
XX
PD 25-NOV-2004.
XX
PF 10-MAY-2004; 2004WO-US014866.
XX
PR 08-MAY-2003; 2003US-0469211P.
PR 29-MAR-2004; 2004US-0557620P.
PR 29-MAR-2004; 2004US-0557621P.
PR 29-MAR-2004; 2004US-0557622P.
XX
PA (PROT-) PROTEIN DESIGN LABS INC.
XX
PI Williams M, Tso YJ, Landolfi NF;
XX
DR WPI; 2004-821790/81.
XX
PT New anti-CS1 antibodies, useful for diagnosing, preventing or treating
PT cancer, myeloma, autoimmune disorder, inflammatory bowel disease, or
PT systemic lupus erythematosus.
XX
PS Example 5; SEQ ID NO 45; 151pp; English.
XX
CC The invention relates to an antibody or its antigen-binding fragment,
CC which binds to CS1 (also known as SLAM family member 7, SLAMF7) and
CC inhibits immunoglobulin secretion, where the antibody binds to
CC substantially the same epitope as an antibody comprising an amino acid
CC sequence of any one of SEQ ID NOS: 3-26, the antibody comprises an amino
CC acid sequence of SEQ ID NOS: 27-44, and where the heavy chain variable
CC region comprises a complementarity determining region (CDR) of SEQ ID NO:
CC 33. Also disclosed are (i) a heavy chain CDR of an antibody comprising an
CC amino acid sequence of SEQ ID NOS: 9-11, 15-17, 21-23, 29-33, (ii) a

CC light chain CDR of an antibody comprising an amino acid sequence of SEQ
CC ID NOS: 12-14, 18-20, 24-26, 34-370, (iii) a pharmaceutical composition
CC comprising a pharmaceutical carrier and the antibody described above,
CC (iv) a method of inhibiting proliferation of CS1 expressing cells, (v)
CC inhibiting immunoglobulin secretion, and (vi) increasing antibody-
CC dependent cellular cytotoxicity (ADCC) activity of the antibody described
CC above, where the antibody has decreased levels of fucose or is mutated to
CC increase antibody affinity for a FcgammaR receptor. The antibody of the
CC invention inhibits the proliferation of leukocytes or cancer cells. The
CC antibody triggers cytotoxic effects on cells expressing CS1 or enhances
CC cytotoxicity mediated by immune cells, or triggers ADCC-mediated
CC cytotoxicity of cells expressing CS1. The antibody binds to substantially
CC the same epitope as the antibody produced by a hybridoma cell line having
CC ATCC accession number PTA-5091 or a Luc63 antibody. The antibody is
CC produced by a hybridoma cell line having ATCC accession number PTA-5091
CC or by a hybridoma cell line expressing Luc63 antibody. The antibody is a
CC monoclonal antibody, e.g. a chimeric antibody, a humanized antibody, or a
CC fully human antibody. The antibody is conjugated with a cytotoxic agent.
CC The antibody comprises a heavy chain variable region comprising amino
CC acid sequences of SEQ ID NOS: 3, 5, 7, or 27, and a light chain variable
CC region comprising amino acid sequences of SEQ ID NOS: 4, 6, 8, or 28. The
CC antibody, compositions, and methods are useful for diagnosing, preventing
CC or treating plasma cell cancer, e.g. myeloma, multiple myeloma, myeloma
CC of bone, extramedullary plasmacytoma, macroglobulinemia (including
CC Waldenstrom's macroglobulinemia), heavy-chain disease, primary
CC amyloidosis or monoclonal gammopathy of unknown significance, non-plasma
CC cell cancer (chronic lymphocytic leukemia), autoimmune disorder,
CC inflammatory bowel disease (IBD), or systemic lupus erythematosus (SLE).
CC This sequence represents the heavy chain variable region of mouse Luc63
CC (MuLuc63 VH).
XX
SQ Sequence 119 AA;

Query Match 87.8%; Score 79; DB 8; Length 119;
Best Local Similarity 88.2%; Pred. No. 7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:||||||| |||||
Db 50 EINPDSSTINYTPSLKD 66

RESULT 50
ADD94119
ID ADD94119 standard; protein; 120 AA.
XX
AC ADD94119;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mouse HUIV26 variable region heavy chain partial amino acid sequence.
XX
KW grafted antibody; complementarity determining region; CDR; light CDR;
KW heavy CDR; cryptic collagen epitope; solid tumour;
KW new blood vessel growth; angiogenesis; tumour growth; cytostatic;
KW collagen agonist; collagen antagonist; cancer metastasis;
KW anti-cryptic collagen; antibody; HUIV26; variable region heavy chain;
KW mouse; murine.
XX
OS Mus musculus.
XX
PN WO2003046204-A2.
XX
PD 05-JUN-2003.
XX
PF 26-NOV-2002; 2002WO-US038147.
XX
PR 26-NOV-2001; 2001US-00995529.
PR 06-DEC-2001; 2001US-00011250.
XX
PA (CELL-) CELL MATRIX INC.
XX
PI Watking JD, Huse WD, Tang Y, Broek D, Brooks PC;
XX
DR WPI; 2003-513649/48.
DR N-PSDB; ADD94118.
XX
PT New cryptic collagen antibody with one or more complementarity
PT determining regions, useful for diagnosing and treating disorders
PT associated with angiogenesis, tumor growth and/or cancer metastasis.
XX
PS Example 1; SEQ ID NO 4; 232pp; English.
XX
CC This invention relates to a novel grafted antibody or its functional
CC fragment comprising one or more complementarity determining regions
CC (CDRs) of a defined light CDR and a heavy CDR with at least one amino
CC acid (aa) substitution where the antibody has specific binding activity
CC for a cryptic collagen epitope. The growth of all solid tumours requires
CC new blood vessel growth, angiogenesis, inhibition of which is an approach
CC to limiting tumour growth. The invention may allow development of
CC therapeutics with a cytostatic activity as a collagen agonist or
CC antagonist. The invention is useful for diagnosing and treating disorders
CC associated with angiogenesis, tumour growth and/or cancer metastasis. The
CC present sequence is the partial amino acid sequence of the mouse anti-
CC cryptic collagen site antibody HUIV26 variable region heavy chain used
CC during the creation of the antibody of the invention.
XX
SQ Sequence 120 AA;

Query Match 87.8%; Score 79; DB 7; Length 120;
Best Local Similarity 88.2%; Pred. No. 7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:||||||| |||||
Db 50 EINPDSSTINYTPSLKD 66

Search completed: March 23, 2006, 01:53:21
Job time : 169.877 secs

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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:54:26 ; Search time 23.5205 Seconds
(without alignments)
69.543 Million cell updates/sec

Title: US-10-755-382-24
Perfect score: 90
Sequence: 1 EIHPDSSTINYAPSLKD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	82	91.1	119	1	AVMSJ5	Ig heavy chain V r
2	79	87.8	94	2	I67528	CD33 antigen homol
3	79	87.8	116	1	HVMS44	Ig heavy chain pre
4	79	87.8	118	2	A47329	Ig heavy chain V r
5	79	87.8	119	1	AVMST6	Ig heavy chain V r
6	79	87.8	119	1	AVMSX4	Ig heavy chain V r
7	79	87.8	139	2	A25912	Ig heavy chain pre
8	73	81.1	117	1	G2MSU1	Ig heavy chain V r
9	72	80.0	95	2	I67527	CD33 antigen homol
10	72	80.0	117	1	G2MS73	Ig heavy chain V r
11	72	80.0	136	2	S13791	Ig heavy chain V r
12	71	78.9	121	2	A30560	Ig heavy chain V r
13	66	73.3	130	2	S06817	Ig heavy chain V r
14	61	67.8	101	2	S13692	Ig heavy chain V r
15	61	67.8	111	2	S13693	Ig heavy chain V r
16	61	67.8	112	2	S13690	Ig heavy chain V r
17	61	67.8	115	2	S13694	Ig heavy chain V r
18	61	67.8	116	2	S13691	Ig heavy chain V r
19	61	67.8	137	2	S03326	Ig heavy chain pre
20	54	60.0	140	2	S06816	Ig heavy chain pre
21	47	52.2	98	2	F47624	Ig heavy chain V-I
22	47	52.2	127	2	PH1421	Ig heavy chain V r
23	46	51.1	117	1	HVCQG4	Ig heavy chain pre
24	46	51.1	125	2	PH1410	Ig heavy chain V r
25	44	48.9	128	2	AF0593	probable secreted
26	44	48.9	305	2	T34867	probable chitosana
27	43	47.8	116	2	I84704	gene VH104B protei
28	43	47.8	204	2	A56642	somatotropin precu
29	43	47.8	204	2	I51289	somatotropin - Mor
30	43	47.8	475	2	S76734	hypothetical prote
31	43	47.8	920	2	A36887	endo-alpha-sialida
32	42	46.7	249	2	AB3063	mandelate racemase
33	42	46.7	372	2	F98223	hypothetical prote
34	42	46.7	577	2	I50731	Ig heavy chain - n
35	42	46.7	584	2	T49320	related to heterok
36	42	46.7	811	2	S77577	endo-alpha-sialida
37	41	45.6	117	2	S19669	Ig heavy chain V r
38	41	45.6	126	2	PH1416	Ig heavy chain V r
39	41	45.6	126	2	PH1417	Ig heavy chain V r
40	41	45.6	126	2	PH1418	Ig heavy chain V r
41	41	45.6	126	2	PH1419	Ig heavy chain V r
42	41	45.6	203	2	S00747	somatotropin precu
43	41	45.6	262	2	B70699	hypothetical prote
44	41	45.6	291	2	T23051	hypothetical prote
45	41	45.6	301	1	S12864	retinal isomerase
46	41	45.6	319	2	E86240	protein T16B5.15 [
47	41	45.6	320	1	G72061	probable phosphoes
48	41	45.6	320	1	G86562	probable phosphoes
49	41	45.6	388	2	D75353	yellow-related pro
50	41	45.6	419	2	H81667	transcription term
51	41	45.6	464	2	G86566	transcription term
52	41	45.6	464	2	D72058	transcription term
53	41	45.6	464	2	A71509	probable transcrip
54	41	45.6	525	2	T30187	hypothetical prote
55	41	45.6	672	2	T12524	hypothetical prote
56	41	45.6	735	2	AC1946	adenylate cyclase
57	41	45.6	795	2	F82858	dipeptidyl-peptida
58	40.5	45.0	368	2	JQ1613	cyanide hydratase
59	40.5	45.0	619	2	C81905	probable dihydroxy
60	40.5	45.0	619	2	E81117	dihydroxy-acid deh
61	40	44.4	65	2	AI2513	hypothetical prote
62	40	44.4	88	2	PH1161	Ig heavy chain V r
63	40	44.4	151	2	T27111	hypothetical prote
64	40	44.4	185	2	T49660	glucan 1,4-alpha-g
65	40	44.4	259	2	A97303	uncharacterized pr
66	40	44.4	264	2	D87217	conserved hypothet
67	40	44.4	313	2	C83874	arsenical pump-dri
68	40	44.4	316	2	T33180	hypothetical prote
69	40	44.4	321	2	AE2170	hypothetical prote
70	40	44.4	355	2	C81405	probable oxidoredu
71	40	44.4	355	2	AI3624	spermidine/putresc
72	40	44.4	360	2	B96618	probable proline-r
73	40	44.4	360	2	T52463	hypothetical prote
74	40	44.4	415	1	TVHUSA	transforming prote
75	40	44.4	416	2	D75531	folyl-polyglutamat
76	40	44.4	684	1	TVHUSN	transforming prote
77	40	44.4	773	2	D89010	protein R08F11.7 [
78	40	44.4	807	2	F85647	probable outer mem
79	40	44.4	807	2	F64844	ycdS protein precu
80	40	44.4	807	2	F90787	probable outer mem
81	40	44.4	955	2	S52959	male-specific leth
82	40	44.4	1611	2	T38236	hypothetical prote
83	39.5	43.9	214	2	S10026	GTP-binding protei
84	39.5	43.9	296	1	B28255	hypothetical 34K p
85	39	43.3	97	2	JH0428	Ig gamma chain V r
86	39	43.3	98	2	PH1154	Ig heavy chain V r
87	39	43.3	102	2	PH1235	Ig heavy chain V r
88	39	43.3	114	2	I72667	cold agglutinin FS
89	39	43.3	116	2	S38718	Ig heavy chain V r
90	39	43.3	119	2	PH1510	Ig heavy chain V r
91	39	43.3	119	2	PH1503	Ig heavy chain V r
92	39	43.3	127	2	PH1415	Ig heavy chain V r
93	39	43.3	132	2	PH1427	Ig heavy chain V r
94	39	43.3	134	2	S54906	Ig heavy chain V r
95	39	43.3	140	2	PH1483	Ig heavy chain V r
96	39	43.3	145	2	S11239	Ig heavy chain V r
97	39	43.3	187	2	PC1082	somatotropin - Jap
98	39	43.3	187	2	PC1087	somatotropin - dus
99	39	43.3	204	2	A56904	somatotropin precu
100	39	43.3	204	2	S30491	somatotropin - Aca
101	39	43.3	284	2	T33586	hypothetical prote
102	39	43.3	307	2	D90394	purine nucleosidas

103	39	43.3	334	2	H64079	ornithine carbamoy
104	39	43.3	336	1	OWPSCA	ornithine carbamoy
105	39	43.3	352	2	F90155	hypothetical prote
106	39	43.3	367	1	S24411	dual specificity p
107	39	43.3	367	2	S52265	dual specificity p
108	39	43.3	379	2	AG2358	hypothetical prote
109	39	43.3	392	2	A84564	hypothetical prote
110	39	43.3	392	2	E88108	protein C46E10.3 [
111	39	43.3	415	2	T50106	hst4p [imported] -
112	39	43.3	463	2	E65017	hypothetical prote
113	39	43.3	480	2	T46925	hypothetical prote
114	39	43.3	538	2	E96492	hypothetical prote
115	39	43.3	581	2	T23396	hypothetical prote
116	39	43.3	583	1	S20495	ferredoxin-nitrite
117	39	43.3	597	2	H82328	hypothetical prote
118	39	43.3	617	2	S77077	hypothetical prote
119	39	43.3	622	2	E83160	two-component sens
120	39	43.3	626	1	D70699	probable pknB prot
121	39	43.3	891	2	T32079	hypothetical prote
122	39	43.3	950	2	S64405	MIC1 protein - yea
123	39	43.3	1392	2	T51947	probable transcrip
124	39	43.3	1407	2	S59823	probable membrane
125	39	43.3	1465	1	S78555	copper-transportin
126	39	43.3	1473	2	T38791	probable ferredoxi
127	39	43.3	1630	2	A53577	ascites sialoglyco
128	39	43.3	3071	2	T45584	hypothetical prote
129	38.5	42.8	98	2	S26905	Ig heavy chain V r
130	38.5	42.8	134	2	B24672	Ig heavy chain pre
131	38.5	42.8	145	2	S78055	Ig heavy chain pre
132	38.5	42.8	231	2	AC2027	hypothetical prote
133	38.5	42.8	425	2	AD1149	O-acetylhomoserine
134	38.5	42.8	425	2	AD1508	O-acetylhomoserine
135	38.5	42.8	1611	1	WMTMPV	183K protein - pep
136	38	42.2	99	2	AB3551	hypothetical cytos
137	38	42.2	119	1	E37831	phenol 2-monooxyge
138	38	42.2	119	1	S44307	phenol 2-monooxyge
139	38	42.2	126	2	E90726	probable homeobox
140	38	42.2	126	2	F85577	probable homeobox
141	38	42.2	143	1	E1HUND	Ig heavy chain pre
142	38	42.2	187	2	A61123	somatotropin - Moz
143	38	42.2	204	2	JN0484	somatotropin precu
144	38	42.2	212	2	I51034	prolactin-I - Moza
145	38	42.2	212	2	A32477	prolactin I precur
146	38	42.2	230	2	S73229	ribosomal protein
147	38	42.2	239	2	AG1569	transcription regu
148	38	42.2	249	1	A31841	bile acid dehydrox
149	38	42.2	249	1	B37762	bile acid 7-dehydr
150	38	42.2	253	2	D69498	peptidyl-prolyl ci
151	38	42.2	268	2	S74772	hypothetical prote
152	38	42.2	280	2	S13108	ECA39 protein - mo
153	38	42.2	317	2	C87420	N-acetyl-gamma-glu
154	38	42.2	325	2	T24689	hypothetical prote
155	38	42.2	329	2	T32760	hypothetical prote
156	38	42.2	377	2	G69937	lipopolysaccharide
157	38	42.2	401	2	T15607	hypothetical prote
158	38	42.2	406	2	C64802	N-acetylglucosamin
159	38	42.2	406	2	B85567	N-acetylglucosamin
160	38	42.2	406	2	B90717	N-acetylglucosamin
161	38	42.2	420	2	T32426	hypothetical prote
162	38	42.2	428	2	C75110	translation elonga
163	38	42.2	428	2	G71023	translation elonga
164	38	42.2	430	2	S19000	translation elonga
165	38	42.2	466	2	D90638	hypothetical prote
166	38	42.2	466	2	D85489	hypothetical prote
167	38	42.2	466	2	H64728	3-isopropylmalate
168	38	42.2	466	2	F69331	conserved hypothet
169	38	42.2	505	2	T43488	hypothetical prote
170	38	42.2	507	2	T33024	hypothetical prote
171	38	42.2	521	2	S62794	probable lipoprote
172	38	42.2	530	2	T18596	hypothetical prote
173	38	42.2	567	2	JA0172	ferredoxin-nitrite
174	38	42.2	597	2	JC7615	alpha-glucosidase
175	38	42.2	597	2	T15324	hypothetical prote
176	38	42.2	599	2	A83740	hypothetical prote
177	38	42.2	808	2	B97303	hypothetical prote
178	38	42.2	817	2	A48721	titin, muscle - ch
179	38	42.2	976	2	C84500	probable retroelem
180	38	42.2	994	2	I49276	c-mer tyrosine kin
181	38	42.2	1044	2	T43800	protein kinase bub
182	38	42.2	1217	2	F97177	alpha-glucosidase
183	38	42.2	2269	1	JQ1750	genome polyprotein
184	38	42.2	3131	2	S39842	enniatin synthetas
185	38	42.2	6260	2	T30228	polyketide synthas
186	38	42.2	6831	2	A88852	protein unc-22 [im
187	38	42.2	6839	2	S57242	twitchin [similari
188	38	42.2	7160	2	T27935	hypothetical prote
189	37.5	41.7	97	2	S26898	Ig heavy chain V r
190	37.5	41.7	97	2	S26806	Ig heavy chain V r
191	37.5	41.7	97	2	S26805	Ig heavy chain V r
192	37.5	41.7	106	2	S37454	Ig mu chain - huma
193	37.5	41.7	122	2	JL0047	Ig heavy chain V r
194	37.5	41.7	126	2	S47010	Ig heavy chain V4.
195	37.5	41.7	133	2	PS0341	Ig heavy chain V-D
196	37.5	41.7	140	2	S78052	Ig heavy chain pre
197	37.5	41.7	140	2	A49045	Ig heavy chain V r
198	37.5	41.7	143	2	B49028	Ig heavy chain V-I
199	37.5	41.7	231	2	B23746	Ig Fab region IV-J
200	37.5	41.7	370	1	HVRKC5	Ig mu chain C regi
201	37.5	41.7	431	2	H84392	O-acetyl homoserin
202	37.5	41.7	436	2	T42982	hypothetical prote
203	37.5	41.7	501	2	T26466	hypothetical prote
204	37.5	41.7	514	2	B87711	coenzyme A transfe
205	37.5	41.7	1023	2	B38932	phospholipase C (E
206	37.5	41.7	1176	1	A48047	phospholipase C (E
207	37	41.1	31	2	S22023	Ig mu chain - mous
208	37	41.1	86	2	S21595	Ig heavy chain V r
209	37	41.1	98	2	S26894	Ig heavy chain V r
210	37	41.1	98	2	PH1429	Ig heavy chain V r
211	37	41.1	99	2	D34964	Ig heavy chain V-V
212	37	41.1	101	2	S12431	Ig heavy chain V r
213	37	41.1	110	2	S36282	Ig heavy chain V r
214	37	41.1	115	2	PH1560	Ig heavy chain V r
215	37	41.1	116	2	S22558	Ig heavy chain V r
216	37	41.1	117	2	S21980	Ig heavy chain V-g
217	37	41.1	121	2	S19969	Ig heavy chain V r
218	37	41.1	122	2	PH1426	Ig heavy chain V r
219	37	41.1	123	2	S26794	Ig heavy chain V r
220	37	41.1	125	2	S30531	Ig heavy chain V r
221	37	41.1	137	2	PH1562	Ig heavy chain V r
222	37	41.1	138	2	PH1564	Ig heavy chain V r
223	37	41.1	138	2	PH1565	yycE protein - Bac
224	37	41.1	139	2	S65969	Ig heavy chain V r
225	37	41.1	143	2	S23624	Ig heavy chain V r
226	37	41.1	144	2	PH1563	Ig heavy chain V r
227	37	41.1	147	2	PH1561	hypothetical prote
228	37	41.1	152	2	AG1292	hypothetical prote
229	37	41.1	152	2	AE1664	hypothetical prote
230	37	41.1	165	2	H69851	hypothetical prote
231	37	41.1	188	2	H70562	recombinase [impor
232	37	41.1	248	2	AG3459	hypothetical prote
233	37	41.1	264	2	F70828	hypothetical prote
234	37	41.1	322	2	F85783	hypothetical prote
235	37	41.1	322	2	B90935	endo-1,4-beta-xyla
236	37	41.1	347	2	B72423	uroporphyrinogen d
237	37	41.1	350	2	S75977	DNA-binding protei
238	37	41.1	353	2	T09887	hypothetical prote
239	37	41.1	366	2	B64413	hypothetical prote
240	37	41.1	389	2	T47178	hypothetical prote
241	37	41.1	391	2	T34935	hypothetical prote
242	37	41.1	415	2	T23215	translation elonga
243	37	41.1	428	2	S10248	hypothetical prote
244	37	41.1	438	2	T50991	Glu-tRNA amidotran
245	37	41.1	453	2	A69494	hypothetical prote
246	37	41.1	458	2	AD2060	hypothetical prote
247	37	41.1	466	2	T08914	S-receptor kinase-
248	37	41.1	482	2	T48397	

249	37	41.1	489	2	S63401	hypothetical prote
250	37	41.1	492	2	S53111	enniatin synthetas
251	37	41.1	509	2	T06300	hypothetical prote
252	37	41.1	510	2	S42626	ER-golgi intermedi
253	37	41.1	543	2	JC4991	detergent sensitiv
254	37	41.1	547	2	T46059	MAP kinase - Arabi
255	37	41.1	549	2	T51099	MAP kinase [import
256	37	41.1	555	2	D71714	ABC transporter AT
257	37	41.1	561	2	G84012	oligo-1,6-glucosid
258	37	41.1	601	2	T46819	rhbF protein [impo
259	37	41.1	601	2	G95419	RhbF Rhizobactin s
260	37	41.1	622	2	T10009	probable serine/th
261	37	41.1	622	2	H86910	probable serine/th
262	37	41.1	659	2	AG1806	AA3-600 quinol oxi
263	37	41.1	659	2	AG1434	AA3-600 quinol oxi
264	37	41.1	667	2	T40727	probable chloride
265	37	41.1	693	2	T19598	hypothetical prote
266	37	41.1	732	1	JU0132	acylaminoacyl-pept
267	37	41.1	758	2	S30948	ferrichrome recept
268	37	41.1	839	2	S62963	hypothetical prote
269	37	41.1	849	2	H84668	Mutator-like trans
270	37	41.1	923	2	S50482	hypothetical prote
271	37	41.1	1036	2	S22383	axonin 1 precursor
272	37	41.1	1147	2	F86297	hypothetical prote
273	37	41.1	1518	2	S37928	probable purine nu
274	37	41.1	1520	1	TVFFA	protein-tyrosine k
275	37	41.1	1630	2	T40217	hypothetical prote
276	37	41.1	2242	2	A57541	pyrimidine synthes
277	36.5	40.6	312	2	AF0806	outer membrane pro
278	36.5	40.6	403	2	T39697	DNAJ protein - fis
279	36.5	40.6	419	2	D69051	3-isopropylmalate
280	36.5	40.6	544	2	AI3266	integral membrane
281	36.5	40.6	1808	2	T47792	hypothetical prote
282	36.5	40.6	3924	2	S37431	ankyrin 2, neurona
283	36	40.0	52	2	AC2566	hypothetical prote
284	36	40.0	68	2	AD2495	hypothetical prote
285	36	40.0	87	2	S27394	colicin E7 immunit
286	36	40.0	92	2	S41662	L-phenylalanine ox
287	36	40.0	94	2	S42185	Ig gamma chain V r
288	36	40.0	97	2	S14474	Ig heavy chain V r
289	36	40.0	98	2	G47624	Ig heavy chain V-V
290	36	40.0	102	2	PH1236	Ig heavy chain V r
291	36	40.0	102	2	PH1263	Ig heavy chain V r
292	36	40.0	104	2	S16310	bchA protein - Ery
293	36	40.0	117	1	HVMS02	Ig heavy chain pre
294	36	40.0	119	2	D25114	Ig heavy chain V r
295	36	40.0	120	2	B22769	Ig heavy chain V r
296	36	40.0	122	2	S24287	Ig heavy chain V r
297	36	40.0	126	2	PH1424	Ig heavy chain V r
298	36	40.0	145	2	G69312	hypothetical prote
299	36	40.0	157	2	AF2708	conserved hypothet
300	36	40.0	157	2	G97490	hypothetical prote
301	36	40.0	162	2	A72690	hypothetical prote
302	36	40.0	204	2	JH0577	somatotropin precu
303	36	40.0	220	2	A70742	hypothetical prote
304	36	40.0	232	2	AI0019	phosphoglycolate p
305	36	40.0	254	2	S56688	globulin G1 precur
306	36	40.0	285	2	A34469	envelope protein p
307	36	40.0	300	1	S75015	ribosomal protein
308	36	40.0	305	2	B82873	conserved hypothet
309	36	40.0	322	2	H64933	succinylglutamate
310	36	40.0	365	2	T15478	hypothetical prote
311	36	40.0	370	2	C40585	recF protein - Sta
312	36	40.0	372	2	C97791	nifs protein homol
313	36	40.0	374	2	A83838	gamma-glutamyl kin
314	36	40.0	376	2	S29089	alpha-centractin -
315	36	40.0	376	2	S29075	centractin - dog
316	36	40.0	376	2	B71652	iron-sulfur cofact
317	36	40.0	379	2	G82233	phosphoserine amin
318	36	40.0	379	2	F90601	probable thiamin b
319	36	40.0	391	2	S61704	probable transcrip
320	36	40.0	395	2	S73531	CDP-diglyceride sy
321	36	40.0	406	2	H64793	ybdN protein - Esc
322	36	40.0	406	2	A99709	hypothetical prote
323	36	40.0	406	2	B85559	hypothetical prote
324	36	40.0	422	2	C85028	hypothetical prote
325	36	40.0	427	2	AB3025	methionine gamma-l
326	36	40.0	427	2	G98259	methionine gamma-l
327	36	40.0	428	2	D96934	cytosine/guanine d
328	36	40.0	436	2	E84071	spore outer layer
329	36	40.0	437	2	C72570	probable translati
330	36	40.0	439	2	T01428	hypothetical prote
331	36	40.0	456	2	S30922	ferredoxin-nitrite
332	36	40.0	457	2	T49169	hypothetical prote
333	36	40.0	467	2	H82070	3-isopropylmalate
334	36	40.0	467	2	A71431	hypothetical prote
335	36	40.0	480	1	A30065	trigramin precurso
336	36	40.0	485	2	S73422	probable lipoprote
337	36	40.0	485	2	AG3221	conserved hypothet
338	36	40.0	489	2	S76768	hypothetical prote
339	36	40.0	489	2	B72767	hypothetical prote
340	36	40.0	489	2	A47259	corticosteroid-bin
341	36	40.0	504	2	S17248	regulatory protein
342	36	40.0	510	2	A71816	hypothetical prote
343	36	40.0	534	2	B71445	probable glycerol-
344	36	40.0	535	2	S19729	xylan 1,4-beta-xyl
345	36	40.0	550	2	H86516	fructose-6-P phosp
346	36	40.0	550	2	A72106	pyrophosphate-fruc
347	36	40.0	552	2	H83392	probable decarboxy
348	36	40.0	557	2	T49811	probable vacuolar
349	36	40.0	562	2	A82743	probable malate de
350	36	40.0	563	2	T09378	hypothetical prote
351	36	40.0	568	2	S42225	major envelope gly
352	36	40.0	583	2	S38789	ferredoxin-nitrite
353	36	40.0	587	2	D81881	probable succinate
354	36	40.0	608	2	A97685	hypothetical prote
355	36	40.0	608	2	AC2910	hypothetical prote
356	36	40.0	623	2	B82536	ABC transporter AT
357	36	40.0	636	2	T38010	hypothetical prote
358	36	40.0	733	2	S44254	alpha-galactosidas
359	36	40.0	752	2	T16508	hypothetical prote
360	36	40.0	776	2	D98354	oligo alginate lya
361	36	40.0	776	2	AC2928	oligo alginate lya
362	36	40.0	778	2	B70667	hypothetical prote
363	36	40.0	779	2	A96758	hypothetical prote
364	36	40.0	798	2	S40052	glycogen phosphory
365	36	40.0	811	2	AB1980	two-component hybr
366	36	40.0	815	2	H69775	hypothetical prote
367	36	40.0	930	2	B84505	probable retroelem
368	36	40.0	948	2	F64672	D-lactate dehydrog
369	36	40.0	951	2	B88042	protein F56D12.6 [
370	36	40.0	962	2	AG2444	hypothetical prote
371	36	40.0	1079	2	A86220	protein F22D3.29
372	36	40.0	1116	2	B88612	protein Y76A2A.2 [
373	36	40.0	1171	2	S57829	genome polyprotein
374	36	40.0	1238	1	JC5573	copper-transportin
375	36	40.0	1325	2	T25753	hypothetical prote
376	36	40.0	1680	2	T01367	hypothetical prote
377	36	40.0	1747	2	T43162	vitellogenin - gyp
378	36	40.0	1820	1	CHEE	sodium channel pro
379	36	40.0	1908	2	T42707	hypothetical prote
380	36	40.0	3898	2	S57437	genome polyprotein
381	36	40.0	26926	1	I38344	titin, cardiac mus
382	35.5	39.4	216	1	BVECKB	alkB protein - Esc
383	35.5	39.4	216	2	E91016	alkylated DNA repa
384	35.5	39.4	216	2	G85860	DNA repair system
385	35.5	39.4	317	1	JC4827	protein kinase (EC
386	35.5	39.4	363	2	T22107	hypothetical prote
387	35.5	39.4	393	1	HVRKC1	Ig mu chain C regi
388	35.5	39.4	397	2	S30023	antiviral protein
389	35.5	39.4	438	1	HVRKC2	Ig mu chain C regi
390	35.5	39.4	438	1	HVRKCS	Ig mu chain C regi
391	35.5	39.4	461	1	HVRKC0	Ig mu chain C regi
392	35.5	39.4	489	1	A53766	phosphoinositide-s
393	35.5	39.4	626	2	A42891	beta-galactosidase
394	35.5	39.4	739	2	H75001	methyl-accepting c

395	35.5	39.4	967	2	D96573	protein F12M16.21
396	35.5	39.4	1095	1	A31225	phospholipase C (E
397	35.5	39.4	1116	2	S26358	hypothetical prote
398	35.5	39.4	1195	2	S76592	5-methyltetrahydro
399	35.5	39.4	1615	1	WMTM18	183.3K protein - t
400	35.5	39.4	1615	1	WMTM8T	180K protein - tom
401	35.5	39.4	1866	1	GNWE2C	genome polyprotein
402	35.5	39.4	1884	2	JC4975	plexin 2 precursor
403	35	38.9	50	2	S26941	Ig heavy chain V r
404	35	38.9	86	1	IMECE2	colicin E2 immunit
405	35	38.9	97	2	S26804	Ig heavy chain V r
406	35	38.9	97	2	S26808	Ig heavy chain V r
407	35	38.9	97	2	S26906	Ig heavy chain V r
408	35	38.9	97	2	S12416	Ig heavy chain V r
409	35	38.9	98	2	S29545	Ig heavy chain V r
410	35	38.9	99	2	S12412	Ig heavy chain V r
411	35	38.9	101	2	PH0983	Ig heavy chain V r
412	35	38.9	101	2	PH0982	Ig heavy chain V r
413	35	38.9	102	2	PH1268	Ig heavy chain V r
414	35	38.9	102	2	PH1241	Ig heavy chain V r
415	35	38.9	102	2	PH1233	Ig heavy chain V r
416	35	38.9	102	2	S07974	12K protein - phag
417	35	38.9	104	2	PH0981	Ig heavy chain V r
418	35	38.9	105	2	S44125	Ig lambda chain V
419	35	38.9	109	2	PH1673	Ig heavy chain V r
420	35	38.9	110	2	E71083	hypothetical prote
421	35	38.9	111	2	S26463	Ig heavy chain V r
422	35	38.9	114	2	F82782	hypothetical prote
423	35	38.9	116	2	B26340	Ig heavy chain pre
424	35	38.9	116	2	S18557	Ig heavy chain V r
425	35	38.9	117	2	A28966	Ig heavy chain pre
426	35	38.9	118	2	A26340	Ig heavy chain pre
427	35	38.9	119	2	D30562	Ig heavy chain V r
428	35	38.9	130	2	S30534	Ig heavy chain V r
429	35	38.9	130	2	S31690	Ig heavy chain V r
430	35	38.9	135	2	A30577	Ig heavy chain pre
431	35	38.9	137	2	S31676	Ig heavy chain V r
432	35	38.9	138	2	E32513	Ig heavy chain pre
433	35	38.9	139	2	S31696	Ig heavy chain V r
434	35	38.9	139	2	S31586	Ig heavy chain V r
435	35	38.9	140	2	I37782	Ig variable region
436	35	38.9	160	2	A64210	single-stranded DN
437	35	38.9	160	2	JU0342	rhizopuspepsin (EC
438	35	38.9	174	2	T35829	acetolactate synth
439	35	38.9	191	2	B70042	hypothetical prote
440	35	38.9	192	2	B82103	conserved hypothet
441	35	38.9	193	2	D82509	Sco1-related prote
442	35	38.9	199	2	F64585	cag pathogenicity
443	35	38.9	200	2	AF1622	integral membrane
444	35	38.9	203	2	I51363	growth hormone - S
445	35	38.9	206	2	S13161	epidermal growth f
446	35	38.9	215	2	D75342	conserved hypothet
447	35	38.9	224	2	H97709	formylmethionine d
448	35	38.9	226	2	AF2362	transcription regu
449	35	38.9	230	2	T48962	hypothetical prote
450	35	38.9	238	2	C70321	Rieske iron-sulfur
451	35	38.9	250	2	T13459	hypothetical prote
452	35	38.9	260	1	CRHU2	carbonate dehydrat
453	35	38.9	260	2	E75592	probable chromosom
454	35	38.9	263	2	T24705	hypothetical prote
455	35	38.9	290	2	T48880	beta-lactamase (EC
456	35	38.9	303	2	AI2935	hypothetical prote
457	35	38.9	304	2	G69995	hypothetical prote
458	35	38.9	305	2	T15960	hypothetical prote
459	35	38.9	317	2	A37204	phospholipase C (E
460	35	38.9	317	2	AB1100	phosphatidylinosit
461	35	38.9	319	2	C69049	ABC transporter (A
462	35	38.9	326	2	G83881	transcription regu
463	35	38.9	326	2	E96923	glycosyltransferas
464	35	38.9	328	2	T17789	chitosanase homolo
465	35	38.9	333	2	A95039	sugar binding tran
466	35	38.9	333	2	F98346	probable permease
467	35	38.9	341	2	T50053	probable esterase
468	35	38.9	347	2	S30921	ferredoxin-nitrite
469	35	38.9	348	1	T31766	phosphoprotein pho
470	35	38.9	348	2	T11429	NADH2 dehydrogenas
471	35	38.9	351	2	A88103	protein W10G11.7 [
472	35	38.9	351	2	H71432	probable glucosylt
473	35	38.9	355	2	B97909	transcription regu
474	35	38.9	358	1	S71887	serine/threonine-s
475	35	38.9	360	2	A84722	probable GDSL-moti
476	35	38.9	362	2	H71187	probable ribosomal
477	35	38.9	366	2	G97305	spore germination
478	35	38.9	372	2	T16971	probable GTP-bindi
479	35	38.9	373	2	A86859	hypothetical prote
480	35	38.9	392	2	T18023	hypothetical prote
481	35	38.9	394	2	T51494	stearoyl-acyl carr
482	35	38.9	395	2	S36029	hypothetical prote
483	35	38.9	395	2	H96513	hypothetical prote
484	35	38.9	398	2	T02161	hypothetical prote
485	35	38.9	399	1	OHSPAD	acyl-[acyl-carrier
486	35	38.9	404	2	S57178	2-nitropropane dio
487	35	38.9	423	2	A69367	translation elonga
488	35	38.9	424	2	JC7102	histone deacetylas
489	35	38.9	427	2	D82197	hypothetical prote
490	35	38.9	428	2	D64340	translation elonga
491	35	38.9	428	2	JC5834	histone deacetylas
492	35	38.9	436	2	A37953	transcription regu
493	35	38.9	436	2	C90043	IgG-binding protei
494	35	38.9	438	2	F90005	transcription term
495	35	38.9	444	2	E96584	hypothetical prote
496	35	38.9	444	2	AH2965	hypothetical prote
497	35	38.9	444	2	D98317	probable pyridoxal
498	35	38.9	445	2	AB0359	hypothetical prote
499	35	38.9	446	2	T09960	mitosis-specific c
500	35	38.9	449	2	S27098	pectate lyase (EC
501	35	38.9	464	2	S10171	3-isopropylmalate
502	35	38.9	466	2	AD0516	3-isopropylmalate
503	35	38.9	470	2	T20851	hypothetical prote
504	35	38.9	478	2	S61192	hypothetical prote
505	35	38.9	479	2	S66578	ORD protein - frui
506	35	38.9	480	2	G64360	phenylalanine-tRNA
507	35	38.9	483	2	T17346	hypothetical prote
508	35	38.9	486	2	T21566	hypothetical prote
509	35	38.9	508	2	T20355	hypothetical prote
510	35	38.9	510	2	T20850	hypothetical prote
511	35	38.9	511	2	AG0636	periplasmic glucan
512	35	38.9	512	2	E59437	F02569_2 protein [
513	35	38.9	515	2	T40021	hypothetical prote
514	35	38.9	522	2	T45540	moaA protein [impo
515	35	38.9	526	2	F82873	hypothetical prote
516	35	38.9	554	2	T33894	hypothetical prote
517	35	38.9	575	2	JC7794	lammer kinase homo
518	35	38.9	586	2	T08293	hypothetical prote
519	35	38.9	608	2	C96527	protein F27J15.26
520	35	38.9	611	2	B86387	unknown protein [i
521	35	38.9	612	2	E82756	beta-galactosidase
522	35	38.9	623	2	T40685	phosphatidylcholin
523	35	38.9	638	2	B35816	transcription regu
524	35	38.9	639	2	T23658	hypothetical prote
525	35	38.9	649	1	B37953	transcription regu
526	35	38.9	649	2	A35816	transcription regu
527	35	38.9	652	2	T39722	serine/threonine p
528	35	38.9	664	2	G86692	penicillin-binding
529	35	38.9	686	2	A55665	microtubule-associ
530	35	38.9	690	2	T38052	probable protein k
531	35	38.9	699	2	A70300	translation elonga
532	35	38.9	701	2	C97302	hypothetical prote
533	35	38.9	708	2	T43109	cytolysin B transp
534	35	38.9	710	2	S66313	phenylalanine ammo
535	35	38.9	731	2	S46813	lanosterol synthas
536	35	38.9	731	2	B83904	hypothetical prote
537	35	38.9	758	2	S65169	hypothetical prote
538	35	38.9	799	1	IJMSFB	fibronectin recept
539	35	38.9	807	2	A32582	protein kinase YAK
540	35	38.9	819	2	B87580	conserved hypothet

541	35	38.9	821	2	B84509	probable Na/H anti
542	35	38.9	822	2	S68210	chloride channel p
543	35	38.9	825	2	B89944	hypothetical prote
544	35	38.9	845	2	S32819	translation elonga
545	35	38.9	875	2	AB1125	E. col YbgG protei
546	35	38.9	875	2	AI1485	E. col YbgG protei
547	35	38.9	885	2	T38387	hypothetical prote
548	35	38.9	907	2	S23399	chloride channel p
549	35	38.9	993	2	A36873	protein-tyrosine k
550	35	38.9	996	2	S76194	hypothetical prote
551	35	38.9	1042	2	S23738	pyr1-3 protein - s
552	35	38.9	1080	2	AF2467	hypothetical prote
553	35	38.9	1087	2	S02035	period clock prote
554	35	38.9	1090	2	AG1749	glycosidase homolo
555	35	38.9	1211	2	T41702	probable cation-tr
556	35	38.9	1290	2	A57190	ebnerin precursor
557	35	38.9	1293	1	A46350	RNA-directed RNA p
558	35	38.9	1294	2	S01085	hypothetical prote
559	35	38.9	1376	2	G00043	osteonidogen - hum
560	35	38.9	1377	2	D90538	hypothetical prote
561	35	38.9	1398	2	T25568	hypothetical prote
562	35	38.9	1441	2	T00335	hypothetical prote
563	35	38.9	1481	1	QZDOP3	pyrimidine synthes
564	35	38.9	1495	2	S60255	transcription co-r
565	35	38.9	1524	2	S68553	surface layer prot
566	35	38.9	1576	2	S65774	homeotic protein H
567	35	38.9	1767	2	T00458	hypothetical prote
568	35	38.9	1792	2	T08878	supervillin P205 -
569	35	38.9	1950	2	S12332	ubiquitin-protein
570	35	38.9	2115	2	S38480	nonstructural prot
571	35	38.9	2205	1	MNWVRN	nonstructural poly
572	35	38.9	3972	2	S75251	hypothetical prote
573	35	38.9	6658	2	T13931	projectin - fruit
574	35	38.9	8563	2	T30226	polyketide synthas
575	34.5	38.3	86	2	T01496	hypothetical prote
576	34.5	38.3	129	2	S44114	Ig heavy chain V r
577	34.5	38.3	184	2	S64020	hypothetical prote
578	34.5	38.3	186	2	S30221	nonhistone chromos
579	34.5	38.3	207	2	JC1129	nonhistone chromos
580	34.5	38.3	207	2	JC1114	high-mobility grou
581	34.5	38.3	209	1	NSHUH2	nonhistone chromos
582	34.5	38.3	210	2	A34719	nonhistone chromos
583	34.5	38.3	210	2	S54774	high mobility grou
584	34.5	38.3	239	2	T51270	hypothetical prote
585	34.5	38.3	244	2	E65128	hypothetical prote
586	34.5	38.3	244	2	A85999	hypothetical prote
587	34.5	38.3	244	2	E91153	hypothetical prote
588	34.5	38.3	246	2	T16403	hypothetical prote
589	34.5	38.3	251	1	F64559	conserved hypothet
590	34.5	38.3	263	2	T39487	hypothetical prote
591	34.5	38.3	390	2	G81742	conserved hypothet
592	34.5	38.3	394	2	A97244	moaA/NirJ family F
593	34.5	38.3	423	2	C81271	probable O-acetylh
594	34.5	38.3	427	2	D97242	o-acetylhomoserine
595	34.5	38.3	457	2	AF0003	oxygen-independent
596	34.5	38.3	524	2	B97864	hypothetical prote
597	34.5	38.3	536	1	EUHUGC	glucosylceramidase
598	34.5	38.3	665	2	T46570	dosage-dependent c
599	34.5	38.3	739	2	F71161	probable chemotaxi
600	34.5	38.3	1216	2	T09224	spindle assembly c
601	34.5	38.3	1353	2	T26301	hypothetical prote
602	34.5	38.3	1820	2	S71853	genome polyprotein
603	34.5	38.3	13055	2	T16580	hypothetical prote
604	34	37.8	94	2	D25913	Ig heavy chain V r
605	34	37.8	96	2	S17230	Ig heavy chain V r
606	34	37.8	96	2	S17614	Ig heavy chain V r
607	34	37.8	96	2	S17620	Ig heavy chain V r
608	34	37.8	96	2	S17618	Ig heavy chain V r
609	34	37.8	96	2	S17610	Ig heavy chain V r
610	34	37.8	97	2	S60846	M protein precurso
611	34	37.8	98	2	PH1274	Ig heavy chain V r
612	34	37.8	98	2	S26907	Ig heavy chain V r
613	34	37.8	98	2	S26932	Ig heavy chain V r
614	34	37.8	98	2	S26896	Ig heavy chain V r
615	34	37.8	101	2	S12428	Ig heavy chain V r
616	34	37.8	101	2	S12424	Ig heavy chain V r
617	34	37.8	102	2	PH1266	Ig heavy chain V r
618	34	37.8	102	2	PH1279	Ig heavy chain V r
619	34	37.8	102	2	PH1281	Ig heavy chain V r
620	34	37.8	102	2	PH1277	Ig heavy chain V r
621	34	37.8	102	2	PH1244	Ig heavy chain V r
622	34	37.8	102	2	PH1267	Ig heavy chain V r
623	34	37.8	102	2	PH1247	Ig heavy chain V r
624	34	37.8	102	2	PH1272	Ig heavy chain V r
625	34	37.8	102	2	PH1282	Ig heavy chain V r
626	34	37.8	102	2	PH1248	Ig heavy chain V r
627	34	37.8	102	2	PH1280	Ig heavy chain V r
628	34	37.8	102	2	PH1258	Ig heavy chain V r
629	34	37.8	102	2	PH1264	Ig heavy chain V r
630	34	37.8	102	2	PH1259	Ig heavy chain V r
631	34	37.8	102	2	PH1273	Ig heavy chain V r
632	34	37.8	102	2	PH1265	Ig heavy chain V r
633	34	37.8	102	2	PH1249	Ig heavy chain V r
634	34	37.8	102	2	PH1271	Ig heavy chain V r
635	34	37.8	102	2	PH1278	Ig heavy chain V r
636	34	37.8	104	2	B36006	Ig heavy chain V r
637	34	37.8	104	2	F81814	hypothetical prote
638	34	37.8	106	2	S59639	Ig heavy chain V r
639	34	37.8	107	2	S76457	hypothetical prote
640	34	37.8	112	2	T16317	hypothetical prote
641	34	37.8	113	2	PH1428	Ig heavy chain V r
642	34	37.8	115	2	PH1557	Ig heavy chain V r
643	34	37.8	116	2	S15672	Ig heavy chain V r
644	34	37.8	117	2	A28846	Ig heavy chain pre
645	34	37.8	117	2	S19670	Ig heavy chain V r
646	34	37.8	117	2	I28195	Ig heavy chain V r
647	34	37.8	117	2	PL0234	Ig heavy chain V r
648	34	37.8	119	2	S36257	Ig heavy chain V r
649	34	37.8	122	2	S64359	hypothetical prote
650	34	37.8	123	2	PH1423	Ig heavy chain V r
651	34	37.8	123	2	S30529	Ig heavy chain V r
652	34	37.8	123	2	S38492	Ig heavy chain - h
653	34	37.8	123	2	PH1413	Ig heavy chain V r
654	34	37.8	123	2	C36006	Ig heavy chain V r
655	34	37.8	127	2	PH1414	Ig heavy chain V r
656	34	37.8	127	2	PH1409	Ig heavy chain V r
657	34	37.8	127	2	PH1411	Ig heavy chain V r
658	34	37.8	128	2	S16685	Ig heavy chain V r
659	34	37.8	134	2	PH1422	Ig heavy chain V r
660	34	37.8	134	2	S52351	hypothetical prote
661	34	37.8	136	1	G1MS21	Ig heavy chain pre
662	34	37.8	136	2	A49047	Ig heavy chain V r
663	34	37.8	136	2	PH1559	Ig heavy chain V r
664	34	37.8	136	2	C72644	hypothetical prote
665	34	37.8	137	2	S34149	Ig mu chain - axol
666	34	37.8	138	2	S71145	H+-transporting tw
667	34	37.8	139	2	PH1558	Ig heavy chain V r
668	34	37.8	140	2	AH2559	transposase alr807
669	34	37.8	142	2	A41122	protein-tyrosine k
670	34	37.8	147	2	S09762	hypothetical prote
671	34	37.8	155	2	D70235	conserved hypothet
672	34	37.8	157	2	G75560	conserved hypothet
673	34	37.8	157	2	B70221	conserved hypothet
674	34	37.8	170	2	B64713	hypothetical prote
675	34	37.8	176	2	F95863	probable cytochrom
676	34	37.8	183	2	T48689	hypothetical prote
677	34	37.8	187	2	F71063	hypothetical prote
678	34	37.8	188	2	B28106	prolactin, 24K - M
679	34	37.8	188	2	G85572	probable fimbriae
680	34	37.8	188	2	B65174	hypothetical prote
681	34	37.8	188	2	B91210	hypothetical prote
682	34	37.8	188	2	E86056	hypothetical prote
683	34	37.8	193	2	H90721	probable fimbrial-
684	34	37.8	200	2	AD1260	integral membrane
685	34	37.8	213	2	S75247	hypothetical prote
686	34	37.8	214	2	H85359	hypothetical prote

687	34	37.8	215	2	S18228	replication initia
688	34	37.8	219	2	A82888	d-ribulose-5-phosp
689	34	37.8	221	2	B64155	hypothetical prote
690	34	37.8	225	2	C86563	CT465 hypothetical
691	34	37.8	225	2	C72062	conserved hypothet
692	34	37.8	226	2	B41378	cytochrome c553i p
693	34	37.8	228	2	A90043	hypothetical prote
694	34	37.8	240	1	VCWGN4	coat protein - nar
695	34	37.8	248	2	T12096	peptidylprolyl iso
696	34	37.8	249	2	S41374	single chain Fv an
697	34	37.8	251	2	E69297	diphthine synthase
698	34	37.8	252	2	E64313	hypothetical prote
699	34	37.8	256	2	AE3549	6-aminohexanoate-d
700	34	37.8	259	2	A22612	carbonate dehydrat
701	34	37.8	259	2	G90042	hypothetical prote
702	34	37.8	261	2	T18320	hypothetical prote
703	34	37.8	262	2	S24718	ornithine carbamoy
704	34	37.8	262	2	S24719	ornithine carbamoy
705	34	37.8	262	2	S24734	ornithine carbamoy
706	34	37.8	262	2	S24741	ornithine carbamoy
707	34	37.8	262	2	S24727	ornithine carbamoy
708	34	37.8	262	2	S24749	ornithine carbamoy
709	34	37.8	275	2	S40007	trypsin (EC 3.4.21
710	34	37.8	280	2	S24720	ornithine carbamoy
711	34	37.8	280	2	C69343	diaminopimelate ep
712	34	37.8	281	2	C72712	probable methionin
713	34	37.8	282	2	F72297	hypothetical prote
714	34	37.8	287	2	T46874	ribokinase homolog
715	34	37.8	296	2	S53960	CTK3 protein - yea
716	34	37.8	306	2	T19412	hypothetical prote
717	34	37.8	307	2	T50493	syntaxin-like prot
718	34	37.8	311	2	C89968	leukotoxin LukE [i
719	34	37.8	313	2	S17757	rRNA N-glycosidase
720	34	37.8	317	2	T45985	hypothetical prote
721	34	37.8	321	2	T42591	gene 48 protein -
722	34	37.8	325	2	T40529	cyclin - fission y
723	34	37.8	330	2	C90090	ATP(GTP)-binding p
724	34	37.8	331	1	OWNHG	ornithine carbamoy
725	34	37.8	331	2	E81066	ornithine carbamoy
726	34	37.8	331	2	B81801	ornithine carbamoy
727	34	37.8	333	2	C84127	high-alkaline pect
728	34	37.8	334	2	JC4870	pepsin A (EC 3.4.2
729	34	37.8	334	2	C82935	recombination prot
730	34	37.8	336	2	H70693	hypothetical prote
731	34	37.8	336	2	T20946	hypothetical prote
732	34	37.8	336	2	T19567	hypothetical prote
733	34	37.8	337	2	T29474	hypothetical prote
734	34	37.8	338	2	H96765	hypothetical prote
735	34	37.8	340	2	C75004	hypothetical prote
736	34	37.8	340	2	T22741	hypothetical prote
737	34	37.8	341	1	S26603	hypothetical prote
738	34	37.8	341	2	G83077	competence protein
739	34	37.8	351	2	T42421	hypothetical prote
740	34	37.8	351	2	T26840	hypothetical prote
741	34	37.8	354	2	A55454	decorin precursor
742	34	37.8	359	2	H84706	probable GDSL-moti
743	34	37.8	361	2	T45860	cyclin D3-like pro
744	34	37.8	363	2	B90482	dehydrogenase, pro
745	34	37.8	365	2	S17885	TcD37 protein - fr
746	34	37.8	371	2	B39625	T-cell receptor al
747	34	37.8	372	2	B89898	LytN protein [impo
748	34	37.8	376	2	F96619	protein T30E16.13
749	34	37.8	381	1	JQ1725	nucleocapsid prote
750	34	37.8	381	2	T11440	ubiquinol-cytochro
751	34	37.8	382	1	A44056	nucleocapsid prote
752	34	37.8	385	2	S46529	polygalacturonase
753	34	37.8	386	2	G83723	hypothetical prote
754	34	37.8	387	1	RSBPIP	integrase - phage
755	34	37.8	388	2	S41940	oligogalacturonide
756	34	37.8	390	2	C42477	malY protein (EC 2
757	34	37.8	392	2	AF3445	spore-cortex-lytic
758	34	37.8	393	2	F86853	aspartate transami
759	34	37.8	395	2	D72339	hypothetical prote
760	34	37.8	397	2	T10793	acyl-[acyl-carrier
761	34	37.8	397	2	A39565	lymphoid enhancer-
762	34	37.8	399	2	T18853	probable transcrip
763	34	37.8	399	2	A39625	T-cell receptor al
764	34	37.8	400	2	T15459	hypothetical prote
765	34	37.8	402	2	A41594	Na+/H+-exchanging
766	34	37.8	403	2	S07825	hypothetical prote
767	34	37.8	404	2	S42578	gene prune protein
768	34	37.8	406	2	AG0584	N-acetylglucosamin
769	34	37.8	410	2	T46034	branched-chain-ami
770	34	37.8	419	2	B89788	hypothetical prote
771	34	37.8	419	2	F83673	PTS system, galact
772	34	37.8	421	2	AD1204	hypothetical prote
773	34	37.8	427	2	AB3265	O-succinylhomoseri
774	34	37.8	427	2	A47051	transcription term
775	34	37.8	434	2	AI3578	glutamate-ammonia
776	34	37.8	437	2	H70301	nucleotide sugar d
777	34	37.8	440	2	E82213	sensor histidine k
778	34	37.8	441	2	T25183	hypothetical prote
779	34	37.8	446	2	B70776	probable gln2 - My
780	34	37.8	448	2	A87113	glutamine synthase
781	34	37.8	451	1	GBECAG	alpha-galactosidas
782	34	37.8	451	2	E91266	alpha-galactosidas
783	34	37.8	452	2	AF1014	maltoporin precurs
784	34	37.8	456	2	G91251	probable DNA circu
785	34	37.8	459	2	T11398	NADH2 dehydrogenas
786	34	37.8	461	2	AI0279	hypothetical prote
787	34	37.8	462	2	S10397	finger protein kox
788	34	37.8	469	2	A90166	conserved hypothet
789	34	37.8	470	1	S56565	hypothetical 53K p
790	34	37.8	474	2	A35732	protective protein
791	34	37.8	474	2	E83587	two-component sens
792	34	37.8	483	1	A46746	glycine hydroxymet
793	34	37.8	484	2	A40202	glycine hydroxymet
794	34	37.8	489	2	T04862	probable serine/th
795	34	37.8	501	2	I46701	cholesterol 7alpha
796	34	37.8	506	2	T08927	probable protein k
797	34	37.8	517	2	H86452	MUDRA-like transpo
798	34	37.8	518	2	G71646	probable protoporp
799	34	37.8	525	2	B83957	flagellar basal-bo
800	34	37.8	527	2	T38265	hypothetical serin
801	34	37.8	531	2	S20900	titin - mouse (fra
802	34	37.8	533	2	D83468	probable decarboxy
803	34	37.8	538	2	A41042	microbial metallop
804	34	37.8	540	2	T14748	hypothetical prote
805	34	37.8	560	2	AD0359	probable membrane
806	34	37.8	567	2	C82183	catalase VC1585 [i
807	34	37.8	570	2	A45249	alpha-glucosidase
808	34	37.8	571	2	F84718	hypothetical prote
809	34	37.8	580	2	E82114	flagellar M-ring p
810	34	37.8	580	2	E84477	Mutator-like trans
811	34	37.8	580	2	C84526	Mutator-like trans
812	34	37.8	580	2	T01865	hypothetical prote
813	34	37.8	584	2	E71643	poly-beta-hydroxyb
814	34	37.8	586	2	C84531	ferredoxin-nitrite
815	34	37.8	589	2	T50698	probable mandeloni
816	34	37.8	590	1	WMBECB	64K capsid assembl
817	34	37.8	594	2	T33686	hypothetical prote
818	34	37.8	596	2	T08847	ferredoxin-nitrite
819	34	37.8	596	2	T03908	hypothetical prote
820	34	37.8	601	2	T52017	fumarate reductase
821	34	37.8	601	2	F64116	endopeptidase La h
822	34	37.8	602	2	G75278	N-acetylmuramoyl-L
823	34	37.8	607	2	H88065	protein T16A1.1 [i
824	34	37.8	607	2	F84525	Mutator-like trans
825	34	37.8	612	2	A54282	reversed polarity
826	34	37.8	616	2	E84463	Mutator-like trans
827	34	37.8	618	1	S38004	probable transport
828	34	37.8	622	2	D82055	conserved hypothet
829	34	37.8	625	2	S69707	hypothetical prote
830	34	37.8	628	2	S37795	hypothetical prote
831	34	37.8	639	2	A24333	tetracycline resis
832	34	37.8	646	1	KJKM	arylsulfatase (EC

833	34	37.8	655	2	AI2556	hypothetical prote
834	34	37.8	658	2	T41309	hypothetical threo
835	34	37.8	662	2	I37892	IL12 receptor comp
836	34	37.8	664	2	PC4002	phosphatidylinosit
837	34	37.8	673	2	A97947	conserved hypothet
838	34	37.8	676	2	F69394	H+-transporting AT
839	34	37.8	685	2	T12139	NADH2 dehydrogenas
840	34	37.8	686	2	E87490	NADH dehydrogenase
841	34	37.8	711	2	T25281	hypothetical prote
842	34	37.8	720	2	A36526	choline O-acetyltr
843	34	37.8	728	2	A24889	choline O-acetyltr
844	34	37.8	729	2	C69038	transcription regu
845	34	37.8	729	2	T15076	hypothetical prote
846	34	37.8	739	2	T12983	hypothetical prote
847	34	37.8	748	2	H84913	probable ATP-depen
848	34	37.8	755	2	T32971	hypothetical prote
849	34	37.8	758	2	AE2022	hypothetical prote
850	34	37.8	760	2	AB2225	hypothetical prote
851	34	37.8	786	2	T26811	hypothetical prote
852	34	37.8	790	2	E86383	hypothetical prote
853	34	37.8	798	2	S01659	integrin beta-1 ch
854	34	37.8	799	2	JC4126	integrin beta olig
855	34	37.8	801	1	T52538	1-phosphatidylinos
856	34	37.8	808	1	T04982	dynamin-like prote
857	34	37.8	811	2	T25166	hypothetical prote
858	34	37.8	816	2	C83917	DNA topoisomerase
859	34	37.8	818	2	T33689	hypothetical prote
860	34	37.8	818	2	T33687	hypothetical prote
861	34	37.8	838	2	T04449	hypothetical prote
862	34	37.8	849	2	C97303	hypothetical prote
863	34	37.8	884	2	B96492	probable polyprote
864	34	37.8	900	2	E71623	protein with DnaJ
865	34	37.8	941	2	B96553	hypothetical prote
866	34	37.8	966	2	S28614	phosphoenolpyruvat
867	34	37.8	1011	1	JH0581	NAD ADP-ribosyltra
868	34	37.8	1068	2	G86452	hypothetical prote
869	34	37.8	1070	2	T34385	hypothetical prote
870	34	37.8	1091	2	AF1380	glycosidase homolo
871	34	37.8	1108	2	JC4037	alpha-mannosidase
872	34	37.8	1128	1	QQBE47	DNA-binding protei
873	34	37.8	1146	2	AH1208	pyruvate carboxyla
874	34	37.8	1146	2	AC1565	pyruvate carboxyla
875	34	37.8	1151	2	S48431	probable membrane
876	34	37.8	1160	2	T13713	beta3 protein - fr
877	34	37.8	1193	2	F83264	hypothetical prote
878	34	37.8	1220	2	S64916	probable membrane
879	34	37.8	1224	2	S73171	DNA-directed RNA p
880	34	37.8	1237	2	E86457	probable RNA helic
881	34	37.8	1357	2	T29265	hypothetical prote
882	34	37.8	1358	2	S33653	probable serine/th
883	34	37.8	1461	2	T13157	mitotic checkpoint
884	34	37.8	1468	2	S58250	DNA-directed DNA p
885	34	37.8	1478	2	S20117	protein kinase BCK
886	34	37.8	1491	1	S43793	copper-transportin
887	34	37.8	1603	2	D89407	protein R10E8.6 [i
888	34	37.8	1608	1	WMTMGM	183K protein - tob
889	34	37.8	1627	1	IJYMAP	adhesin P1 precurs
890	34	37.8	1635	2	A41480	adhesin P1, group
891	34	37.8	1668	2	A60272	IgA-specific metal
892	34	37.8	1696	2	T24146	hypothetical prote
893	34	37.8	1764	2	S37827	hypothetical prote
894	34	37.8	1778	2	T50074	probable nucleopor
895	34	37.8	1798	2	T27149	hypothetical prote
896	34	37.8	2004	2	F95133	immunoglobulin A1
897	34	37.8	2105	1	A44059	genome polyprotein
898	34	37.8	2431	1	MNWVSF	nonstructural poly
899	34	37.8	2539	2	B71619	hypothetical prote
900	34	37.8	2549	2	S45340	FKBP-rapamycin-ass
901	34	37.8	2549	2	A54837	rapamycin/FKBP12 t
902	34	37.8	2958	2	S64921	probable membrane
903	34	37.8	3228	2	T21381	hypothetical prote
904	34	37.8	3262	2	AH2137	hypothetical prote
905	34	37.8	3600	2	D86161	F10O3.12 protein -
906	34	37.8	3869	2	A48205	All-1 protein +GTE
907	34	37.8	6805	2	S20901	titin - rabbit (fr
908	34	37.8	7576	2	T17428	FK506 polyketide s
909	34	37.8	10223	2	T30225	polyketide synthas
910	33.5	37.2	97	2	G34964	Ig heavy chain V-I
911	33.5	37.2	120	2	A25114	Ig heavy chain V r
912	33.5	37.2	123	2	E84752	hypothetical prote
913	33.5	37.2	139	2	S54247	Ig mu heavy chain
914	33.5	37.2	140	2	T39107	hypothetical prote
915	33.5	37.2	142	2	S54243	Ig mu heavy chain
916	33.5	37.2	145	2	T17931	IgA Fc receptor-li
917	33.5	37.2	197	2	A97912	dTDP-4-dehydrorham
918	33.5	37.2	216	2	AF0789	AlkB protein [impo
919	33.5	37.2	231	2	F81089	6-phosphogluconola
920	33.5	37.2	251	2	A70113	methionine aminope
921	33.5	37.2	251	2	G71947	hypothetical prote
922	33.5	37.2	325	2	T23309	hypothetical prote
923	33.5	37.2	358	2	S07594	hypothetical prote
924	33.5	37.2	367	2	H84397	hypothetical prote
925	33.5	37.2	370	2	D83818	heat-shock protein
926	33.5	37.2	373	2	T36591	hypothetical prote
927	33.5	37.2	390	2	G71479	hypothetical prote
928	33.5	37.2	407	2	A72691	probable spermidin
929	33.5	37.2	419	2	B49418	spermatogenesis fa
930	33.5	37.2	450	2	A57426	puc expression act
931	33.5	37.2	474	2	S71322	glutathione syntha
932	33.5	37.2	490	2	A55141	GlcNAc beta-1,4-N-
933	33.5	37.2	494	1	CSPM	catalase (EC 1.11.
934	33.5	37.2	496	2	A49418	spermatogenesis fa
935	33.5	37.2	501	2	A87474	enoyl-CoA hydratas
936	33.5	37.2	554	1	SYECQT	glutamine-tRNA lig
937	33.5	37.2	554	2	F85567	glutamine tRNA syn
938	33.5	37.2	554	2	F90717	glutamine tRNA syn
939	33.5	37.2	559	2	A42807	phosphoglycerate m
940	33.5	37.2	561	1	A41365	rhodopsin kinase (
941	33.5	37.2	601	2	A28577	NADPH-ferrihemopro
942	33.5	37.2	630	2	G87753	protein C43E11.8 [
943	33.5	37.2	650	2	T38692	probable serine/th
944	33.5	37.2	651	2	T49986	lectin-like protei
945	33.5	37.2	857	2	A42861	protein kinase TTK
946	33.5	37.2	859	2	S66827	aluminium resistan
947	33.5	37.2	894	2	C90719	hypothetical prote
948	33.5	37.2	894	2	D85569	hypothetical prote
949	33.5	37.2	894	2	B42372	histidine kinase k
950	33.5	37.2	1021	2	T51497	hypothetical prote
951	33.5	37.2	1196	2	S40908	TyB protein - yeas
952	33.5	37.2	1278	2	B22671	TyB protein - yeas
953	33.5	37.2	1328	2	B22999	TyB protein - yeas
954	33.5	37.2	1328	2	S52481	TyB protein - yeas
955	33.5	37.2	1328	2	S50948	TyB protein - yeas
956	33.5	37.2	1328	2	S52894	TyB protein - yeas
957	33.5	37.2	1328	2	B28097	TyB protein - yeas
958	33.5	37.2	1348	2	B23496	TyB protein - yeas
959	33.5	37.2	1598	2	S69967	TyB protein - yeas
960	33.5	37.2	1604	2	S70227	TyB protein - yeas
961	33.5	37.2	1616	1	JQ2144	183K protein - tom
962	33.5	37.2	1749	2	S69972	TyB protein - yeas
963	33.5	37.2	1755	2	S69979	TyB protein - yeas
964	33.5	37.2	1755	2	S69975	TyB protein - yeas
965	33.5	37.2	1755	2	S69866	TyB protein - yeas
966	33.5	37.2	1755	2	S69955	TyB protein - yeas
967	33.5	37.2	1755	2	S50663	TyB protein - yeas
968	33.5	37.2	1755	2	S50641	TyB protein YER138
969	33.5	37.2	1755	2	S57047	TyB protein - yeas
970	33.5	37.2	1755	2	S69951	TyB protein - yeas
971	33.5	37.2	1755	2	S45736	TyB protein - yeas
972	33.5	37.2	1755	2	S69838	TyB protein - yeas
973	33.5	37.2	1755	2	S61763	TyB protein - yeas
974	33.5	37.2	1755	2	S57045	TyB protein - yeas
975	33.5	37.2	1755	2	S70298	TyB protein - yeas
976	33.5	37.2	1755	2	S69982	TyB protein - yeas
977	33.5	37.2	1755	2	S69960	TyB protein - yeas
978	33.5	37.2	1755	2	S69969	TyB protein - yeas

979	33.5	37.2	1755	2	S69949	TyB protein - yeas
980	33.5	37.2	1755	2	S69957	TyB protein - yeas
981	33.5	37.2	1755	2	S69963	TyB protein - yeas
982	33.5	37.2	1755	2	S69839	TyB protein - yeas
983	33.5	37.2	1755	2	S69845	TyB protein - yeas
984	33.5	37.2	1755	2	S69980	TyB protein - yeas
985	33.5	37.2	1756	2	S45867	TyB protein - yeas
986	33.5	37.2	1756	2	S69983	TyB protein - yeas
987	33.5	37.2	1770	2	S69953	TyB protein - yeas
988	33.5	37.2	1770	2	S58651	TyB protein - yeas
989	33.5	37.2	1770	2	S70233	TyB protein - yeas
990	33.5	37.2	1770	2	S69948	TyB protein - yeas
991	33.5	37.2	1770	2	S69966	TyB protein - yeas
992	33.5	37.2	1770	2	S45842	TyB protein - yeas
993	33.5	37.2	1770	2	S70230	TyB protein - yeas
994	33.5	37.2	1770	2	S69950	TyB protein - yeas
995	33.5	37.2	1771	2	S53592	TyB protein - yeas
996	33.5	37.2	1793	2	S52601	TyB protein - yeas
997	33.5	37.2	1810	2	S69973	TyB protein - yeas
998	33.5	37.2	2129	2	T14182	fxbC protein - Myc
999	33.5	37.2	4976	2	T14165	peptide synthetase
1000	33	36.7	94	2	PN0142	histone H2B - Neur

ALIGNMENTS

RESULT 1
AVMSJ5
Ig heavy chain V region (J539) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Apr-1980 #sequence_revision 30-Apr-1980 #text_change 09-Jul-2004
C;Accession: A02080
R;Rao, D.N.; Rudikoff, S.; Krutzsch, H.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 76, 2890-2894, 1979
A;Title: Structural evidence for independent joining region gene in immunoglobulin heavy
etermining regions.
A;Reference number: A93832; MUID:79223895; PMID:111245
A;Accession: A02080
A;Molecule type: protein
A;Residues: 1-119 <RAO>
A;Cross-references: UNIPROT:P01810; UNIPARC:UPI0000027262
C;Comment: This chain was isolated from a myeloma protein that binds galactan.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted

Query Match 91.1%; Score 82; DB 1; Length 119;
Best Local Similarity 88.2%; Pred. No. 3.2e-06;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||||||:|||| |||||
Db 50 EIHPDSGTINYTPSLKD 66

RESULT 2
I67528
CD33 antigen homolog - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C;Accession: I67528
R;Chies, J.A.; Lembezat, M.P.; Freitas, A.A.
Eur. J. Immunol. 24, 1657-1664, 1994
A;Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is r
A;Reference number: I53392; MUID:94298870; PMID:8026526
A;Accession: I67528
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-94 <RES>
A;Cross-references: UNIPARC:UPI0000176EB4; GB:S71357; NID:g550040
C;Genetics:
A;Gene: Ig VHX24b
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;11-94/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 79; DB 2; Length 94;
Best Local Similarity 88.2%; Pred. No. 7.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:|||||||| |||||
Db 46 EINPDSSTINYTPSLKD 62

RESULT 3
HVMS44
Ig heavy chain precursor V region (441) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A02076
R;Ollo, R.; Auffray, C.; Sikorav, J.L.; Rougeon, F.
Nucleic Acids Res. 9, 4099-4109, 1981
A;Title: Mouse heavy chain variable regions: nucleotide sequence of a germ-line V-H gene
A;Reference number: A02076; MUID:82059449; PMID:6795591
A;Accession: A02076
A;Molecule type: DNA
A;Residues: 1-116 <OLL>
A;Cross-references: UNIPROT:P01806; UNIPARC:UPI000002724C; GB:V00774; GB:J00541; NID:g516
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Introns: 15/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-116/Product: Ig heavy chain V region (441) #status predicted <MAT>
F;33-116/Domain: immunoglobulin homology <IMM>
F;40-114/Disulfide bonds: #status predicted

Query Match 87.8%; Score 79; DB 1; Length 116;
Best Local Similarity 88.2%; Pred. No. 9.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:|||||||| |||||
Db 68 EINPDSSTINYTPSLKD 84

RESULT 4
A47329
Ig heavy chain V region (PR1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 17-Jul-1994 #text_change 30-May-1997
C;Accession: A47329
R;Brinkmann, U.; Gallo, M.; Brinkmann, E.; Kunwar, S.; Pastan, I.
Proc. Natl. Acad. Sci. U.S.A. 90, 547-551, 1993
A;Title: A recombinant immunotoxin that is active on prostate cancer cells and that is cc
A;Reference number: A47329; MUID:93133825; PMID:8421689
A;Accession: A47329
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <BRI>
A;Cross-references: UNIPARC:UPI0000176E3C
A;Experimental source: Balb/c
A;Note: sequence modified after extraction from NCBI backbone
A;Note: sequence extracted from NCBI backbone (NCBIN:122874)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-99/Domain: immunoglobulin homology <IMM>

Query Match 87.8%; Score 79; DB 2; Length 118;
Best Local Similarity 88.2%; Pred. No. 9.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17

```
              ||:|||||||| |||||
Db         51 EINPDSSTINYTPSLKD 67


RESULT 5
AVMST6
Ig heavy chain V region (T601) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Apr-1980 #sequence_revision 30-Apr-1980 #text_change 09-Jul-2004
C;Accession: A02078
R;Rao, D.N.; Rudikoff, S.; Krutzsch, H.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 76, 2890-2894, 1979
A;Title: Structural evidence for independent joining region gene in immunoglobulin heavy
etermining regions.
A;Reference number: A93832; MUID:79223895; PMID:111245
A;Accession: A02078
A;Molecule type: protein
A;Residues: 1-119 <RAO>
A;Cross-references: UNIPROT:P01808; UNIPARC:UPI0000027253
C;Comment: This chain was isolated from an IgA myeloma protein that binds galactan.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted

  Query Match             87.8%;  Score 79;  DB 1;  Length 119;
  Best Local Similarity   88.2%;  Pred. No. 1e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         50 EINPDSSTINYTPSLKD 66


RESULT 6
AVMSX4
Ig heavy chain V region (X44) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Apr-1980 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C;Accession: A02077; S06815
R;Rao, D.N.; Rudikoff, S.; Krutzsch, H.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 76, 2890-2894, 1979
A;Title: Structural evidence for independent joining region gene in immunoglobulin heavy
etermining regions.
A;Reference number: A93832; MUID:79223895; PMID:111245
A;Accession: A02077
A;Molecule type: protein
A;Residues: 1-119 <RAO>
A;Cross-references: UNIPROT:P01807; UNIPARC:UPI0000027250
A;Note: this chain was isolated from an IgA myeloma protein that binds galactan
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06815
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-118 <MIL>
A;Cross-references: UNIPARC:UPI0000173738
A;Experimental source: clone IIIB
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted

  Query Match             87.8%;  Score 79;  DB 1;  Length 119;
  Best Local Similarity   88.2%;  Pred. No. 1e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         50 EINPDSSTINYTPSLKD 66


RESULT 7
A25912
Ig heavy chain precursor V region (W3129) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999
C;Accession: A25912
R;Borden, P.; Kabat, E.A.
Proc. Natl. Acad. Sci. U.S.A. 84, 2440-2443, 1987
A;Title: Nucleotide sequence of the cDNAs encoding the variable region heavy and light ch
A;Reference number: A94147; MUID:87175689; PMID:2436230
A;Accession: A25912
A;Molecule type: mRNA
A;Residues: 1-139 <BOR>
A;Cross-references: UNIPARC:UPI0000114C7B; GB:M15873; NID:g195268; PIDN:AAA38228.1; PID:g
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-139/Product: Ig heavy chain V region W3129 #status predicted <VAR>
F;33-116/Domain: immunoglobulin homology <IMM>

  Query Match             87.8%;  Score 79;  DB 2;  Length 139;
  Best Local Similarity   88.2%;  Pred. No. 1.2e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         68 EINPDSSTINYTPSLKD 84


RESULT 8
G2MSU1
Ig heavy chain V region (UPC10) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C;Accession: A02081
R;Auffray, C.; Sikorav, J.L.; Ollo, R.; Rougeon, F.
Ann. Immunol. (Paris) 132D, 77-88, 1981
A;Title: Correlation between D region structure and antigen-binding specifity: evidences
A;Reference number: A02081; MUID:83021113; PMID:6181731
A;Accession: A02081
A;Molecule type: mRNA
A;Residues: 1-117 <AUF>
A;Cross-references: UNIPROT:P01811; UNIPARC:UPI0000027263
C;Comment: This chain was isolated from an Ig gamma-2a myeloma protein binding 2,6-levan
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted

  Query Match             81.1%;  Score 73;  DB 1;  Length 117;
  Best Local Similarity   82.4%;  Pred. No. 9.6e-05;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| | |||
Db         50 EINPDSSTINYTPFLKD 66


RESULT 9
I67527
CD33 antigen homolog - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C;Accession: I67527
R;Chies, J.A.; Lembezat, M.P.; Freitas, A.A.
Eur. J. Immunol. 24, 1657-1664, 1994
A;Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is nc
A;Reference number: I53392; MUID:94298870; PMID:8026526
A;Accession: I67527
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-95 <RES>
```

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A;Cross-references: UNIPARC:UPI0000176EB3; GB:S71351; NID:g550039
C;Genetics:
A;Gene: Ig VHX24a
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;12-95/Domain: immunoglobulin homology <IMM>

  Query Match             80.0%;  Score 72;  DB 2;  Length 95;
  Best Local Similarity   82.4%;  Pred. No. 0.00011;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:| |||||| |||||
Db         47 EINPGSSTINYTPSLKD 63


RESULT 10
G2MS73
Ig heavy chain V region (MOPC 173) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change 09-Jul-2004
C;Accession: A91190; A91235; A93886; A02082
R;Bourgois, A.; Fougereau, M.; de Preval, C.
Eur. J. Biochem. 24, 446-455, 1972
A;Title: Sequence of amino acids of the NH-2-terminal region of a mouse-clonal immunoglo
A;Reference number: A91190; MUID:72105531; PMID:5062012
A;Accession: A91190
A;Molecule type: protein
A;Residues: 1-104 <BOU>
A;Cross-references: UNIPROT:P01812; UNIPARC:UPI0000173739
R;Rocca-Serra, J.; Milili, M.; Fougereau, M.
Eur. J. Biochem. 59, 511-523, 1975
A;Title: Determination of the primary structure of a mouse IgG2a immunoglobulin. Amino-a
A;Reference number: A91235; MUID:76091933; PMID:812695
A;Accession: A91235
A;Molecule type: protein
A;Residues: 'D',106-117 <ROC>
A;Cross-references: UNIPARC:UPI000017373A
R;Gough, N.M.; Bernard, O.
Proc. Natl. Acad. Sci. U.S.A. 78, 509-513, 1981
A;Title: Sequences of the joining region genes for immunoglobulin heavy chains and their
A;Reference number: A93886; MUID:81223769; PMID:6787590
A;Accession: A93886
A;Molecule type: DNA
A;Residues: 96-117 <GOU>
A;Cross-references: UNIPARC:UPI000017373B
R;Bourgois, A.; Fougereau, M.
FEBS Lett. 8, 265-268, 1970
A;Title: Partial amino acid sequence of the variable region of a mouse gammaG2a immunogl
A;Reference number: A91439
A;Contents: annotation; disulfide bond
C;Comment: This gamma-2a chain was isolated from a myeloma protein.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status experimental

  Query Match             80.0%;  Score 72;  DB 1;  Length 117;
  Best Local Similarity   82.4%;  Pred. No. 0.00014;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              || |:|||||| |||||
Db         50 EIDPNSSTINYTPSLKD 66


RESULT 11
S13791
Ig heavy chain V region (X-24) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S13791
R;Arepalli, S.R.; Heller, M.; Glaudemans, C.P.J.
Nucleic Acids Res. 18, 7152, 1990
A;Title: Sequence of the V(H) gene for murine IgA X-24.
A;Reference number: S13791; MUID:91088313; PMID:2124679
A;Accession: S13791
A;Molecule type: DNA
A;Residues: 1-136 <ARE>
A;Cross-references: UNIPARC:UPI0000176C85; EMBL:X55984
A;Note: the authors translated the codon GGG for residue 15 as Lys
C;Genetics:
A;Introns: 15/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-116/Domain: immunoglobulin homology <IMM>

  Query Match             80.0%;  Score 72;  DB 2;  Length 136;
  Best Local Similarity   82.4%;  Pred. No. 0.00016;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:| |||||| |||||
Db         68 EINPGSSTINYTPSLKD 84


RESULT 12
A30560
Ig heavy chain V region (16.4.12E) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 23-Jul-1999
C;Accession: A30560
R;Matsuda, T.; Kabat, E.A.
J. Immunol. 142, 863-870, 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclor
.
A;Reference number: A30560; MUID:89110062; PMID:2464028
A;Accession: A30560
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-121 <MAT>
A;Cross-references: UNIPARC:UPI0000114E07; GB:M22955; NID:g195610; PIDN:AAA38368.1; PID:9
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             78.9%;  Score 71;  DB 2;  Length 121;
  Best Local Similarity   82.4%;  Pred. No. 0.00021;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||| ||||| |||
Db         50 EINPDSSIINYAPFLKD 66


RESULT 13
S06817
Ig heavy chain V region (clone 11C7) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 11-Nov-1994 #text_change 23-Jul-1999
C;Accession: S06817
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morph
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06817
A;Molecule type: mRNA
A;Residues: 1-130 <MIL>
A;Cross-references: UNIPARC:UPI0000115E39; EMBL:X17165; NID:g51917; PIDN:CAA35043.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted

  Query Match             73.3%;  Score 66;  DB 2;  Length 130;
  Best Local Similarity   70.6%;  Pred. No. 0.0015;
  Matches   12;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          1 EIHPDSSTINYAPSLKD 17
              ||:| |:|||| ||||:
Db         50 EINPSSNTINYTPSLKE 66


RESULT 14
S13692
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-May-1997
C;Accession: S13692
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13692
A;Molecule type: mRNA
A;Residues: 1-101 <PEN>
A;Cross-references: UNIPARC:UPI0000176D57; EMBL:X53345
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             67.8%;  Score 61;  DB 2;  Length 101;
  Best Local Similarity   64.7%;  Pred. No. 0.0077;
  Matches   11;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              :|: | | ||||||:||
Db         32 DINSDGSAINYAPSIKD 48


RESULT 15
S13693
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 30-May-1997
C;Accession: S13693
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13693
A;Molecule type: mRNA
A;Residues: 1-111 <PEN>
A;Cross-references: UNIPARC:UPI0000176E3D; EMBL:X53346
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             67.8%;  Score 61;  DB 2;  Length 111;
  Best Local Similarity   64.7%;  Pred. No. 0.0086;
  Matches   11;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              :|: | | ||||||:||
Db         50 DINSDGSAINYAPSIKD 66


RESULT 16
S13690
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Jun-1997
C;Accession: S13690
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to cl
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13690
A;Molecule type: mRNA
A;Residues: 1-112 <PEN>
A;Cross-references: UNIPARC:UPI0000176E5F; EMBL:X53343
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             67.8%;  Score 61;  DB 2;  Length 112;
  Best Local Similarity   64.7%;  Pred. No. 0.0087;
  Matches   11;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              :|: | | ||||||:||
Db         50 DINSDGSAINYAPSIKD 66


RESULT 17
S13694
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S13694
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clo
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13694
A;Molecule type: mRNA
A;Residues: 1-115 <PEN>
A;Cross-references: UNIPARC:UPI0000113776; EMBL:X53347; NID:g55240; PIDN:CAA37433.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             67.8%;  Score 61;  DB 2;  Length 115;
  Best Local Similarity   64.7%;  Pred. No. 0.0089;
  Matches   11;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              :|: | | ||||||:||
Db         50 DINSDGSAINYAPSIKD 66


RESULT 18
S13691
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S13691
R;Pennell, C.A.; Mercolino, T.J.; Grdina, T.A.; Arnold, L.W.; Haughton, G.; Clarke, S.H.
Eur. J. Immunol. 19, 1289-1295, 1989
A;Title: Biased immunoglobulin variable region gene expression by Ly-1 B cells due to clo
A;Reference number: S13685; MUID:89338557; PMID:2503389
A;Accession: S13691
A;Molecule type: mRNA
A;Residues: 1-116 <PEN>
A;Cross-references: UNIPARC:UPI0000113773; EMBL:X53344; NID:g55235; PIDN:CAA37430.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             67.8%;  Score 61;  DB 2;  Length 116;
  Best Local Similarity   64.7%;  Pred. No. 0.009;
  Matches   11;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              :|: | | ||||||:||
Db         50 DINSDGSAINYAPSIKD 66


RESULT 19
S03326
Ig heavy chain precursor V-D-J region (clone pCP12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999
C;Accession: S03326
```

```
R;Reininger, L.; Kaushik, A.; Izui, S.; Jaton, J.C.
Eur. J. Immunol. 18, 1521-1526, 1988
A;Title: A member of a new V(H) gene family encodes antibromelinized mouse red blood cel
A;Reference number: S03326; MUID:89052754; PMID:2903828
A;Accession: S03326
A;Molecule type: mRNA
A;Residues: 1-137 <REI>
A;Cross-references: UNIPARC:UPI0000115093; EMBL:Y00743; NID:g52483; PIDN:CAA68712.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region pCP12 #status predicted <MAT>
F;34-117/Domain: immunoglobulin homology <IMM>
F;118-120/Domain: D region #status predicted <DRE>
F;121-137/Domain: J region #status predicted <JRE>

  Query Match             67.8%;  Score 61;  DB 2;  Length 137;
  Best Local Similarity   64.7%;  Pred. No. 0.011;
  Matches   11;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              :|: | | ||||||:||
Db         69 DINSDGSAINYAPSIKD 85


RESULT 20
S06816
Ig heavy chain precursor V region (clone 10C3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1991 #sequence_revision 11-Nov-1994 #text_change 23-Jul-1999
C;Accession: S06816
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06815; MUID:90064531; PMID:2555519
A;Accession: S06816
A;Molecule type: mRNA
A;Residues: 1-140 <MIL>
A;Cross-references: UNIPARC:UPI0000115E38; EMBL:X17164; NID:g51916; PIDN:CAA35042.1; PID
A;Note: part of this sequence, including the amino end of the mature protein, was confir
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-140/Product: Ig heavy chain V region #status experimental <MAT>
F;33-115/Domain: immunoglobulin homology <IMM>
F;40-113/Disulfide bonds: #status predicted

  Query Match             60.0%;  Score 54;  DB 2;  Length 140;
  Best Local Similarity   64.7%;  Pred. No. 0.16;
  Matches   11;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:| |:|| | ||| |
Db         67 EINPHSTTIFYTPSLMD 83


RESULT 21
F47624
Ig heavy chain V-I region - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: F47624
R;Haire, R.N.; Amemiya, C.T.; Suzuki, D.; Litman, G.W.
J. Exp. Med. 171, 1721-1737, 1990
A;Title: Eleven distinct V-H gene families and additional patterns of sequence variation
A;Reference number: A47624; MUID:90237760; PMID:2110243
A;Accession: F47624
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-98 <HAI>
A;Cross-references: UNIPARC:UPI0000176E6C
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             52.2%;  Score 47;  DB 2;  Length 98;
  Best Local Similarity   60.0%;  Pred. No. 1.5;
  Matches    9;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              |||| |:  || |:|
Db         51 IHPDGSSAYYADSVK 65


RESULT 22
PH1421
Ig heavy chain V region (clone P2-56) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: PH1421
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of sl
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1421
A;Molecule type: mRNA
A;Residues: 1-127 <VAN>
A;Cross-references: UNIPARC:UPI0000176A2D
A;Experimental source: PBMC
A;Note: the authors translated the codon GCA for residue 123 as Ser
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             52.2%;  Score 47;  DB 2;  Length 127;
  Best Local Similarity   53.3%;  Pred. No. 2;
  Matches    8;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              |:|| | | |:|| :
Db         51 IYPDDSDIKYSPSFR 65


RESULT 23
HVCQG4
Ig heavy chain precursor V region (G4) - spectacled caiman
C;Species: Caiman crocodilus, Caiman sclerops (spectacled caiman)
C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C;Accession: A02085
R;Litman, G.W.; Murphy, K.; Berger, L.; Litman, R.; Hinds, K.; Erickson, B.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 844-848, 1985
A;Title: Complete nucleotide sequences of three V-H genes in Caiman, a phylogenetically a
n of recombination elements.
A;Reference number: A94080; MUID:85140192; PMID:2983316
A;Accession: A02085
A;Molecule type: DNA
A;Residues: 1-117 <LIT>
A;Cross-references: UNIPROT:P03982; UNIPARC:UPI000012CEDC; GB:M12770; NID:g213027; PIDN:A
C;Genetics:
A;Gene: G4
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-117/Product: Ig heavy chain V region (G4) #status predicted <MAT>
F;20-49/Region: framework 1
F;34-117/Domain: immunoglobulin homology <IMM>
F;50-54/Region: complementarity-determining 1
F;55-68/Region: framework 2
F;69-85/Region: complementarity-determining 2
F;86-117/Region: framework 3
F;41-115/Disulfide bonds: #status predicted

  Query Match             51.1%;  Score 46;  DB 1;  Length 117;
  Best Local Similarity   56.2%;  Pred. No. 2.7;
```

```
  Matches    9;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLK 16
              ||: :| || ||| :|
Db         69 EINGNSETIRYAPEVK 84


RESULT 24
PH1410
Ig heavy chain V region (clone P1-52) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: PH1410
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of s
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1410
A;Molecule type: mRNA
A;Residues: 1-125 <VAN>
A;Cross-references: UNIPARC:UPI0000176A31
A;Experimental source: PBMC
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             51.1%;  Score 46;  DB 2;  Length 125;
  Best Local Similarity   53.3%;  Pred. No. 2.9;
  Matches    8;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              |:|| | | |:|| :
Db         51 IYPDDSDIRYSPSFQ 65


RESULT 25
AF0593
probable secreted protein [imported] - Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF0593
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF0593
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-128 <PAR>
A;Cross-references: UNIPARC:UPI000005A10E; GB:AL513382; PIDN:CAD05216.1; PID:g16501986;
C;Genetics:
A;Gene: STY0800

  Query Match             48.9%;  Score 44;  DB 2;  Length 128;
  Best Local Similarity   53.3%;  Pred. No. 6.3;
  Matches    8;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 HPDSSTINYAPSLKD 17
              ||| ||:|:    ||
Db         75 HPDGSTMNHDGMTKD 89


RESULT 26
T34867
probable chitosanase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T34867
R;Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21560
A;Accession: T34867
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-305 <SEE>
A;Cross-references: UNIPROT:Q9S2Z1; UNIPARC:UPI00000DB32C; EMBL:AL109849; PIDN:CAB52859.1
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC3A3.02
C;Superfamily: chitosanase

  Query Match             48.9%;  Score 44;  DB 2;  Length 305;
  Best Local Similarity   41.2%;  Pred. No. 16;
  Matches    7;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              | |||:    | |:|::
Db        135 EDHPDNGLAEYLPALRE 151


RESULT 27
I84704
gene VH104B protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: I84704
R;Cohen, J.B.; Givol, D.
EMBO J. 2, 2013-2018, 1983
A;Title: Allelic immunoglobulin VH genes in two mouse strains: possible germline gene rec
A;Reference number: I48457; MUID:84057727; PMID:6416826
A;Accession: I84704
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-116 <RES>
A;Cross-references: UNIPARC:UPI00001148C0; GB:K00707; NID:g196075; PIDN:AAA38516.1; PID:g
C;Genetics:
A;Gene: VH104B
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-115/Domain: immunoglobulin homology <IMM>

  Query Match             47.8%;  Score 43;  DB 2;  Length 116;
  Best Local Similarity   50.0%;  Pred. No. 8.3;
  Matches    8;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLK 16
              ||||:   |||    |
Db         69 EIHPNCGNINYNEKFK 84


RESULT 28
A56642
somatotropin precursor - European sea bass
N;Alternate names: growth hormone
C;Species: Dicentrarchus labrax (European sea bass)
C;Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 01-Aug-1997
C;Accession: A56642
R;Doliana, R.; Bortolussi, M.; Colombo, L.
DNA Seq. 3, 185-189, 1992
A;Title: Cloning and sequencing of European sea bass (Dicentrarchus labrax L.) growth hor
A;Reference number: A56642; MUID:93113000; PMID:1472711
A;Accession: A56642
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-204 <DOL>
A;Cross-references: UNIPARC:UPI00001765EF
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:121471, NCBIP:121472)
C;Superfamily: prolactin
F;1-17/Domain: signal sequence #status predicted <SIG>
```

```
  Query Match             47.8%;  Score 43;  DB 2;  Length 204;
  Best Local Similarity   61.5%;  Pred. No. 15;
  Matches    8;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAP 13
              |: |||||:  ||
Db        142 EMFPDSSTLQLAP 154


RESULT 29
I51289
somatotropin - Morone saxatilis
C;Species: Morone saxatilis
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C;Accession: I51289
R;Cheng, C.M.; Lin, C.M.; Shamblott, M.; Gonzalez-Villasenor, L.I.; Powers, D.A.; Woods,
Mol. Cell. Endocrinol. 108, 75-85, 1995
A;Title: Production of a biologically active recombinant teleostean growth hormone in E.
A;Reference number: I51289; MUID:95278623; PMID:7758842
A;Accession: I51289
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-204 <CHE>
A;Cross-references: UNIPROT:P48248; UNIPARC:UPI0000135CAF; GB:S78253; NID:g1000418; PIDN
C;Superfamily: prolactin

  Query Match             47.8%;  Score 43;  DB 2;  Length 204;
  Best Local Similarity   61.5%;  Pred. No. 15;
  Matches    8;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAP 13
              |: |||||:  ||
Db        142 EMFPDSSTLQLAP 154


RESULT 30
S76734
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76734
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76734
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-475 <KAN>
A;Cross-references: UNIPROT:P74540; UNIPARC:UPI00000C0E90; EMBL:D90916; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

  Query Match             47.8%;  Score 43;  DB 2;  Length 475;
  Best Local Similarity   57.1%;  Pred. No. 38;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 PDSSTINYAPSLKD 17
              ||:  || |||::|
Db        127 PDAPFINLAPSVED 140


RESULT 31
A36887
endo-alpha-sialidase (EC 3.2.1.129), tail - phage K1F
N;Alternate names: endo-N-acylneuraminidase
C;Species: phage K1F
C;Date: 18-Nov-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A36887
R;Petter, J.G.; Vimr, E.R.
J. Bacteriol. 175, 4354-4363, 1993
A;Title: Complete nucleotide sequence of the bacteriophage K1F tail gene encoding endo-N-
A;Reference number: A36887; MUID:93322313; PMID:8331067
A;Accession: A36887
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-920 <PET>
A;Cross-references: UNIPROT:Q04830; UNIPARC:UPI000016D772; GB:M63657; NID:g215082; PIDN:A
A;Note: in the authors' translation residues 875-888 are shown after residue 903 and, cor
C;Keywords: glycosidase; hydrolase; polysaccharide degradation; tail protein

  Query Match             47.8%;  Score 43;  DB 2;  Length 920;
  Best Local Similarity   54.5%;  Pred. No. 79;
  Matches    6;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINY 11
              ::|||  |:||
Db        377 DLHPDYPTVNY 387


RESULT 32
AB3063
mandelate racemase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AB3063
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClella
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, B
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AB3063
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <KUR>
A;Cross-references: UNIPROT:Q8U8H2; UNIPARC:UPI00001648DC; GB:AE008689; PIDN:AAL44920.1;
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu4120
A;Map position: linear chromosome

  Query Match             46.7%;  Score 42;  DB 2;  Length 249;
  Best Local Similarity   46.7%;  Pred. No. 28;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 HPDSSTINYAPSLKD 17
              || |: : | | :||
Db        197 HPASTILEYIPWIKD 211


RESULT 33
F98223
hypothetical protein AGR_L_1470 [imported] - Agrobacterium tumefaciens (strain C58, Cerec
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: F98223
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F98223
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-372 <KUR>
A;Cross-references: UNIPROT:Q8U8H2; UNIPARC:UPI00000D2452; GB:AE007870; PIDN:AAK89312.1;
C;Genetics:
A;Gene: AGR_L_1470
A;Map position: linear chromosome

  Query Match             46.7%;  Score 42;  DB 2;  Length 372;
```

```
  Best Local Similarity   46.7%;  Pred. No. 43;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 HPDSSTINYAPSLKD 17
              || |: : | | :||
Db        320 HPASTILEYIPWIKD 334


RESULT 34
I50731
Ig heavy chain - nurse shark
C;Species: Ginglymostoma cirratum (nurse shark)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: I50731
R;Vazquez, M.; Mizuki, N.; Flajnik, M.F.; McKinney, E.C.; Kasahara, M.
Mol. Immunol. 29, 1157-1158, 1992
A;Title: Nucleotide sequence of a nurse shark immunoglobulin heavy chain cDNA clone.
A;Reference number: I50731; MUID:92357056; PMID:1495502
A;Accession: I50731
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-577 <VAZ>
A;Cross-references: UNIPARC:UPI0000115352; GB:M92851; NID:g213264; PIDN:AAA50817.1; PID:
C;Genetics:
A;Gene: IgH
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;469-539/Domain: immunoglobulin homology <IMM>

  Query Match             46.7%;  Score 42;  DB 2;  Length 577;
  Best Local Similarity   66.7%;  Pred. No. 69;
  Matches    8;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 SSTINYAPSLKD 17
              ||  ||||::||
Db         74 SSMNNYAPAIKD 85


RESULT 35
T49320
related to heterokaryon incompatibility protein [imported] - Neurospora crassa
N;Alternate names: protein B13N20.50
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49320
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: Z25022
A;Accession: T49320
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-584 <SCH>
A;Cross-references: UNIPROT:Q9P5Z4; UNIPARC:UPI000017B4F7; EMBL:AL355925; GSPDB:GN00116;
A;Experimental source: BAC clone B13N20; strain OR74A
C;Genetics:
A;Gene: NCSP:B13N20.50
A;Map position: 6

  Query Match             46.7%;  Score 42;  DB 2;  Length 584;
  Best Local Similarity   53.3%;  Pred. No. 70;
  Matches    8;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 HPDSSTINYAPSLKD 17
              || ::| | || | |
Db         90 HPKANTENLAPELGD 104


RESULT 36
S77577
endo-alpha-sialidase (EC 3.2.1.129) - phage E
N;Alternate names: Endo NE protein; endo-N-acylneuraminidase; endoneuraminidase; endosia
C;Species: phage E
A;Note: host Escherichia coli K1
C;Date: 21-Apr-1997 #sequence_revision 18-Jul-1997 #text_change 08-Oct-1999
C;Accession: S77577; S77940; S56130; S56126; S52299
R;Gerardy-Schahn, R.; Bethe, A.; Brennecke, T.; Muehlenhoff, M.; Eckhardt, M.; Ziesing, S
Mol. Microbiol. 16, 441-450, 1995
A;Title: Molecular cloning and functional expression of bacteriophage PK1E-encoded endone
A;Reference number: S77577; MUID:96037789; PMID:7565105
A;Accession: S77577
A;Molecule type: DNA
A;Residues: 1-811 <GER1>
A;Cross-references: UNIPARC:UPI000016D73D; EMBL:Z36986; NID:g662881; PIDN:CAA85449.1; PII
A;Note: in the authors' translation residues 166-170 are shown between residue 190 and 19
A;Accession: S77940
A;Molecule type: protein
A;Residues: 1-17;530-535;542-553;593-599 <GER2>
A;Cross-references: UNIPARC:UPI000017CA8C; UNIPARC:UPI000017CA8D; UNIPARC:UPI000017CA8E;
R;Long, G.S.; Bryant, J.M.; Taylor, P.W.; Luzio, J.P.
Biochem. J. 309, 543-550, 1995
A;Title: Complete nucleotide sequence of the gene encoding bacteriophage E endosialidase
A;Reference number: S56126; MUID:95351985; PMID:7626018
A;Accession: S56130
A;Molecule type: DNA
A;Residues: 1-52,'A',54,'MA',57-522,'K',524-538,'C',540-811 <LON>
A;Cross-references: UNIPARC:UPI000011D898; EMBL:X78310; NID:g536777; PIDN:CAA55120.1; PII
A;Accession: S56126
A;Molecule type: protein
A;Residues: 1-6;330-349;613-632 <LOW>
A;Cross-references: UNIPARC:UPI000017CA90; UNIPARC:UPI000017CA91; UNIPARC:UPI000017CA92
C;Genetics:
A;Gene: endo NE
C;Keywords: glycosidase; homotrimer; hydrolase
F;1-811/Product: endo-alpha-sialidase #status experimental <MAT>

  Query Match             46.7%;  Score 42;  DB 2;  Length 811;
  Best Local Similarity   54.5%;  Pred. No. 1e+02;
  Matches    6;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINY 11
              ::|||  |:||
Db        167 DMHPDYPTVNY 177


RESULT 37
S19669
Ig heavy chain V region (VH5DJ) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19669
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on pha
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19669
A;Molecule type: mRNA
A;Residues: 1-117 <MAR>
A;Cross-references: UNIPARC:UPI0000115FEA; EMBL:X61651; NID:g37731; PIDN:CAA43832.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

  Query Match             45.6%;  Score 41;  DB 2;  Length 117;
  Best Local Similarity   46.7%;  Pred. No. 18;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              |:|| |   |:|| :
Db         51 IYPDDSDTRYSPSFE 65


RESULT 38
PH1416
Ig heavy chain V region (clone P2-51) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1416
```

R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of s
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1416
A;Molecule type: mRNA
A;Residues: 1-126 <VAN>
A;Cross-references: UNIPARC:UPI0000176950
A;Experimental source: PBMC
A;Note: the authors translated the codon CTG for residue 6 as Gln
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

 Query Match 45.6%; Score 41; DB 2; Length 126;
 Best Local Similarity 46.7%; Pred. No. 19;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IHPDSSTINYAPSLK 16
 |:|| | |:|| :
Db 51 IYPDDSDTRYSPSFQ 65

RESULT 39
PH1417
Ig heavy chain V region (clone P2-52) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999
C;Accession: PH1417
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of s
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1417
A;Molecule type: mRNA
A;Residues: 1-126 <VAN>
A;Cross-references: UNIPARC:UPI0000176951
A;Experimental source: PBMC
A;Note: the authors translated the codon ATC for residue 111 as Thr
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

 Query Match 45.6%; Score 41; DB 2; Length 126;
 Best Local Similarity 46.7%; Pred. No. 19;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IHPDSSTINYAPSLK 16
 |:|| | |:|| :
Db 51 IYPDDSDARYSPSFQ 65

RESULT 40
PH1418
Ig heavy chain V region (clone P2-53) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1418
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of s
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1418
A;Molecule type: mRNA
A;Residues: 1-126 <VAN>
A;Cross-references: UNIPARC:UPI0000176952
A;Experimental source: PBMC
A;Note: the authors translated the codon CTG for residue 6 as Gln
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

 Query Match 45.6%; Score 41; DB 2; Length 126;
 Best Local Similarity 46.7%; Pred. No. 19;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IHPDSSTINYAPSLK 16
 |:|| | |:|| :
Db 51 IYPDDSDARYSPSFQ 65

RESULT 41
PH1419
Ig heavy chain V region (clone P2-54) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C;Accession: PH1419
R;van der Stoep, N.; van der Linden, J.; Logtenberg, T.
J. Exp. Med. 177, 99-107, 1993
A;Title: Molecular evolution of the human immunoglobulin E response: High incidence of sl
dermatitis.
A;Reference number: PH1409; MUID:93115676; PMID:8418213
A;Accession: PH1419
A;Molecule type: mRNA
A;Residues: 1-126 <VAN>
A;Cross-references: UNIPARC:UPI0000176953
A;Experimental source: PBMC
A;Note: the authors translated the codon ACT for residue 107 as Ser
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

 Query Match 45.6%; Score 41; DB 2; Length 126;
 Best Local Similarity 46.7%; Pred. No. 19;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 IHPDSSTINYAPSLK 16
 |:|| | |:|| :
Db 51 IYPDDSDTRYSPSFQ 65

RESULT 42
S00747
somatotropin precursor - red sea bream
N;Alternate names: growth hormone
C;Species: Chrysophrys major (red sea bream)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S00747
R;Momota, H.; Kosugi, R.; Hiramatsu, H.; Ohgai, H.; Hara, A.; Ishioka, H.
Nucleic Acids Res. 16, 3107, 1988
A;Title: Nucleotide sequence of cDNA encoding the pregrowth hormone of red sea bream (Pag
A;Reference number: S00747; MUID:88217528; PMID:3368321
A;Accession: S00747
A;Molecule type: mRNA
A;Residues: 1-203 <MOM>
A;Cross-references: UNIPROT:P08591; UNIPARC:UPI0000135CB7; EMBL:X06962; NID:g64219; PIDN:
A;Note: the source is designated as Pagrus major
C;Superfamily: prolactin
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-203/Product: somatotropin #status predicted <MAT>

 Query Match 45.6%; Score 41; DB 2; Length 203;
 Best Local Similarity 61.5%; Pred. No. 33;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAP 13
 || |||| : ||
Db 141 EIFPDSSALQLAP 153

RESULT 43
B70699
hypothetical protein Rv0012 - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: B70699
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: B70699
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-262 <COL>
A;Cross-references: UNIPROT:P71582; UNIPARC:UPI00000CCC1C; GB:Z80233; GB:AL123456; NID:g
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv0012

 Query Match 45.6%; Score 41; DB 2; Length 262;
 Best Local Similarity 37.5%; Pred. No. 43;
 Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLK 16
|:||| : || ::
Db 235 EVHPDLQIVGYADPVR 250

RESULT 44
T23051
hypothetical protein H06A10.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23051
R;Lennard, N.
submitted to the EMBL Data Library, October 1997
A;Reference number: Z19663
A;Accession: T23051
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-291 <WIL>
A;Cross-references: UNIPROT:Q9XTR0; UNIPARC:UPI0000074B61; EMBL:Z99773; PIDN:CAB16924.1;
A;Experimental source: clone H06A10
C;Genetics:
A;Gene: CESP:H06A10.1
A;Map position: X
A;Introns: 16/1; 59/1; 94/2; 129/3; 189/1; 218/2
C;Superfamily: Caenorhabditis elegans hypothetical protein H06A10.1

 Query Match 45.6%; Score 41; DB 2; Length 291;
 Best Local Similarity 70.0%; Pred. No. 48;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TINYAPSLKD 17
|:|| | |||
Db 216 TLNYCPMLKD 225

RESULT 45
S12864
retinal isomerase (EC 5.2.1.3) [validated] - Japanese flying squid
N;Alternate names: retinochrome
C;Species: Todarodes pacificus (Japanese flying squid)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: S12864; S39449
R;Hara-Nishimura, I.; Matsumoto, T.; Mori, H.; Nishimura, M.; Hara, R.; Hara, T.
FEBS Lett. 271, 106-110, 1990
A;Title: Cloning and nucleotide sequence of cDNA for retinochrome, retinal photoisomeras
A;Reference number: S12864; MUID:91032043; PMID:2226795
A;Accession: S12864
A;Molecule type: mRNA
A;Residues: 1-301 <HAR>
A;Cross-references: UNIPROT:P23820; UNIPARC:UPI0000133655; EMBL:X57143; NID:g10776; PID:

R;Hara-Nishimura, I.; Kondo, M.; Nishimura, M.; Hara, R.; Hara, T.
FEBS Lett. 335, 94-98, 1993
A;Title: Amino acid sequence surrounding the retinal-binding site in retinochrome of the
A;Reference number: S39449; MUID:94063090; PMID:8243675
A;Accession: S39449
A;Status: preliminary
A;Molecule type: protein
A;Residues: 274-277,'X',279-282 <HA2>
A;Cross-references: UNIPARC:UPI000017411D
C;Superfamily: vertebrate rhodopsin
C;Keywords: chromoprotein; cis-trans-isomerase; G protein-coupled receptor; glycoprotein;
F;1-301/Product: retinal isomerase #status experimental <MAT>
F;19-43/Domain: transmembrane #status predicted <TM1>
F;54-75/Domain: transmembrane #status predicted <TM2>
F;95-120/Domain: transmembrane #status predicted <TM3>
F;133-153/Domain: transmembrane #status predicted <TM4>
F;181-208/Domain: transmembrane #status predicted <TM5>
F;231-255/Domain: transmembrane #status predicted <TM6>
F;265-288/Domain: transmembrane #status predicted <TM7>
F;170/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;275/Binding site: retinal (Lys) (covalent) #status experimental

 Query Match 45.6%; Score 41; DB 1; Length 301;
 Best Local Similarity 57.1%; Pred. No. 50;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPS 14
|:| | ||||: |
Db 161 EVHGTSCTINYSVS 174

RESULT 46
E86240
protein T16B5.15 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E86240
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E86240
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <STO>
A;Cross-references: UNIPROT:Q9SAD1; UNIPARC:UPI000009D0F4; GB:AE005172; NID:g4874277; PID
C;Genetics:
A;Gene: T16B5.15
A;Map position: 1

 Query Match 45.6%; Score 41; DB 2; Length 319;
 Best Local Similarity 50.0%; Pred. No. 53;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IHPDSSTINYAPSL 15
::| ||:| |||
Db 245 LYPSQSTLNQIPSL 258

RESULT 47
G72061
probable phosphoesterase (EC 3.1.-.-) yaeI [similarity] - Chlamydophila pneumoniae (strai
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 05-Oct-2004
C;Accession: G72061
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;

```
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: G72061
A;Molecule type: DNA
A;Residues: 1-320 <ARN>
A;Cross-references: UNIPROT:Q9Z7X6; UNIPARC:UPI0000139ACD; GB:AE001642; GB:AE001363; NID
A;Experimental source: strain CWL029
C;Comment: This sequence has motifs characteristic of a variety of phosphoesterases.
C;Genetics:
A;Gene: yaeI
C;Superfamily: phosphoesterase, YkuE type; phosphoesterase core homology
C;Keywords: hydrolase
F;46-118/Domain: phosphoesterase core homology <PEC>

  Query Match             45.6%;  Score 41;  DB 1;  Length 320;
  Best Local Similarity   46.7%;  Pred. No. 54;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSL 15
              : ||: :  || |||
Db        209 QFHPEQAFKNYDPSL 223


RESULT 48
G86562
probable phosphoesterase (EC 3.1.-.-) yaeI [similarity] - Chlamydophila pneumoniae (stra
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 05-Oct-2004
C;Accession: G86562
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: G86562
A;Molecule type: DNA
A;Residues: 1-320 <STO>
A;Cross-references: UNIPROT:Q9Z7X6; UNIPARC:UPI0000139ACD; GB:BA000008; NID:g8978950; PI
A;Experimental source: strain J138
C;Comment: This sequence has motifs characteristic of a variety of phosphoesterases.
C;Genetics:
A;Gene: yaeI
C;Superfamily: phosphoesterase, YkuE type; phosphoesterase core homology
C;Keywords: hydrolase
F;46-118/Domain: phosphoesterase core homology <PEC>

  Query Match             45.6%;  Score 41;  DB 1;  Length 320;
  Best Local Similarity   46.7%;  Pred. No. 54;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSL 15
              : ||: :  || |||
Db        209 QFHPEQAFKNYDPSL 223


RESULT 49
D75353
yellow-related protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: D75353
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: D75353
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-388 <WHI>
A;Cross-references: UNIPROT:Q9RTH4; UNIPARC:UPI00000D3ED5; GB:AE002021; GB:AE000513; NID
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1790
A;Map position: 1

  Query Match             45.6%;  Score 41;  DB 2;  Length 388;
  Best Local Similarity   53.8%;  Pred. No. 66;
  Matches    7;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPS 14
              | || :|: |||:
Db        249 ISPDGATLYYAPT 261


RESULT 50
H81667
transcription termination factor Rho TC0778 [imported] - Chlamydia muridarum (strain Nigg
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: H81667
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, E
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: H81667
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-419 <TET>
A;Cross-references: UNIPROT:Q9PJQ0; UNIPARC:UPI0000057A61; GB:AE002345; GB:AE002160; NID:
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0778
C;Superfamily: transcription termination factor rho
C;Keywords: transcription termination

  Query Match             45.6%;  Score 41;  DB 2;  Length 419;
  Best Local Similarity   43.5%;  Pred. No. 72;
  Matches   10;  Conservative    2;  Mismatches    5;  Indels    6;  Gaps    1;

Qy          1 EIHPD------SSTINYAPSLKD 17
              |: ||      | | || || :|
Db         60 EVLPDGFGFLRSPTYNYLPSAED 82


Search completed: March 23, 2006, 02:04:53
Job time : 32.5205 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:40:40 ; Search time 146.247 Seconds
(without alignments)
82.012 Million cell updates/sec

Title: US-10-755-382-24
Perfect score: 90
Sequence: 1 EIHPDSSTINYAPSLKD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	92.2	476	2	Q4V9Z4_MOUSE	Q4v9z4 mus musculu
2	82	91.1	119	1	HV40_MOUSE	P01810 mus musculu
3	79	87.8	116	1	HV36_MOUSE	P01806 mus musculu
4	79	87.8	119	1	HV37_MOUSE	P01807 mus musculu
5	79	87.8	119	1	HV38_MOUSE	P01808 mus musculu
6	73	81.1	117	1	HV41_MOUSE	P01811 mus musculu
7	72	80.0	117	1	HV42_MOUSE	P01812 mus musculu
8	72	80.0	118	1	HV39_MOUSE	P01809 mus musculu
9	51	56.7	594	2	Q4TCI9_TETNG	Q4tc19 tetraodon n
10	49	54.4	3969	2	Q600K8_MYCHY	Q600k8 mycoplasma
11	48	53.3	281	2	Q74LE0_LACJO	Q74le0 lactobacill
12	48	53.3	450	2	Q817S5_BACCR	Q817s5 bacillus ce
13	47	52.2	179	2	Q6YRI1_ONYPE	Q6yri1 onion yello
14	47	52.2	872	2	Q4WK85_ASPFU	Q4wk85 aspergillus
15	47	52.2	4547	2	Q52US9_OMPOL	Q52us9 omphalotus
16	46	51.1	117	1	HV03_CAICR	P03982 caiman croc
17	46	51.1	204	1	SOMA_SCIOC	Q9ib11 sciaenops o
18	46	51.1	212	2	Q7ZME2_9HIV1	Q7zme2 human immun
19	46	51.1	516	2	Q8GAV2_9RICK	Q8gav2 wolbachia e
20	46	51.1	533	2	Q73G99_WOLPM	Q73g99 wolbachia p
21	46	51.1	1052	2	Q65MN3_BACLD	Q65mn3 bacillus li
22	46	51.1	1445	2	Q4RXT1_TETNG	Q4rxt1 tetraodon n
23	45.5	50.6	361	2	Q517J8_ENTHI	Q517j8 entamoeba h
24	45	50.0	79	2	Q7QSK1_GIALA	Q7qsk1 giardia lam
25	45	50.0	249	2	Q9RB46_9CLOT	Q9rb46 clostridium
26	45	50.0	378	2	Q4S517_TETNG	Q4s517 tetraodon n
27	45	50.0	400	2	Q7MZB1_PHOLL	Q7mzb1 photorhabdu
28	45	50.0	505	2	Q6T7E8_TOBAC	Q6t7e8 nicotiana t
29	45	50.0	513	2	Q9V8D9_DROME	Q9v8d9 drosophila
30	45	50.0	746	2	Q55EX4_DICDI	Q55ex4 dictyosteli
31	45	50.0	2047	2	Q601N7_MYCHY	Q601n7 mycoplasma
32	44	48.9	128	1	YBGS_SALTI	P64438 salmonella
33	44	48.9	128	1	YBGS_SALTY	P64437 salmonella
34	44	48.9	128	2	Q57RJ7_SALCH	Q57rj7 salmonella
35	44	48.9	128	2	Q5PG71_SALPA	Q5pg71 salmonella
36	44	48.9	305	2	Q9S2Z1_STRCO	Q9s2z1 streptomyce
37	44	48.9	967	2	Q60LS4_CAEBR	Q60ls4 caenorhabdi
38	44	48.9	1066	2	Q4SEC3_TETNG	Q4sec3 tetraodon n
39	44	48.9	1122	2	Q5TWD0_ANOGA	Q5twd0 anopheles g
40	44	48.9	1776	2	Q963L7_SCHMA	Q963l7 schistosoma
41	44	48.9	2324	2	Q4SMH7_TETNG	Q4smh7 tetraodon n
42	43.5	48.3	108	2	Q6LJK3_PHOPR	Q6ljk3 photobacter
43	43	47.8	117	2	Q63656_RAT	Q63656 rattus norv
44	43	47.8	117	2	Q63658_RAT	Q63658 rattus norv
45	43	47.8	204	1	SOMA_DICLA	Q05163 dicentrarch
46	43	47.8	204	1	SOMA_MORSA	P48248 morone saxa
47	43	47.8	232	2	Q9ERB8_MOUSE	Q9erb8 mus musculu
48	43	47.8	233	2	Q6N2Q7_RHOPA	Q6n2q7 rhodopseudo
49	43	47.8	341	2	Q503N3_BRARE	Q503n3 brachydanio
50	43	47.8	371	2	Q9GNR4_LEIMA	Q9gnr4 leishmania
51	43	47.8	382	2	O85003_STRPN	O85003 streptococc
52	43	47.8	382	2	Q9R922_STRPN	Q9r922 streptococc
53	43	47.8	384	2	Q4K0H5_STRPN	Q4k0h5 streptococc
54	43	47.8	389	2	Q5PP31_ARATH	Q5pp31 arabidopsis
55	43	47.8	435	2	Q73GY4_WOLPM	Q73gy4 wolbachia p
56	43	47.8	444	2	Q5HLZ5_STAEQ	Q5hlz5 staphylococ
57	43	47.8	444	2	Q8CRF8_STAEP	Q8crf8 staphylococ
58	43	47.8	475	2	P74540_SYNY3	P74540 synechocyst
59	43	47.8	511	2	Q585X9_9TRYP	Q585x9 trypanosoma
60	43	47.8	527	2	Q74JA0_LACJO	Q74ja0 lactobacill
61	43	47.8	528	2	Q669J0_YERPS	Q669j0 yersinia ps
62	43	47.8	566	2	Q8BRP9_MOUSE	Q8brp9 mus musculu
63	43	47.8	585	2	Q6GPX4_XENLA	Q6gpx4 xenopus lae
64	43	47.8	759	2	Q5AUY7_EMENI	Q5auy7 aspergillus
65	43	47.8	767	2	Q4WK80_ASPFU	Q4wk80 aspergillus
66	43	47.8	768	2	Q8FRA2_COREF	Q8fra2 corynebacte
67	43	47.8	789	2	Q93M73_XANOR	Q93m73 xanthomonas
68	43	47.8	800	2	Q8PF79_XANAC	Q8pf79 xanthomonas
69	43	47.8	811	2	Q9AZ46_BPSP6	Q9az46 enterobacte
70	43	47.8	812	2	Q5GUP4_XANOR	Q5gup4 xanthomonas
71	43	47.8	866	2	Q80UQ4_MOUSE	Q80uq4 mus musculu
72	43	47.8	901	2	Q4XZM4_PLACH	Q4xzm4 plasmodium
73	43	47.8	919	1	ENAN_BPK1F	Q04830 bacteriopha
74	43	47.8	1064	2	Q858B1_BPK1F	Q858b1 bacteriopha
75	43	47.8	1248	2	Q80TW8_MOUSE	Q80tw8 mus musculu
76	43	47.8	1334	2	Q8CAP0_MOUSE	Q8cap0 mus musculu
77	43	47.8	1334	2	Q6PGL7_MOUSE	Q6pgl7 mus musculu
78	43	47.8	1363	2	Q5DZN6_VIBF1	Q5dzn6 vibrio fisc
79	43	47.8	1372	2	Q87JN6_VIBPA	Q87jn6 vibrio para
80	43	47.8	1780	2	Q6TV07_HUMAN	Q6tv07 homo sapien
81	42.5	47.2	138	2	Q5BWK7_SCHJA	Q5bwk7 schistosoma
82	42.5	47.2	207	2	Q550K4_DICDI	Q550k4 dictyosteli
83	42.5	47.2	763	2	Q525Z6_MAGGR	Q525z6 magnaporthe
84	42.5	47.2	909	2	Q6FLK8_CANGA	Q6flk8 candida gla
85	42.5	47.2	1947	2	Q5AGH1_CANAL	Q5agh1 candida alb
86	42.5	47.2	2091	2	Q5AG35_CANAL	Q5ag35 candida alb
87	42	46.7	160	2	Q89GY1_BRAJA	Q89gy1 bradyrhizob
88	42	46.7	162	2	Q6CUQ9_KLULA	Q6cuq9 kluyveromyc
89	42	46.7	163	2	Q704V3_ORYSA	Q704v3 oryza sativ
90	42	46.7	196	2	P71510_METEX	P71510 methylobact
91	42	46.7	208	2	Q7LDZ4_HUMAN	Q7ldz4 homo sapien
92	42	46.7	233	2	Q89HQ7_BRAJA	Q89hq7 bradyrhizob
93	42	46.7	246	2	Q8SUT3_ENCCU	Q8sut3 encephalito
94	42	46.7	249	2	Q8U8H2_AGRT5	Q8u8h2 agrobacteri
95	42	46.7	303	2	Q4UIV6_THEAN	Q4uiv6 theileria a
96	42	46.7	342	2	Q8H598_ORYSA	Q8h598 oryza sativ
97	42	46.7	348	2	Q8D4Y2_VIBVU	Q8d4y2 vibrio vuln
98	42	46.7	351	2	Q4WBF0_ASPFU	Q4wbf0 aspergillus
99	42	46.7	364	1	SERC_VIBVU	Q8d900 vibrio vuln
100	42	46.7	364	1	SERC_VIBVY	Q7mlh6 vibrio vuln
101	42	46.7	366	1	GCST_BORBR	Q7wp31 bordetella
102	42	46.7	366	1	GCST_BORPA	Q7w1c6 bordetella
103	42	46.7	366	1	GCST_BORPE	Q7w0e5 bordetella
104	42	46.7	372	2	Q7CU39_AGRT5	Q7cu39 agrobacteri

105	42	46.7	395	2	Q5KX79_GEOKA	Q5kx79	geobacillus
106	42	46.7	419	2	Q5RC64_PONPY	Q5rc64	pongo pygma
107	42	46.7	419	2	Q4H4E7_BACCI	Q4h4e7	bacillus ci
108	42	46.7	428	2	Q4HVC3_GIBZE	Q4hvc3	gibberella
109	42	46.7	433	2	Q74MI6_NANEQ	Q74mi6	nanoarchaeu
110	42	46.7	435	2	Q7NHT9_GLOVI	Q7nht9	gloeobacter
111	42	46.7	444	2	Q5XTP6_TRYCR	Q5xtp6	trypanosoma
112	42	46.7	471	2	Q5GSA8_WOLTR	Q5gsa8	wolbachia s
113	42	46.7	488	2	Q4MPF7_BACCE	Q4mpf7	bacillus ce
114	42	46.7	488	2	Q63EK6_BACCZ	Q63ek6	bacillus ce
115	42	46.7	488	2	Q6HM27_BACHK	Q6hm27	bacillus th
116	42	46.7	488	2	Q81TU8_BACAN	Q81tu8	bacillus an
117	42	46.7	515	2	Q7N4H6_PHOLL	Q7n4h6	photorhabdu
118	42	46.7	521	2	Q9BYI3_HUMAN	Q9byi3	homo sapien
119	42	46.7	521	2	Q96MX1_HUMAN	Q96mx1	homo sapien
120	42	46.7	521	2	Q99NC4_MOUSE	Q99nc4	mus musculu
121	42	46.7	521	2	Q6P9N1_MOUSE	Q6p9n1	mus musculu
122	42	46.7	522	2	Q9P5Z4_NEUCR	Q9p5z4	neurospora
123	42	46.7	527	2	Q74J63_LACJO	Q74j63	lactobacill
124	42	46.7	582	2	Q8NPT3_CORGL	Q8npt3	corynebacte
125	42	46.7	584	2	Q7RUZ5_NEUCR	Q7ruz5	neurospora
126	42	46.7	754	2	Q5ZBI2_ORYSA	Q5zbi2	oryza sativ
127	42	46.7	811	1	ENAN_BPK1E	P49714	bacteriopha
128	42	46.7	1037	2	Q9N437_CAEEL	Q9n437	caenorhabdi
129	42	46.7	1434	2	Q6P2J3_HUMAN	Q6p2j3	homo sapien
130	42	46.7	1610	2	Q6EBW9_PSESX	Q6ebw9	pseudomonas
131	42	46.7	1871	1	RRP5_HUMAN	Q14690	homo sapien
132	42	46.7	1871	2	Q5W093_HUMAN	Q5w093	homo sapien
133	42	46.7	1939	2	Q5CRH8_CRYPV	Q5crh8	cryptospori
134	42	46.7	2148	2	Q9BJD3_PHYPO	Q9bjd3	physarum po
135	42	46.7	2209	2	Q54JI4_DICDI	Q54ji4	dictyosteli
136	41.5	46.1	448	2	Q4MR79_BACCE	Q4mr79	bacillus ce
137	41.5	46.1	688	2	Q6FJQ0_CANGA	Q6fjq0	candida gla
138	41.5	46.1	1157	2	Q6BG49_PARTE	Q6bg49	paramecium
139	41	45.6	110	2	Q9JL77_MOUSE	Q9jl77	mus musculu
140	41	45.6	110	2	Q5UQB3_MIMIV	Q5uqb3	mimivirus.
141	41	45.6	203	1	SOMA_PAGMA	P08591	pagrus majo
142	41	45.6	204	1	SOMA_SPAAU	P29971	sparus aura
143	41	45.6	204	2	Q7SYG9_SINKN	Q7syg9	siniperca k
144	41	45.6	204	2	Q56V58_9PERO	Q56v58	rhabdosargu
145	41	45.6	209	2	Q50A30_9HIV1	Q50a30	human immun
146	41	45.6	211	2	Q75SX9_ECOLI	Q75sx9	escherichia
147	41	45.6	221	2	Q7RID7_PLAYO	Q7rid7	plasmodium
148	41	45.6	258	2	Q6Q5X6_9ARAE	Q6q5x6	arisaema lo
149	41	45.6	261	2	Q4TML0_9SPHN	Q4tml0	erythrobact
150	41	45.6	262	2	Q7DAK7_MYCTU	Q7dak7	mycobacteri
151	41	45.6	262	2	P71582_MYCTU	P71582	mycobacteri
152	41	45.6	262	2	Q7U308_MYCBO	Q7u308	mycobacteri
153	41	45.6	264	2	Q73SW3_MYCPA	Q73sw3	mycobacteri
154	41	45.6	284	2	Q5FMD5_LACAC	Q5fmd5	lactobacill
155	41	45.6	289	2	Q8DVP3_STRMU	Q8dvp3	streptococc
156	41	45.6	291	2	Q9XTR0_CAEEL	Q9xtr0	caenorhabdi
157	41	45.6	301	1	REIS_TODPA	P23820	todarodes p
158	41	45.6	319	2	Q9SAD1_ARATH	Q9sad1	arabidopsis
159	41	45.6	320	1	Y578_CHLPN	Q9z7x6	chlamydia p
160	41	45.6	324	2	Q824I3_CHLCV	Q824i3	chlamydophi
161	41	45.6	365	2	Q65KU8_BACLD	Q65ku8	bacillus li
162	41	45.6	384	2	Q4W6C8_LEPDE	Q4w6c8	leptinotars
163	41	45.6	388	2	Q9RTH4_DEIRA	Q9rth4	deinococcus
164	41	45.6	410	2	Q5BQ17_ARATH	Q5bq17	arabidopsis
165	41	45.6	413	2	Q99984_HUMAN	Q99984	homo sapien
166	41	45.6	413	2	Q53G44_HUMAN	Q53g44	homo sapien
167	41	45.6	413	2	Q96B64_HUMAN	Q96b64	homo sapien
168	41	45.6	419	2	Q9PJQ0_CHLMU	Q9pjq0	chlamydia m
169	41	45.6	427	2	Q9VU19_DROME	Q9vu19	drosophila
170	41	45.6	427	2	Q9VS67_DROME	Q9vs67	drosophila
171	41	45.6	440	2	Q6ADC1_LEIXX	Q6adc1	leifsonia x
172	41	45.6	442	2	Q7X5M1_9LACO	Q7x5m1	lactobacill
173	41	45.6	461	2	Q9SGX9_ARATH	Q9sgx9	arabidopsis
174	41	45.6	464	2	Q5L6Y3_CHLAB	Q516y3	chlamydophi
175	41	45.6	464	2	O84498_CHLTR	O84498	chlamydia t
176	41	45.6	464	2	Q824L5_CHLCV	Q82415	chlamydophi
177	41	45.6	464	2	Q9Z7U4_CHLPN	Q9z7u4	chlamydia p
178	41	45.6	474	2	Q88JV5_PSEPK	Q88jv5	pseudomonas
179	41	45.6	488	2	Q81GN6_BACCR	Q81gn6	bacillus ce
180	41	45.6	525	2	O33908_9GAMM	O33908	shewanella
181	41	45.6	538	2	Q7SD85_NEUCR	Q7sd85	neurospora
182	41	45.6	539	2	Q51JD4_MAGGR	Q51jd4	magnaporthe
183	41	45.6	542	2	Q4PCL7_USTMA	Q4pcl7	ustilago ma
184	41	45.6	550	2	Q4I961_GIBZE	Q4i961	gibberella
185	41	45.6	550	2	Q5LFH5_BACFN	Q5lfh5	bacteroides
186	41	45.6	550	2	Q64W99_BACFR	Q64w99	bacteroides
187	41	45.6	553	2	Q51EL4_ENTHI	Q51el4	entamoeba h
188	41	45.6	562	2	Q4N6J1_THEPA	Q4n6j1	theileria p
189	41	45.6	576	2	Q5ANC3_CANAL	Q5anc3	candida alb
190	41	45.6	595	2	Q5AYJ1_EMENI	Q5ayj1	aspergillus
191	41	45.6	666	2	Q7UX94_RHOBA	Q7ux94	rhodopirell
192	41	45.6	672	2	Q9UG38_HUMAN	Q9ug38	homo sapien
193	41	45.6	684	1	SKIL_PONPY	Q5r431	pongo pygma
194	41	45.6	717	2	Q4I9G2_GIBZE	Q4i9g2	gibberella
195	41	45.6	735	2	P94180_9NOST	P94180	anabaena sp
196	41	45.6	735	2	Q7A2G7_ANASP	Q7a2g7	anabaena sp
197	41	45.6	763	2	Q9XZ01_DROME	Q9xz01	drosophila
198	41	45.6	795	2	Q87FB4_XYLFT	Q87fb4	xylella fas
199	41	45.6	795	2	Q9PHC9_XYLFA	Q9phc9	xylella fas
200	41	45.6	800	2	O75466_HUMAN	O75466	homo sapien
201	41	45.6	803	2	O60545_HUMAN	O60545	homo sapien
202	41	45.6	803	2	O75214_HUMAN	O75214	homo sapien
203	41	45.6	846	2	O93920_MAGGR	O93920	magnaporthe
204	41	45.6	846	2	Q9UNW0_HUMAN	Q9unw0	homo sapien
205	41	45.6	846	2	Q5T396_HUMAN	Q5t396	homo sapien
206	41	45.6	846	2	Q96IJ1_HUMAN	Q96ij1	homo sapien
207	41	45.6	846	2	Q9UQ84_HUMAN	Q9uq84	homo sapien
208	41	45.6	847	2	Q529E0_MAGGR	Q529e0	magnaporthe
209	41	45.6	854	2	Q90VG7_9HIV1	Q90vg7	human immun
210	41	45.6	908	2	Q4P7F1_USTMA	Q4p7f1	ustilago ma
211	41	45.6	933	2	Q677U1_9VIRU	Q677u1	lymphocysti
212	41	45.6	951	2	Q6FQ85_CANGA	Q6fq85	candida gla
213	41	45.6	967	2	Q61MX8_CAEBR	Q61mx8	caenorhabdi
214	41	45.6	1015	2	Q5WS95_LEGPA	Q5ws95	legionella
215	41	45.6	1326	2	Q6FV20_CANGA	Q6fv20	candida gla
216	41	45.6	1579	2	Q90X96_XENLA	Q90x96	xenopus lae
217	41	45.6	1610	2	Q4ZPR9_PSESY	Q4zpr9	pseudomonas
218	41	45.6	1857	2	Q6C4B9_YARLI	Q6c4b9	yarrowia li
219	41	45.6	3443	2	Q8JZM8_MOUSE	Q8jzm8	mus musculu
220	40.5	45.0	368	1	CYHY_GLOSO	P32964	gloeocercos
221	40.5	45.0	619	1	ILVD_NEIMA	Q9jue0	neisseria m
222	40.5	45.0	619	1	ILVD_NEIMB	Q9js61	neisseria m
223	40	44.4	65	2	Q8YKK6_ANASP	Q8ykk6	anabaena sp
224	40	44.4	147	2	Q5WNL3_CAEBR	Q5wnl3	caenorhabdi
225	40	44.4	151	2	Q9XXB9_CAEEL	Q9xxb9	caenorhabdi
226	40	44.4	154	2	Q92NY6_RHIME	Q92ny6	rhizobium m
227	40	44.4	177	2	Q4X150_ASPFU	Q4x150	aspergillus
228	40	44.4	181	2	Q8MQZ4_DROME	Q8mqz4	drosophila
229	40	44.4	192	2	Q61IZ4_CAEBR	Q61iz4	caenorhabdi
230	40	44.4	209	2	Q5FJ42_LACAC	Q5fj42	lactobacill
231	40	44.4	216	2	Q6ABZ3_LEIXX	Q6abz3	leifsonia x
232	40	44.4	237	2	Q7V5G0_PROMM	Q7v5g0	prochloroco
233	40	44.4	240	2	Q6CZV9_ERWCT	Q6czv9	erwinia car
234	40	44.4	246	2	Q8XM92_CLOPE	Q8xm92	clostridium
235	40	44.4	256	2	Q5EGS1_SPAAU	Q5egs1	sparus aura
236	40	44.4	259	2	Q97E38_CLOAB	Q97e38	clostridium
237	40	44.4	264	2	Q9CB38_MYCLE	Q9cb38	mycobacteri
238	40	44.4	294	2	Q88BQ6_PSESM	Q88bq6	pseudomonas
239	40	44.4	301	2	Q5U3X0_BRARE	Q5u3x0	brachydanio
240	40	44.4	306	2	Q9P5R1_NEUCR	Q9p5r1	neurospora
241	40	44.4	306	2	Q68WY8_RICTY	Q68wy8	rickettsia
242	40	44.4	309	2	Q6AKE2_DESPS	Q6ake2	desulfotale
243	40	44.4	311	2	Q6NWD2_BRARE	Q6nwd2	brachydanio
244	40	44.4	313	2	Q9KBX9_BACHD	Q9kbx9	bacillus ha
245	40	44.4	315	2	Q61KG7_CAEBR	Q61kg7	caenorhabdi
246	40	44.4	316	1	PTH2_CAEEL	O76387	caenorhabdi
247	40	44.4	320	2	Q8N4L9_HUMAN	Q8n4l9	homo sapien
248	40	44.4	321	2	Q65X50_ORYSA	Q65x50	oryza sativ
249	40	44.4	321	2	Q8YT11_ANASP	Q8yt11	anabaena sp
250	40	44.4	323	2	Q7V544_PROMM	Q7v544	prochloroco

251	40	44.4	355	2	Q577D9_BRUAB	Q577d9	brucella ab
252	40	44.4	355	2	Q5HVJ0_CAMJR	Q5hvj0	campylobact
253	40	44.4	355	2	Q9PHT6_CAMJE	Q9pht6	campylobact
254	40	44.4	355	2	Q8FWW6_BRUSU	Q8fww6	brucella su
255	40	44.4	355	2	Q8YBH8_BRUME	Q8ybh8	brucella me
256	40	44.4	360	2	Q8LB77_ARATH	Q8lb77	arabidopsis
257	40	44.4	360	2	Q9C648_ARATH	Q9c648	arabidopsis
258	40	44.4	360	2	Q9SM03_ARATH	Q9sm03	arabidopsis
259	40	44.4	375	2	Q6VSX5_9VIRU	Q6vsx5	vibrio para
260	40	44.4	377	2	Q8A0C7_BACTN	Q8a0c7	bacteroides
261	40	44.4	381	2	Q8EIY3_SHEON	Q8eiy3	shewanella
262	40	44.4	385	1	BCAT1_SHEEP	Q9gkm4	ovis aries
263	40	44.4	385	2	Q68DQ7_HUMAN	Q68dq7	homo sapien
264	40	44.4	386	1	BCAT1_HUMAN	P54687	homo sapien
265	40	44.4	387	2	Q65E78_BACLD	Q65e78	bacillus li
266	40	44.4	388	2	Q6EHZ7_TRIVA	Q6ehz7	trichomonas
267	40	44.4	391	2	Q5JJT2_ORYSA	Q5jjt2	oryza sativ
268	40	44.4	413	2	Q5BLI7_BRARE	Q5bli7	brachydanio
269	40	44.4	416	2	Q9RXH3_DEIRA	Q9rxh3	deinococcus
270	40	44.4	421	2	Q5FUL6_GLUOX	Q5ful6	gluconobact
271	40	44.4	425	2	Q9W116_DROME	Q9w116	drosophila
272	40	44.4	426	2	Q8I1E1_DROPS	Q8i1e1	drosophila
273	40	44.4	433	2	Q6PFK3_BRARE	Q6pfk3	brachydanio
274	40	44.4	435	2	Q55W75_CRYNE	Q55w75	cryptococcu
275	40	44.4	448	2	Q72YC9_BACC1	Q72yc9	bacillus ce
276	40	44.4	448	2	Q505G3_MOUSE	Q505g3	mus musculu
277	40	44.4	479	2	Q4XQX8_PLACH	Q4xqx8	plasmodium
278	40	44.4	480	2	Q51GN3_ENTHI	Q51gn3	entamoeba h
279	40	44.4	484	2	Q64TB7_BACFR	Q64tb7	bacteroides
280	40	44.4	490	2	Q6FR73_CANGA	Q6fr73	candida gla
281	40	44.4	490	2	Q5LCC3_BACFN	Q5lcc3	bacteroides
282	40	44.4	495	2	Q5A2W6_CANAL	Q5a2w6	candida alb
283	40	44.4	522	2	Q6D6A8_ERWCT	Q6d6a8	erwinia car
284	40	44.4	526	2	Q6FTA0_CANGA	Q6fta0	candida gla
285	40	44.4	530	2	Q4FZ16_LEIMA	Q4fz16	leishmania
286	40	44.4	530	2	Q9W629_BRARE	Q9w629	brachydanio
287	40	44.4	533	2	Q5U5D3_XENLA	Q5u5d3	xenopus lae
288	40	44.4	538	2	Q57U34_9TRYP	Q57u34	trypanosoma
289	40	44.4	540	2	Q7T6I0_9LUTE	Q7t6i0	sugarcane y
290	40	44.4	551	2	Q822S1_CHLCV	Q822s1	chlamydophi
291	40	44.4	552	2	Q5L5R0_CHLAB	Q5l5r0	chlamydophi
292	40	44.4	578	2	Q6SGA1_9BACT	Q6sga1	uncultured
293	40	44.4	578	2	Q64YP4_BACFR	Q64yp4	bacteroides
294	40	44.4	588	2	Q4RKP2_TETNG	Q4rkp2	tetraodon n
295	40	44.4	612	2	Q55KL3_CRYNE	Q55kl3	cryptococcu
296	40	44.4	612	2	Q5KAV8_CRYNE	Q5kav8	cryptococcu
297	40	44.4	620	2	Q670I3_9LUTE	Q670i3	carrot red
298	40	44.4	642	2	Q6NQ84_ARATH	Q6nq84	arabidopsis
299	40	44.4	644	2	Q55JT3_CRYNE	Q55jt3	cryptococcu
300	40	44.4	644	2	Q5K9R8_CRYNE	Q5k9r8	cryptococcu
301	40	44.4	662	2	Q7QSP2_GIALA	Q7qsp2	giardia lam
302	40	44.4	671	2	Q4WU61_ASPFU	Q4wu61	aspergillus
303	40	44.4	684	1	SKIL_HUMAN	P12757	homo sapien
304	40	44.4	720	2	Q4I4D0_GIBZE	Q4i4d0	gibberella
305	40	44.4	740	2	Q67Z21_ARATH	Q67z21	arabidopsis
306	40	44.4	746	2	Q6BQT6_DEBHA	Q6bqt6	debaryomyce
307	40	44.4	761	2	Q9D9U3_MOUSE	Q9d9u3	mus musculu
308	40	44.4	773	2	O01892_CAEEL	O01892	caenorhabdi
309	40	44.4	775	2	Q9C284_NEUCR	Q9c284	neurospora
310	40	44.4	778	2	Q6PCQ0_MOUSE	Q6pcq0	mus musculu
311	40	44.4	793	2	Q560C5_CRYNE	Q560c5	cryptococcu
312	40	44.4	801	2	Q4UP79_XANCP	Q4up79	xanthomonas
313	40	44.4	801	2	Q8P3Q3_XANCP	Q8p3q3	xanthomonas
314	40	44.4	807	1	PGAA_ECO57	P69435	escherichia
315	40	44.4	807	1	PGAA_ECOLI	P69434	escherichia
316	40	44.4	807	2	Q8CW69_ECOL6	Q8cw69	escherichia
317	40	44.4	811	2	Q51H45_ENTHI	Q51h45	entamoeba h
318	40	44.4	812	2	Q5KPC8_CRYNE	Q5kpc8	cryptococcu
319	40	44.4	865	2	Q5CNG4_CRYHO	Q5cng4	cryptospori
320	40	44.4	880	2	O73879_BRARE	O73879	brachydanio
321	40	44.4	906	2	Q51SU1_MAGGR	Q51su1	magnaporthe
322	40	44.4	936	2	Q5TT82_ANOGA	Q5tt82	anopheles g
323	40	44.4	994	2	Q7RWT6_NEUCR	Q7rwt6	neurospora
324	40	44.4	1025	2	Q6NXM0_MOUSE	Q6nxm0	mus musculu
325	40	44.4	1039	1	MSL1_DROME	P50535	drosophila
326	40	44.4	1045	2	Q670I5_9LUTE	Q670i5	carrot red
327	40	44.4	1087	2	Q8NJ48_9ASCO	Q8nj48	ericoid myc
328	40	44.4	1209	2	Q69ZU2_MOUSE	Q69zu2	mus musculu
329	40	44.4	1240	2	Q7TQM8_MOUSE	Q7tqm8	mus musculu
330	40	44.4	1248	2	Q8BWH3_MOUSE	Q8bwh3	mus musculu
331	40	44.4	1391	2	Q4WXL5_ASPFU	Q4wxl5	aspergillus
332	40	44.4	1519	2	Q7QAM8_ANOGA	Q7qam8	anopheles g
333	40	44.4	1611	2	O42854_SCHPO	O42854	schizosacch
334	40	44.4	1813	2	Q75F75_ASHGO	Q75f75	ashbya goss
335	40	44.4	1884	2	Q4QGV3_LEIMA	Q4qgv3	leishmania
336	40	44.4	1927	2	Q59L14_CANAL	Q59l14	candida alb
337	40	44.4	1927	2	Q59L18_CANAL	Q59l18	candida alb
338	40	44.4	2209	2	Q4QEP0_LEIMA	Q4qep0	leishmania
339	40	44.4	2773	2	Q8IBF4_PLAF7	Q8ibf4	plasmodium
340	40	44.4	3620	2	Q5XWC6_BARVI	Q5xwc6	bartonella
341	40	44.4	3855	2	Q4SYK6_TETNG	Q4syk6	tetraodon n
342	39.5	43.9	214	1	YPT3_SCHPO	P17610	schizosacch
343	39.5	43.9	312	1	PGTE_SALTY	P06185	salmonella
344	39.5	43.9	312	2	Q57LW0_SALCH	Q57lw0	salmonella
345	39.5	43.9	419	2	Q6CL06_KLULA	Q6cl06	kluyveromyc
346	39.5	43.9	555	2	Q9U6X2_ONCVO	Q9u6x2	onchocerca
347	39.5	43.9	619	2	Q5F8G6_NEIG1	Q5f8g6	neisseria g
348	39.5	43.9	619	2	Q4LUY2_9BURK	Q4luy2	burkholderi
349	39.5	43.9	1116	2	Q9IBK4_9VIRU	Q9ibk4	tobacco mos
350	39.5	43.9	1616	2	Q9IBK5_9VIRU	Q9ibk5	tobacco mos
351	39.5	43.9	1808	2	Q6E7J4_9CYAN	Q6e7j4	lyngbya maj
352	39	43.3	54	2	Q6F907_ACIAD	Q6f907	acinetobact
353	39	43.3	68	2	Q9T1H5_9CAUD	Q9t1h5	lactobacill
354	39	43.3	142	2	Q6FYF0_BARQU	Q6fyf0	bartonella
355	39	43.3	149	2	Q5QZI7_IDILO	Q5qzi7	idiomarina
356	39	43.3	151	2	Q801A0_EPIAK	Q801a0	epinephelus
357	39	43.3	164	2	Q9CQ46_MOUSE	Q9cq46	m mus muscu
358	39	43.3	170	2	Q5CF19_CRYHO	Q5cf19	cryptospori
359	39	43.3	174	2	Q5FLV6_LACAC	Q5flv6	lactobacill
360	39	43.3	175	2	Q5TWW1_ANOGA	Q5tww1	anopheles g
361	39	43.3	185	2	Q4LTQ1_9BURK	Q4ltq1	burkholderi
362	39	43.3	186	2	Q6QW49_AZOBR	Q6qw49	azospirillu
363	39	43.3	187	2	Q91077_LATJA	Q91077	lateolabrax
364	39	43.3	187	2	Q91454_9PERC	Q91454	sebastiscus
365	39	43.3	192	2	Q5C4Z0_SCHJA	Q5c4z0	schistosoma
366	39	43.3	202	2	Q9X3T1_ERWAM	Q9x3t1	erwinia amy
367	39	43.3	204	1	SOMA_ACABU	Q01282	acanthopagr
368	39	43.3	204	1	SOMA_ACALA	P45654	acanthopagr
369	39	43.3	204	1	SOMA_PERFV	Q9dev3	perca flave
370	39	43.3	204	1	SOMA_SEBSC	P87391	sebastes sc
371	39	43.3	204	2	Q6QPJ2_9PERO	Q6qpj2	lepomis cya
372	39	43.3	204	2	Q90VV6_EPICO	Q90vv6	epinephelus
373	39	43.3	204	2	Q5J3Q3_ACASC	Q5j3q3	acanthopagr
374	39	43.3	204	2	Q8UW02_EPIAW	Q8uw02	epinephelus
375	39	43.3	204	2	Q5Y163_ACASC	Q5y163	acanthopagr
376	39	43.3	204	2	Q53YN5_SEBSC	Q53yn5	sebastes sc
377	39	43.3	208	2	Q839U8_ENTFA	Q839u8	enterococcu
378	39	43.3	209	2	Q7ZP21_9HIV1	Q7zp21	human immun
379	39	43.3	222	2	Q5ABB4_CANAL	Q5abb4	candida alb
380	39	43.3	223	2	Q50V15_ENTHI	Q50v15	entamoeba h
381	39	43.3	234	2	Q6GQ47_XENLA	Q6gq47	xenopus lae
382	39	43.3	238	2	Q8X0T6_NEUCR	Q8x0t6	neurospora
383	39	43.3	244	2	Q5MI37_9HIV1	Q5mi37	human immun
384	39	43.3	245	2	Q6BT26_DEBHA	Q6bt26	debaryomyce
385	39	43.3	245	2	Q5CNG2_CRYHO	Q5cng2	cryptospori
386	39	43.3	253	2	Q8TTX8_METAC	Q8ttx8	methanosarc
387	39	43.3	256	2	Q9XY51_CTEFE	Q9xy51	ctenocephal
388	39	43.3	258	2	Q7QCU7_ANOGA	Q7qcu7	anopheles g
389	39	43.3	261	2	Q4SQ53_TETNG	Q4sq53	tetraodon n
390	39	43.3	274	2	Q4LJ76_9BURK	Q4lj76	burkholderi
391	39	43.3	277	2	Q4UA37_THEAN	Q4ua37	theileria a
392	39	43.3	284	2	Q9TZB2_CAEEL	Q9tzb2	caenorhabdi
393	39	43.3	294	2	Q5ZZ27_LEGPH	Q5zz27	legionella
394	39	43.3	297	2	Q4YYB3_PLABE	Q4yyb3	plasmodium
395	39	43.3	307	2	Q97WH6_SULSO	Q97wh6	sulfolobus
396	39	43.3	309	2	Q4R6Z8_MACFA	Q4r6z8	macaca fasc

397	39	43.3	312	2	Q8F3E4_LEPIN	Q8f3e4 leptospira
398	39	43.3	312	2	Q72S89_LEPIC	Q72s89 leptospira
399	39	43.3	321	2	Q7VPE0_HAEDU	Q7vpe0 haemophilus
400	39	43.3	321	2	Q7W168_BORPA	Q7w168 bordetella
401	39	43.3	321	2	Q7WNW1_BORBR	Q7wnw1 bordetella
402	39	43.3	325	2	Q8HW98_MOUSE	Q8hw98 mus musculu
403	39	43.3	330	2	Q72M54_LEPIC	Q72m54 leptospira
404	39	43.3	330	2	Q8EYN2_LEPIN	Q8eyn2 leptospira
405	39	43.3	333	2	Q7PCU2_ANOGA	Q7pcu2 anopheles g
406	39	43.3	334	1	OTCC_HAEGA	Q9zix8 haemophilus
407	39	43.3	334	1	OTCC_HAEIN	P44770 haemophilus
408	39	43.3	334	1	OTC_HAEDU	Q7vp68 haemophilus
409	39	43.3	334	2	Q4QMU8_HAEI8	Q4qmu8 haemophilus
410	39	43.3	335	1	OTCC_PSEAE	P08308 pseudomonas
411	39	43.3	335	1	OTCC_PSEME	Q936v7 pseudomonas
412	39	43.3	335	1	OTCC_PSEPK	Q88p53 pseudomonas
413	39	43.3	335	2	Q7WPN2_BORBR	Q7wpn2 bordetella
414	39	43.3	336	2	Q4K7R3_PSEF5	Q4k7r3 pseudomonas
415	39	43.3	342	2	Q7VVI8_BORPE	Q7vvi8 bordetella
416	39	43.3	352	1	ARGC_SULSO	Q980x1 s n-acetyl-
417	39	43.3	353	2	Q5AP60_CANAL	Q5ap60 candida alb
418	39	43.3	353	2	Q9QEL3_9HIV1	Q9qel3 human immun
419	39	43.3	357	2	Q893A1_CLOTE	Q893a1 clostridium
420	39	43.3	367	1	DUS1_MOUSE	P28563 mus musculu
421	39	43.3	367	1	DUS1_RAT	Q64623 rattus norv
422	39	43.3	367	2	Q63683_RAT	Q63683 rattus norv
423	39	43.3	367	2	Q64193_9MURI	Q64193 rattus sp.
424	39	43.3	367	2	Q548G6_RAT	Q548g6 rattus norv
425	39	43.3	376	2	Q4RHB3_TETNG	Q4rhb3 tetraodon n
426	39	43.3	379	2	Q8YNY6_ANASP	Q8yny6 anabaena sp
427	39	43.3	381	2	Q56TM4_9LACO	Q56tm4 lactobacill
428	39	43.3	392	2	O44716_CAEEL	O44716 caenorhabdi
429	39	43.3	392	2	Q9ZPX3_ARATH	Q9zpx3 arabidopsis
430	39	43.3	401	2	Q89UQ2_BRAJA	Q89uq2 bradyrhizob
431	39	43.3	407	2	Q4NTX3_9DELT	Q4ntx3 anaeromyxob
432	39	43.3	410	2	Q5CSH8_CRYPV	Q5csh8 cryptospori
433	39	43.3	415	1	HST4_SCHPO	Q9ur39 schizosacch
434	39	43.3	419	2	Q8I199_DROVI	Q8i199 drosophila
435	39	43.3	420	2	Q521U6_MAGGR	Q521u6 magnaporthe
436	39	43.3	434	1	YFEW_ECOLI	P77619 escherichia
437	39	43.3	435	2	Q5C363_SCHJA	Q5c363 schistosoma
438	39	43.3	467	2	Q55JN3_CRYNE	Q55jn3 cryptococcu
439	39	43.3	467	2	Q5K9W8_CRYNE	Q5k9w8 cryptococcu
440	39	43.3	490	2	Q8CFG4_MOUSE	Q8cfg4 mus musculu
441	39	43.3	491	2	Q7Q631_ANOGA	Q7q631 anopheles g
442	39	43.3	502	2	Q6ZGZ5_ORYSA	Q6zgz5 oryza sativ
443	39	43.3	510	2	Q801V8_BRARE	Q801v8 brachydanio
444	39	43.3	514	2	Q856B6_9CAUD	Q856b6 mycobacteri
445	39	43.3	516	2	Q5K0A0_9FUNG	Q5k0a0 orpinomyces
446	39	43.3	522	1	OPGG_ERWCH	Q9f496 erwinia chr
447	39	43.3	524	2	Q7T6H2_9LUTE	Q7t6h2 sugarcane y
448	39	43.3	525	2	Q704G6_9LUTE	Q704g6 sugarcane y
449	39	43.3	525	2	Q704G9_9LUTE	Q704g9 sugarcane y
450	39	43.3	525	2	Q704K5_9LUTE	Q704k5 sugarcane y
451	39	43.3	525	2	Q704N5_9LUTE	Q704n5 sugarcane y
452	39	43.3	525	2	Q704N2_9LUTE	Q704n2 sugarcane y
453	39	43.3	525	2	Q704M9_9LUTE	Q704m9 sugarcane y
454	39	43.3	525	2	Q704M6_9LUTE	Q704m6 sugarcane y
455	39	43.3	525	2	Q704M3_9LUTE	Q704m3 sugarcane y
456	39	43.3	525	2	Q704M0_9LUTE	Q704m0 sugarcane y
457	39	43.3	525	2	Q704L7_9LUTE	Q704l7 sugarcane y
458	39	43.3	525	2	Q704L4_9LUTE	Q704l4 sugarcane y
459	39	43.3	525	2	Q704L1_9LUTE	Q704l1 sugarcane y
460	39	43.3	525	2	Q704K8_9LUTE	Q704k8 sugarcane y
461	39	43.3	525	2	Q704K2_9LUTE	Q704k2 sugarcane y
462	39	43.3	525	2	Q704J9_9LUTE	Q704j9 sugarcane y
463	39	43.3	525	2	Q704J6_9LUTE	Q704j6 sugarcane y
464	39	43.3	525	2	Q704J3_9LUTE	Q704j3 sugarcane y
465	39	43.3	525	2	Q704J0_9LUTE	Q704j0 sugarcane y
466	39	43.3	525	2	Q704I4_9LUTE	Q704i4 sugarcane y
467	39	43.3	525	2	Q704I1_9LUTE	Q704i1 sugarcane y
468	39	43.3	525	2	Q704H8_9LUTE	Q704h8 sugarcane y
469	39	43.3	525	2	Q704H5_9LUTE	Q704h5 sugarcane y
470	39	43.3	525	2	Q704H2_9LUTE	Q704h2 sugarcane y
471	39	43.3	526	2	Q9V9Y4_DROME	Q9v9y4 drosophila
472	39	43.3	526	2	Q704G5_9LUTE	Q704g5 sugarcane y
473	39	43.3	526	2	Q704G8_9LUTE	Q704g8 sugarcane y
474	39	43.3	526	2	Q704H1_9LUTE	Q704h1 sugarcane y
475	39	43.3	526	2	Q704H4_9LUTE	Q704h4 sugarcane y
476	39	43.3	526	2	Q704H7_9LUTE	Q704h7 sugarcane y
477	39	43.3	526	2	Q704I0_9LUTE	Q704i0 sugarcane y
478	39	43.3	526	2	Q704J2_9LUTE	Q704j2 sugarcane y
479	39	43.3	526	2	Q704J8_9LUTE	Q704j8 sugarcane y
480	39	43.3	526	2	Q704K1_9LUTE	Q704k1 sugarcane y
481	39	43.3	526	2	Q704K4_9LUTE	Q704k4 sugarcane y
482	39	43.3	526	2	Q704L3_9LUTE	Q704l3 sugarcane y
483	39	43.3	526	2	Q704M5_9LUTE	Q704m5 sugarcane y
484	39	43.3	526	2	Q704N1_9LUTE	Q704n1 sugarcane y
485	39	43.3	526	2	Q704N4_9LUTE	Q704n4 sugarcane y
486	39	43.3	526	2	Q704M8_9LUTE	Q704m8 sugarcane y
487	39	43.3	526	2	Q704M2_9LUTE	Q704m2 sugarcane y
488	39	43.3	526	2	Q704L9_9LUTE	Q704l9 sugarcane y
489	39	43.3	526	2	Q704L6_9LUTE	Q704l6 sugarcane y
490	39	43.3	526	2	Q704L0_9LUTE	Q704l0 sugarcane y
491	39	43.3	526	2	Q704K7_9LUTE	Q704k7 sugarcane y
492	39	43.3	526	2	Q704J5_9LUTE	Q704j5 sugarcane y
493	39	43.3	526	2	Q704I9_9LUTE	Q704i9 sugarcane y
494	39	43.3	526	2	Q704I3_9LUTE	Q704i3 sugarcane y
495	39	43.3	534	2	Q63655_RAT	Q63655 rattus norv
496	39	43.3	538	2	Q9FZH1_ARATH	Q9fzh1 arabidopsis
497	39	43.3	540	2	Q7T6H3_9LUTE	Q7t6h3 sugarcane y
498	39	43.3	540	2	Q7T6H4_9LUTE	Q7t6h4 sugarcane y
499	39	43.3	540	2	Q7T6H5_9LUTE	Q7t6h5 sugarcane y
500	39	43.3	540	2	Q7T6H6_9LUTE	Q7t6h6 sugarcane y
501	39	43.3	540	2	Q7T6H7_9LUTE	Q7t6h7 sugarcane y
502	39	43.3	540	2	Q7T6H9_9LUTE	Q7t6h9 sugarcane y
503	39	43.3	540	2	Q7T6I3_9LUTE	Q7t6i3 sugarcane y
504	39	43.3	540	2	Q7T6I6_9LUTE	Q7t6i6 sugarcane y
505	39	43.3	540	2	Q7T6I7_9LUTE	Q7t6i7 sugarcane y
506	39	43.3	540	2	Q7T6I8_9LUTE	Q7t6i8 sugarcane y
507	39	43.3	540	2	Q7T6I9_9LUTE	Q7t6i9 sugarcane y
508	39	43.3	540	2	Q7T6J0_9LUTE	Q7t6j0 sugarcane y
509	39	43.3	540	2	Q7T6J1_9LUTE	Q7t6j1 sugarcane y
510	39	43.3	540	2	Q7T6J2_9LUTE	Q7t6j2 sugarcane y
511	39	43.3	540	2	Q7T6J3_9LUTE	Q7t6j3 sugarcane y
512	39	43.3	540	2	Q7T6I5_9LUTE	Q7t6i5 sugarcane y
513	39	43.3	540	2	Q7T6I4_9LUTE	Q7t6i4 sugarcane y
514	39	43.3	540	2	Q7T6I2_9LUTE	Q7t6i2 sugarcane y
515	39	43.3	540	2	Q7T6I1_9LUTE	Q7t6i1 sugarcane y
516	39	43.3	540	2	Q7T6H8_9LUTE	Q7t6h8 sugarcane y
517	39	43.3	541	2	Q835M9_ENTFA	Q835m9 enterococcu
518	39	43.3	545	2	Q88N22_PSEPK	Q88n22 pseudomonas
519	39	43.3	552	2	Q5ALQ3_CANAL	Q5alq3 candida alb
520	39	43.3	563	2	Q8IWE2_HUMAN	Q8iwe2 homo sapien
521	39	43.3	563	2	Q9BVL6_HUMAN	Q9bvl6 homo sapien
522	39	43.3	569	2	Q655F1_ORYSA	Q655f1 oryza sativ
523	39	43.3	579	2	Q6Z1Y8_ORYSA	Q6z1y8 oryza sativ
524	39	43.3	581	2	P90919_CAEEL	P90919 caenorhabdi
525	39	43.3	583	1	NIR_BETVE	P38500 betula verr
526	39	43.3	597	2	Q9KUW6_VIBCH	Q9kuw6 vibrio chol
527	39	43.3	612	2	Q6ZLW2_9TELE	Q6zlw2 synaphobran
528	39	43.3	617	2	Q4FY33_LEIMA	Q4fy33 leishmania
529	39	43.3	617	2	Q55987_SYNY3	Q55987 synechocyst
530	39	43.3	622	2	O54040_PSEAE	O54040 pseudomonas
531	39	43.3	626	1	PKNB_MYCBO	P0a5s5 mycobacteri
532	39	43.3	626	1	PKNB_MYCTU	P0a5s4 mycobacteri
533	39	43.3	632	2	Q93AE0_PSEOL	Q93ae0 pseudomonas
534	39	43.3	642	2	Q70AE1_9LUTE	Q70ae1 sugarcane y
535	39	43.3	642	2	Q70AF9_9LUTE	Q70af9 sugarcane y
536	39	43.3	642	2	Q70AF6_9LUTE	Q70af6 sugarcane y
537	39	43.3	642	2	Q70AF3_9LUTE	Q70af3 sugarcane y
538	39	43.3	642	2	Q70AF0_9LUTE	Q70af0 sugarcane y
539	39	43.3	642	2	Q70AE7_9LUTE	Q70ae7 sugarcane y
540	39	43.3	642	2	Q70AE4_9LUTE	Q70ae4 sugarcane y
541	39	43.3	642	2	Q70AD9_9LUTE	Q70ad9 sugarcane y
542	39	43.3	649	2	Q617Q6_CAEBR	Q617q6 caenorhabdi

543	39	43.3	649	2	Q688U4_ORYSA	Q688u4	oryza sativ	616	38.5	42.8	425	2	Q8Y9D5_LISMO	Q8y9d5	listeria mo		
544	39	43.3	649	2	Q9XHW1_ORYSA	Q9xhw1	oryza sativ	617	38.5	42.8	425	2	Q92E57_LISIN	Q92e57	listeria in		
545	39	43.3	650	2	Q9JH79_9LUTE	Q9jh79	sugarcane y	618	38.5	42.8	445	2	Q5CKS2_CRYHO	Q5cks2	cryptospori		
546	39	43.3	650	2	Q9QQN9_9LUTE	Q9qqn9	sugarcane y	619	38.5	42.8	476	2	Q4IP01_GIBZE	Q4ip01	gibberella		
547	39	43.3	650	2	Q80FH9_9LUTE	Q80fh9	sugarcane y	620	38.5	42.8	576	2	Q6P4I8_HUMAN	Q6p4i8	homo sapien		
548	39	43.3	655	2	Q9D2Z9_MOUSE	Q9d2z9	mus musculu	621	38.5	42.8	618	2	Q5FN26_GLUOX	Q5fn26	gluconobact		
549	39	43.3	662	2	Q519Z9_ENTHI	Q519z9	entamoeba h	622	38.5	42.8	669	2	Q4KJP4_PSEF5	Q4kjp4	pseudomonas		
550	39	43.3	670	2	Q5P4R5_AZOSE	Q5p4r5	azoarcus sp	623	38.5	42.8	944	2	Q5DMW3_CUCME	Q5dmw3	cucumis mel		
551	39	43.3	679	2	Q9FG18_ARATH	Q9fg18	arabidopsis	624	38.5	42.8	1098	2	Q6RK14_9BROM	Q6rk14	parietaria		
552	39	43.3	681	2	Q8VCB0_MOUSE	Q8vcb0	mus musculu	625	38.5	42.8	1117	2	Q5DWU8_9VIRU	Q5dwu8	pepper mild		
553	39	43.3	697	2	Q9LU16_ARATH	Q9lu16	arabidopsis	626	38.5	42.8	1117	2	Q5I2N8_9VIRU	Q5i2n8	pepper mild		
554	39	43.3	701	2	Q4SU80_TETNG	Q4su80	tetraodon n	627	38.5	42.8	1117	2	Q8QZF3_9VIRU	Q8qzf3	pepper mild		
555	39	43.3	717	2	O04325_ARATH	O04325	arabidopsis	628	38.5	42.8	1117	2	Q91E34_9VIRU	Q91e34	pepper mild		
556	39	43.3	724	2	Q8BZM6_MOUSE	Q8bzm6	mus musculu	629	38.5	42.8	1117	2	Q4W8Q6_9VIRU	Q4w8q6	pepper mild		
557	39	43.3	740	2	Q6BKZ5_DEBHA	Q6bkz5	debaryomyce	630	38.5	42.8	1439	2	Q5CRM3_CRYPV	Q5crm3	cryptospori		
558	39	43.3	755	2	O14167_SCHPO	O14167	schizosacch	631	38.5	42.8	1612	1	RRPO_PMMVJ	P89657	pepper mild		
559	39	43.3	771	2	Q5BGR9_EMENI	Q5bgr9	aspergillus	632	38.5	42.8	1612	1	RRPO_PMMVS	P29098	pepper mild		
560	39	43.3	775	2	Q4J6P8_SULAC	Q4j6p8	sulfolobus	633	38.5	42.8	1612	2	Q5DWU9_9VIRU	Q5dwu9	pepper mild		
561	39	43.3	782	2	Q55D42_DICDI	Q55d42	dictyosteli	634	38.5	42.8	1612	2	Q5I2N9_9VIRU	Q5i2n9	pepper mild		
562	39	43.3	794	2	Q965V2_CAEEL	Q965v2	caenorhabdi	635	38.5	42.8	1612	2	Q91E35_9VIRU	Q91e35	pepper mild		
563	39	43.3	815	2	Q70AE3_9LUTE	Q70ae3	sugarcane y	636	38.5	42.8	1800	2	Q7SB36_NEUCR	Q7sb36	neurospora		
564	39	43.3	815	2	Q70AF5_9LUTE	Q70af5	sugarcane y	637	38.5	42.8	4081	2	Q9VWZ3_DROME	Q9vwz3	drosophila		
565	39	43.3	815	2	Q70AF8_9LUTE	Q70af8	sugarcane y	638	38	42.2	55	2	Q5C6I2_SCHJA	Q5c6i2	schistosoma		
566	39	43.3	815	2	Q70AF2_9LUTE	Q70af2	sugarcane y	639	38	42.2	78	2	Q5BH03_EMENI	Q5bh03	aspergillus		
567	39	43.3	815	2	Q70AE9_9LUTE	Q70ae9	sugarcane y	640	38	42.2	99	2	Q8YD46_BRUME	Q8yd46	brucella me		
568	39	43.3	815	2	Q70AE6_9LUTE	Q70ae6	sugarcane y	641	38	42.2	112	2	Q5B6P4_EMENI	Q5b6p4	aspergillus		
569	39	43.3	815	2	Q70AD8_9LUTE	Q70ad8	sugarcane y	642	38	42.2	112	2	Q6QU05_9HIV1	Q6qu05	human immun		
570	39	43.3	851	2	Q9CS19_MOUSE	Q9cs19	mus musculu	643	38	42.2	113	2	Q75FR4_LEPIC	Q75fr4	leptospira		
571	39	43.3	877	2	Q5SVT3_MOUSE	Q5svt3	mus musculu	644	38	42.2	113	2	Q8EXR0_LEPIN	Q8exr0	leptospira		
572	39	43.3	877	2	Q8K332_MOUSE	Q8k332	mus musculu	645	38	42.2	115	2	Q63660_RAT	Q63660	rattus norv		
573	39	43.3	891	2	Q86B39_CAEEL	Q86b39	caenorhabdi	646	38	42.2	119	1	DMPO_PSEUF	P19733	pseudomonas		
574	39	43.3	910	2	O16720_CAEEL	O16720	caenorhabdi	647	38	42.2	119	2	Q52165_PSEPU	Q52165	pseudomonas		
575	39	43.3	922	2	Q6MIH5_BDEBA	Q6mih5	bdellovibri	648	38	42.2	119	2	Q52174_PSEPU	Q52174	pseudomonas		
576	39	43.3	923	2	Q4I4L5_GIBZE	Q4i4l5	gibberella	649	38	42.2	119	2	Q68J58_PSEPU	Q68j58	pseudomonas		
577	39	43.3	950	1	GYP2_YEAST	P53258	saccharomyc	650	38	42.2	126	2	Q8CW93_ECOL6	Q8cw93	escherichia		
578	39	43.3	1026	2	Q8A5H1_BACTN	Q8a5h1	bacteroides	651	38	42.2	126	2	Q8X948_ECO57	Q8x948	escherichia		
579	39	43.3	1040	2	Q9W675_BRARE	Q9w675	brachydanio	652	38	42.2	135	2	Q9J5G8_FOWPV	Q9j5g8	fowlpox vir		
580	39	43.3	1050	2	Q54Q21_DICDI	Q54q21	dictyosteli	653	38	42.2	135	2	Q70HB5_FOWPV	Q70hb5	fowlpox vir		
581	39	43.3	1066	1	PZRN3_HUMAN	Q9upq7	homo sapien	654	38	42.2	139	2	Q5KTL9_BOMMO	Q5kt19	bombyx mori		
582	39	43.3	1118	2	Q9LJS9_ARATH	Q9ljs9	arabidopsis	655	38	42.2	147	1	HV1C_HUMAN	P01744	homo sapien		
583	39	43.3	1143	2	Q4P100_USTMA	Q4p100	ustilago ma	656	38	42.2	161	2	Q4YMU9_PLABE	Q4ymu9	plasmodium		
584	39	43.3	1147	2	Q5YW29_NOCFA	Q5yw29	nocardia fa	657	38	42.2	161	2	Q4LDU1_9BACT	Q4ldu1	uncultured		
585	39	43.3	1163	2	Q4WJQ8_ASPFU	Q4wjq8	aspergillus	658	38	42.2	161	2	Q4H1S1_9BACT	Q4h1s1	uncultured		
586	39	43.3	1316	2	Q4QGN1_LEIMA	Q4qgn1	leishmania	659	38	42.2	161	2	Q4H1L7_9BACT	Q4h1l7	uncultured		
587	39	43.3	1323	2	Q6BZ91_DEBHA	Q6bz91	debaryomyce	660	38	42.2	172	2	Q9F5I5_AGRRH	Q9f5i5	agrobacteri		
588	39	43.3	1363	2	Q59MA9_CANAL	Q59ma9	candida alb	661	38	42.2	179	2	Q7U8J0_SYNPX	Q7u8j0	synechococc		
589	39	43.3	1375	2	Q54YB9_DICDI	Q54yb9	dictyosteli	662	38	42.2	186	1	CI025_BRARE	Q6dc60	brachydanio		
590	39	43.3	1392	2	Q9XER9_ARATH	Q9xer9	arabidopsis	663	38	42.2	190	2	Q4NVX9_9DELT	Q4nvx9	anaeromyxob		
591	39	43.3	1407	2	Q06211_YEAST	Q06211	saccharomyc	664	38	42.2	194	1	ACPD_VIBPA	Q87pp9	vibrio para		
592	39	43.3	1412	2	Q5ZM88_CHICK	Q5zm88	gallus gall	665	38	42.2	204	1	SOMA_OREMO	P34746	oreochromis		
593	39	43.3	1465	1	ATP7B_HUMAN	P35670	homo sapien	666	38	42.2	204	1	SOMA_ORENI	P13391	oreochromis		
594	39	43.3	1526	2	Q6BL88_DEBHA	Q6bl88	debaryomyce	667	38	42.2	204	1	SOMA_PSECR	Q9i9m4	pseudosciae		
595	39	43.3	1643	2	Q7RYT7_NEUCR	Q7ryt7	neurospora	668	38	42.2	204	2	Q6LAL0_OREMO	Q6lal0	oreochromis		
596	39	43.3	2740	2	Q4P2Z4_USTMA	Q4p2z4	ustilago ma	669	38	42.2	204	2	Q53WZ5_ORENI	Q53wz5	oreochromis		
597	39	43.3	3071	2	Q9SND0_ARATH	Q9snd0	arabidopsis	670	38	42.2	204	2	Q541C7_PSECR	Q541c7	pseudosciae		
598	39	43.3	8601	2	Q6VT95_9BACT	Q6vt95	symbiont ba	671	38	42.2	209	2	Q5FGD3_EHRRG	Q5fgd3	ehrlichia r		
599	39	43.3	18412	2	Q7ZZ61_BRARE	Q7zz61	brachydanio	672	38	42.2	209	2	Q5HA96_EHRRW	Q5ha96	ehrlichia r		
600	38.5	42.8	115	2	Q63AR2_BACCZ	Q63ar2	bacillus ce	673	38	42.2	210	2	Q4SCF1_TETNG	Q4scf1	tetraodon n		
601	38.5	42.8	181	2	Q8E849_SHEON	Q8e849	shewanella	674	38	42.2	212	1	PRL1_OREMO	P09319	oreochromis		
602	38.5	42.8	185	2	Q8E838_SHEON	Q8e838	shewanella	675	38	42.2	212	2	Q4U8X6_THEAN	Q4u8x6	theileria a		
603	38.5	42.8	185	2	Q8E862_SHEON	Q8e862	shewanella	676	38	42.2	214	2	Q831Q1_ENTFA	Q831q1	enterococcu		
604	38.5	42.8	200	2	Q5BFC5_EMENI	Q5bfc5	aspergillus	677	38	42.2	215	2	Q4UMJ4_RICFE	Q4umj4	rickettsia		
605	38.5	42.8	231	2	Q8YW47_ANASP	Q8yw47	anabaena sp	678	38	42.2	219	2	Q4XX60_PLACH	Q4xx60	plasmodium		
606	38.5	42.8	258	2	O36625_9GEMI	O36625	tomato mott	679	38	42.2	223	2	Q977L8_9CREN	Q977l8	uncultured		
607	38.5	42.8	316	2	Q6ZJ42_ORYSA	Q6zj42	oryza sativ	680	38	42.2	230	1	RR3_PORPU	P51308	porphyra pu		
608	38.5	42.8	324	2	Q7R3H8_GIALA	Q7r3h8	giardia lam	681	38	42.2	231	2	Q5ZZZ4_MYCHY	Q5zzz4	mycoplasma		
609	38.5	42.8	331	2	Q9ZP12_CICAR	Q9zp12	cicer ariet	682	38	42.2	238	2	Q5FHH4_EHRRG	Q5fhh4	ehrlichia r		
610	38.5	42.8	353	2	Q9FSY1_9VIRI	Q9fsy1	chara fragi	683	38	42.2	238	2	Q5HBN7_EHRRW	Q5hbn7	ehrlichia r		
611	38.5	42.8	357	2	Q5KTX2_GIALA	Q5ktx2	giardia lam	684	38	42.2	239	2	Q92CS5_LISIN	Q92cs5	listeria in		
612	38.5	42.8	365	2	Q9FSY6_CONCI	Q9fsy6	conocephalu	685	38	42.2	249	1	BAIA1_EUBSP	P07914	eubacterium		
613	38.5	42.8	366	2	Q9FSY2_9VIRI	Q9fsy2	chara fragi	686	38	42.2	249	1	BAIA2_EUBSP	P19337	eubacterium		
614	38.5	42.8	421	2	Q5BEQ3_EMENI	Q5beq3	aspergillus	687	38	42.2	249	2	Q75DZ3_ASHGO	Q75dz3	ashbya goss		
615	38.5	42.8	424	2	Q4WEP0_ASPFU	Q4wep0	aspergillus	688	38	42.2	253	2	O28290_ARCFU	O28290	archaeoglob		

689	38	42.2	256	2	Q567D0_BRARE	Q567d0 brachydanio
690	38	42.2	266	2	Q976V5_SULTO	Q976v5 sulfolobus
691	38	42.2	268	2	P72907_SYNY3	P72907 synechocyst
692	38	42.2	274	2	Q63UR5_BURPS	Q63ur5 burkholderi
693	38	42.2	276	2	Q4HFX5_CAMCO	Q4hfx5 campylobact
694	38	42.2	278	2	Q51A89_ENTHI	Q51a89 entamoeba h
695	38	42.2	280	2	Q62JY4_BURMA	Q62jy4 burkholderi
696	38	42.2	284	2	Q74ZZ8_ASHGO	Q74zz8 ashbya goss
697	38	42.2	289	2	Q8XYX9_RALSO	Q8xyx9 ralstonia s
698	38	42.2	289	2	Q5YRR5_NOCFA	Q5yrr5 nocardia fa
699	38	42.2	290	2	Q6CEA0_YARLI	Q6cea0 yarrowia li
700	38	42.2	304	2	Q5BHD1_EMENI	Q5bhd1 aspergillus
701	38	42.2	308	2	Q4JCK2_SULAC	Q4jck2 sulfolobus
702	38	42.2	308	2	Q7YZF9_CAEEL	Q7yzf9 caenorhabdi
703	38	42.2	310	2	Q7RDL4_PLAYO	Q7rdl4 plasmodium
704	38	42.2	312	2	Q4UEL7_THEAN	Q4uel7 theileria a
705	38	42.2	317	1	ARGC_CAUCR	Q9a8h5 caulobacter
706	38	42.2	322	2	Q7R018_GIALA	Q7r018 giardia lam
707	38	42.2	325	2	Q9XTX8_CAEEL	Q9xtx8 caenorhabdi
708	38	42.2	328	2	Q5LH25_BACFN	Q5lh25 bacteroides
709	38	42.2	328	2	Q64XY2_BACFR	Q64xy2 bacteroides
710	38	42.2	329	2	O44759_CAEEL	O44759 caenorhabdi
711	38	42.2	336	2	Q6ZVW7_HUMAN	Q6zvw7 homo sapien
712	38	42.2	338	2	Q6XRB7_9BACT	Q6xrb7 uncultured
713	38	42.2	349	2	Q83F08_COXBU	Q83f08 coxiella bu
714	38	42.2	350	2	Q4UFZ4_THEAN	Q4ufz4 theileria a
715	38	42.2	350	2	Q6VT40_9VIRU	Q6vt40 vibrio para
716	38	42.2	352	2	Q4WD67_ASPFU	Q4wd67 aspergillus
717	38	42.2	355	2	Q4I6W9_GIBZE	Q4i6w9 gibberella
718	38	42.2	358	2	Q5W9C0_CHICK	Q5w9c0 gallus gall
719	38	42.2	362	2	Q9R170_RAT	Q9r170 rattus norv
720	38	42.2	368	2	Q4IJB6_GIBZE	Q4ijb6 gibberella
721	38	42.2	370	2	Q4QZZ9_EMENI	Q4qzz9 emericella
722	38	42.2	370	2	Q4ZMT4_PSESY	Q4zmt4 pseudomonas
723	38	42.2	372	2	Q57TW0_9TRYP	Q57tw0 trypanosoma
724	38	42.2	376	2	Q7RSF4_PLAYO	Q7rsf4 plasmodium
725	38	42.2	377	1	YPJH_BACSU	P42982 bacillus su
726	38	42.2	379	2	Q55TX8_CRYNE	Q55tx8 cryptococcu
727	38	42.2	379	2	Q5KIG0_CRYNE	Q5kig0 cryptococcu
728	38	42.2	379	2	Q4R7F2_MACFA	Q4r7f2 macaca fasc
729	38	42.2	386	1	BCAT1_MOUSE	P24288 mus musculu
730	38	42.2	389	2	Q50WM7_ENTHI	Q50wm7 entamoeba h
731	38	42.2	393	2	Q62TK2_BACLD	Q62tk2 bacillus li
732	38	42.2	394	2	Q65I53_BACLD	Q65i53 bacillus li
733	38	42.2	397	2	Q55WR0_CRYNE	Q55wr0 cryptococcu
734	38	42.2	397	2	Q5KJI6_CRYNE	Q5kji6 cryptococcu
735	38	42.2	398	2	Q8FV80_BRUSU	Q8fv80 brucella su
736	38	42.2	398	2	Q9CXX6_MOUSE	Q9cxx6 mus musculu
737	38	42.2	399	2	Q99JD5_RAT	Q99jd5 rattus norv
738	38	42.2	401	2	Q18155_CAEEL	Q18155 caenorhabdi
739	38	42.2	402	2	Q8IL48_PLAF7	Q8il48 plasmodium
740	38	42.2	406	1	NAGC_ECOLI	P15301 escherichia
741	38	42.2	407	2	Q9AEU0_STRGN	Q9aeu0 streptococc
742	38	42.2	411	1	BCAT1_RAT	P54690 rattus norv
743	38	42.2	411	2	Q6ZPV0_MOUSE	Q6zpv0 mus musculu
744	38	42.2	416	2	Q753A9_ASHGO	Q753a9 ashbya goss
745	38	42.2	416	2	Q6W4N2_9BACI	Q6w4n2 bacillus sp
746	38	42.2	417	2	Q5B0C8_EMENI	Q5b0c8 aspergillus
747	38	42.2	420	2	Q7SEI7_NEUCR	Q7sei7 neurospora
748	38	42.2	420	2	O17324_CAEEL	O17324 caenorhabdi
749	38	42.2	420	2	Q4H616_9DEIO	Q4h616 deinococcus
750	38	42.2	428	1	EF1A_PYRAB	Q9v0v7 pyrococcus
751	38	42.2	428	1	EF1A_PYRFU	Q8u152 pyrococcus
752	38	42.2	428	1	EF1A_PYRHO	O59153 pyrococcus
753	38	42.2	429	2	Q5W612_CAEEL	Q5w612 caenorhabdi
754	38	42.2	430	1	EF1A_PYRWO	P26751 pyrococcus
755	38	42.2	430	2	Q75EY0_ASHGO	Q75ey0 ashbya goss
756	38	42.2	431	2	Q524D2_MAGGR	Q524d2 magnaporthe
757	38	42.2	437	2	Q9VZZ0_DROME	Q9vzz0 drosophila
758	38	42.2	442	2	Q8ERI7_OCEIH	Q8eri7 oceanobacil
759	38	42.2	448	2	Q66HY4_BRARE	Q66hy4 brachydanio
760	38	42.2	452	2	Q6SYY7_CANAL	Q6syy7 candida alb
761	38	42.2	452	2	Q516V4_ENTHI	Q516v4 entamoeba h
762	38	42.2	453	2	Q8CBC8_MOUSE	Q8cbc8 mus musculu
763	38	42.2	456	2	Q7RGH5_PLAYO	Q7rgh5 plasmodium
764	38	42.2	465	1	LEU2_ECO57	Q8xa00 escherichia
765	38	42.2	465	1	LEU2_ECOL6	P0a6a7 escherichia
766	38	42.2	465	1	LEU2_ECOLI	P0a6a6 escherichia
767	38	42.2	466	1	LEU2_SHIFL	Q821c2 shigella fl
768	38	42.2	466	2	O29603_ARCFU	O29603 archaeoglob
769	38	42.2	474	2	Q560N4_CRYNE	Q560n4 cryptococcu
770	38	42.2	475	2	Q70VZ2_CIOIN	Q70vz2 ciona intes
771	38	42.2	479	2	Q5TDS1_HUMAN	Q5tds1 homo sapien
772	38	42.2	480	2	Q9H951_HUMAN	Q9h951 homo sapien
773	38	42.2	480	2	Q6MEJ1_PARUW	Q6mej1 parachlamyd
774	38	42.2	480	2	Q90220_AGKHP	Q90220 agkistrodon
775	38	42.2	482	2	Q5WYU9_LEGPL	Q5wyu9 legionella
776	38	42.2	484	2	Q4H3J4_CIOIN	Q4h3j4 ciona intes
777	38	42.2	485	2	Q5KPN0_CRYNE	Q5kpn0 cryptococcu
778	38	42.2	485	2	Q9VZL5_DROME	Q9vzl5 drosophila
779	38	42.2	486	2	Q5RI01_BRARE	Q5ri01 brachydanio
780	38	42.2	493	2	Q5DTU7_MOUSE	Q5dtu7 mus musculu
781	38	42.2	503	2	Q965K0_CAEEL	Q965k0 caenorhabdi
782	38	42.2	505	2	Q624F3_CAEBR	Q624f3 caenorhabdi
783	38	42.2	507	2	O45182_CAEEL	O45182 caenorhabdi
784	38	42.2	510	2	Q6AZW0_BRARE	Q6azw0 brachydanio
785	38	42.2	512	1	GMEB2_MOUSE	P58929 mus musculu
786	38	42.2	513	2	Q4HDV6_CAMCO	Q4hdv6 campylobact
787	38	42.2	515	2	Q5ZM13_CHICK	Q5zm13 gallus gall
788	38	42.2	519	2	Q4WDT1_ASPFU	Q4wdt1 aspergillus
789	38	42.2	521	1	Y592_MYCPN	Q50335 mycoplasma
790	38	42.2	522	2	Q61A98_CAEBR	Q61a98 caenorhabdi
791	38	42.2	525	2	Q4UPT8_XANCP	Q4upt8 xanthomonas
792	38	42.2	525	2	Q8P488_XANCP	Q8p488 xanthomonas
793	38	42.2	525	2	Q704I7_9LUTE	Q704i7 sugarcane y
794	38	42.2	526	2	Q704I6_9LUTE	Q704i6 sugarcane y
795	38	42.2	527	2	Q5FK00_LACAC	Q5fk00 lactobacill
796	38	42.2	529	1	GMEB2_RAT	O88873 rattus norv
797	38	42.2	530	1	GMEB2_HUMAN	Q9ukd1 homo sapien
798	38	42.2	530	2	Q6PCY0_MOUSE	Q6pcy0 mus musculu
799	38	42.2	531	2	Q7PRN2_ANOGA	Q7prn2 anopheles g
800	38	42.2	531	2	Q17404_CAEEL	Q17404 caenorhabdi
801	38	42.2	549	2	Q6G957_STAAS	Q6g957 staphylococ
802	38	42.2	549	2	Q6GGJ1_STAAR	Q6ggj1 staphylococ
803	38	42.2	549	2	Q8NWE4_STAAW	Q8nwe4 staphylococ
804	38	42.2	549	2	Q5HFR5_STAAC	Q5hfr5 staphylococ
805	38	42.2	569	1	NIR_MAIZE	P17847 zea mays (m
806	38	42.2	575	2	Q73P57_TREDE	Q73p57 treponema d
807	38	42.2	582	2	Q59SC9_CANAL	Q59sc9 candida alb
808	38	42.2	583	2	Q6BJL2_DEBHA	Q6bjl2 debaryomyce
809	38	42.2	588	2	Q5E387_VIBF1	Q5e387 vibrio fisc
810	38	42.2	590	2	Q4WY86_ASPFU	Q4wy86 aspergillus
811	38	42.2	591	2	Q966U1_HALRO	Q966u1 halocynthia
812	38	42.2	593	2	Q8GYX7_ARATH	Q8gyx7 arabidopsis
813	38	42.2	593	2	Q8L6Y3_ARATH	Q8l6y3 arabidopsis
814	38	42.2	593	2	Q6INM5_XENLA	Q6inm5 xenopus lae
815	38	42.2	597	2	Q9HFG9_PENMI	Q9hfg9 penicillium
816	38	42.2	597	2	Q8BZP3_MOUSE	Q8bzp3 mus musculu
817	38	42.2	599	2	Q9KEX8_BACHD	Q9kex8 bacillus ha
818	38	42.2	600	2	Q7VF42_HELHP	Q7vf42 helicobacte
819	38	42.2	603	2	Q4LBE8_PARTE	Q4lbe8 paramecium
820	38	42.2	624	2	Q4IAH6_GIBZE	Q4iah6 gibberella
821	38	42.2	630	2	O87110_COMAC	O87110 comamonas a
822	38	42.2	650	2	Q584Z2_9TRYP	Q584z2 trypanosoma
823	38	42.2	652	2	Q7U6U0_SYNPX	Q7u6u0 synechococc
824	38	42.2	667	2	Q6BPE9_DEBHA	Q6bpe9 debaryomyce
825	38	42.2	668	2	Q4RMD9_TETNG	Q4rmd9 tetraodon n
826	38	42.2	679	2	Q9W3E3_DROME	Q9w3e3 drosophila
827	38	42.2	689	2	Q5BG42_EMENI	Q5bg42 aspergillus
828	38	42.2	708	2	Q6IS39_MOUSE	Q6is39 mus musculu
829	38	42.2	714	2	Q4H7U2_9DEIO	Q4h7u2 deinococcus
830	38	42.2	722	2	Q86NT1_DROME	Q86nt1 drosophila
831	38	42.2	724	2	Q8VUB6_9BRAD	Q8vub6 bradyrhizob
832	38	42.2	728	2	Q4RNV0_TETNG	Q4rnv0 tetraodon n
833	38	42.2	752	2	Q4XN44_PLACH	Q4xn44 plasmodium
834	38	42.2	755	2	Q9HAK5_HUMAN	Q9hak5 homo sapien

835	38	42.2	764	2	Q6MD16_PARUW	Q6md16 parachlamyd	908	37.5	41.7	436	2	Q9YTJ8_9HERP	Q9ytj8 ateline her		
836	38	42.2	770	2	Q54S16_DICDI	Q54s16 dictyosteli	909	37.5	41.7	437	2	Q9C5P8_ARATH	Q9c5p8 arabidopsis		
837	38	42.2	771	2	Q4ILJ1_GIBZE	Q4ilj1 gibberella	910	37.5	41.7	437	2	Q9LVW4_ARATH	Q9lvw4 arabidopsis		
838	38	42.2	784	2	Q6P5Z3_HUMAN	Q6p5z3 homo sapien	911	37.5	41.7	437	2	Q6QAD0_ARATH	Q6qad0 arabidopsis		
839	38	42.2	789	2	Q5KDC8_CRYNE	Q5kdc8 cryptococcu	912	37.5	41.7	447	2	Q53MM5_ORYSA	Q53mm5 oryza sativ		
840	38	42.2	789	2	Q5FBV2_CRYNE	Q5fbv2 cryptococcu	913	37.5	41.7	475	2	Q54M81_DICDI	Q54m81 dictyosteli		
841	38	42.2	789	2	Q55Q39_CRYNE	Q55q39 cryptococcu	914	37.5	41.7	492	2	Q5K8J7_CRYNE	Q5k8j7 cryptococcu		
842	38	42.2	805	2	Q4JT35_CORJK	Q4jt35 corynebacte	915	37.5	41.7	492	2	Q7UMZ6_RHOBA	Q7umz6 rhodopirell		
843	38	42.2	808	2	Q97E37_CLOAB	Q97e37 clostridium	916	37.5	41.7	507	2	Q9XWR1_CAEEL	Q9xwr1 caenorhabdi		
844	38	42.2	817	2	Q07784_CHICK	Q07784 gallus gall	917	37.5	41.7	510	2	Q55M71_CRYNE	Q55m71 cryptococcu		
845	38	42.2	829	2	Q6DI86_MOUSE	Q6di86 mus musculu	918	37.5	41.7	510	2	Q5K8J8_CRYNE	Q5k8j8 cryptococcu		
846	38	42.2	847	2	Q994F7_9HIV1	Q994f7 human immun	919	37.5	41.7	514	2	Q9A242_CAUCR	Q9a242 caulobacter		
847	38	42.2	855	2	Q5HRV7_STAEQ	Q5hrv7 staphylococ	920	37.5	41.7	533	2	Q4LVT1_9BURK	Q4lvt1 burkholderi		
848	38	42.2	855	2	Q8CQS1_STAEP	Q8cqs1 staphylococ	921	37.5	41.7	595	2	Q8WUX4_HUMAN	Q8wux4 homo sapien		
849	38	42.2	862	2	Q4HYB5_GIBZE	Q4hyb5 gibberella	922	37.5	41.7	597	2	Q9BU10_HUMAN	Q9bu10 homo sapien		
850	38	42.2	884	2	Q7RI40_PLAYO	Q7ri40 plasmodium	923	37.5	41.7	597	2	Q6GMX5_HUMAN	Q6gmx5 homo sapien		
851	38	42.2	903	2	Q5B0N9_EMENI	Q5b0n9 aspergillus	924	37.5	41.7	625	2	Q96AA6_HUMAN	Q96aa6 homo sapien		
852	38	42.2	903	2	Q6DDL5_XENLA	Q6ddl5 xenopus lae	925	37.5	41.7	637	2	Q5CQU6_CRYPV	Q5cqu6 cryptospori		
853	38	42.2	915	2	Q7S6E2_NEUCR	Q7s6e2 neurospora	926	37.5	41.7	712	2	Q9SC94_MENLI	Q9sc94 mentzelia l		
854	38	42.2	915	2	Q4T0U6_TETNG	Q4t0u6 tetraodon n	927	37.5	41.7	747	2	Q5JYT3_HUMAN	Q5jyt3 homo sapien		
855	38	42.2	927	2	Q54PE8_DICDI	Q54pe8 dictyosteli	928	37.5	41.7	823	2	Q6CQ51_KLULA	Q6cq51 kluyveromyc		
856	38	42.2	932	2	Q4PI32_USTMA	Q4pi32 ustilago ma	929	37.5	41.7	919	2	Q5JYS7_HUMAN	Q5jys7 homo sapien		
857	38	42.2	949	2	Q5RGL8_BRARE	Q5rgl8 brachydanio	930	37.5	41.7	958	2	Q51T33_MAGGR	Q51t33 magnaporthe		
858	38	42.2	958	2	Q9UL01_HUMAN	Q9ul01 homo sapien	931	37.5	41.7	1022	2	Q5JYT1_HUMAN	Q5jyt1 homo sapien		
859	38	42.2	958	2	Q8BLI4_MOUSE	Q8bli4 m mus muscu	932	37.5	41.7	1023	1	PLCB4_BOVIN	Q07722 bos taurus		
860	38	42.2	973	2	Q57ZI4_9TRYP	Q57zi4 trypanosoma	933	37.5	41.7	1023	2	Q5JYS9_HUMAN	Q5jys9 homo sapien		
861	38	42.2	983	2	O75039_HUMAN	O75039 homo sapien	934	37.5	41.7	1121	2	Q4RYN8_TETNG	Q4ryn8 tetraodon n		
862	38	42.2	983	2	Q5T799_HUMAN	Q5t799 homo sapien	935	37.5	41.7	1175	1	PLCB4_HUMAN	Q15147 homo sapien		
863	38	42.2	993	1	RAD50_METMP	P62134 methanococc	936	37.5	41.7	1175	1	PLCB4_RAT	Q9qw07 rattus norv		
864	38	42.2	994	1	MERTK_MOUSE	Q60805 mus musculu	937	37.5	41.7	1175	2	Q91UZ1_MOUSE	Q91uz1 mus musculu		
865	38	42.2	1009	2	Q7VFZ6_HELHP	Q7vfz6 helicobacte	938	37.5	41.7	1571	2	Q5B2Y8_EMENI	Q5b2y8 aspergillus		
866	38	42.2	1016	2	Q7QPC1_GIALA	Q7qpc1 giardia lam	939	37.5	41.7	1958	2	Q9VB98_DROME	Q9vb98 drosophila		
867	38	42.2	1023	2	Q4SJH5_TETNG	Q4sjh5 tetraodon n	940	37.5	41.7	2183	2	Q89ZD7_BACTN	Q89zd7 bacteroides		
868	38	42.2	1043	2	Q6LNM7_PHOPR	Q6lnm7 photobacter	941	37	41.1	31	2	Q5R3T6_MOUSE	Q5r3t6 mus musculu		
869	38	42.2	1044	1	BUB1_SCHPO	O94751 schizosacch	942	37	41.1	91	2	Q4HL66_CAMLA	Q4hl66 campylobact		
870	38	42.2	1070	2	Q4U437_POLCB	Q4u437 polyangium	943	37	41.1	91	2	Q7VF12_HELHP	Q7vf12 helicobacte		
871	38	42.2	1095	2	Q4S9T4_TETNG	Q4s9t4 tetraodon n	944	37	41.1	98	2	Q7TU70_PROMP	Q7tu70 prochloroco		
872	38	42.2	1125	2	Q7RPG0_PLAYO	Q7rpg0 plasmodium	945	37	41.1	111	2	Q8DLN5_SYNEL	Q8dln5 synechococc		
873	38	42.2	1139	2	Q7WIM2_BORBR	Q7wim2 bordetella	946	37	41.1	115	2	O37063_9HIV1	O37063 human immun		
874	38	42.2	1139	2	Q7W753_BORPA	Q7w753 bordetella	947	37	41.1	116	2	Q4IHT6_GIBZE	Q4iht6 gibberella		
875	38	42.2	1139	2	Q7VYJ1_BORPE	Q7vyj1 bordetella	948	37	41.1	116	2	Q9WP04_9HIV1	Q9wp04 human immun		
876	38	42.2	1152	2	Q4IFG8_GIBZE	Q4ifg8 gibberella	949	37	41.1	119	2	Q9UL73_HUMAN	Q9ul73 homo sapien		
877	38	42.2	1201	2	Q4P7H7_USTMA	Q4p7h7 ustilago ma	950	37	41.1	120	2	Q7RGC9_PLAYO	Q7rgc9 plasmodium		
878	38	42.2	1206	2	Q4S1I2_TETNG	Q4s1i2 tetraodon n	951	37	41.1	124	2	Q4YTW9_PLABE	Q4ytw9 plasmodium		
879	38	42.2	1217	2	Q97GW3_CLOAB	Q97gw3 clostridium	952	37	41.1	125	2	Q9G2S8_9CUCU	Q9g2s8 pimelia rot		
880	38	42.2	1222	2	Q8IZU8_HUMAN	Q8izu8 homo sapien	953	37	41.1	125	2	Q8FC55_ECOL6	Q8fc55 escherichia		
881	38	42.2	1431	1	STAB2_RAT	Q8cfm6 rattus norv	954	37	41.1	126	2	Q5G8V1_9CAUD	Q5g8v1 salmonella		
882	38	42.2	1452	2	Q6FTD5_CANGA	Q6ftd5 candida gla	955	37	41.1	128	2	Q5X2K2_LEGPA	Q5x2k2 legionella		
883	38	42.2	1543	2	Q61CM8_CAEBR	Q61cm8 caenorhabdi	956	37	41.1	130	2	Q8TKC4_METAC	Q8tkc4 methanosarc		
884	38	42.2	1754	2	Q51FA4_ENTHI	Q51fa4 entamoeba h	957	37	41.1	138	1	TATB_XYLFT	Q87b79 xylella fas		
885	38	42.2	1803	2	Q7R5C6_GIALA	Q7r5c6 giardia lam	958	37	41.1	139	1	YYCE_BACSU	P37479 bacillus su		
886	38	42.2	2057	2	Q7R4F0_GIALA	Q7r4f0 giardia lam	959	37	41.1	140	2	Q65PK7_BACLD	Q65pk7 bacillus li		
887	38	42.2	2151	2	Q54X78_DICDI	Q54x78 dictyosteli	960	37	41.1	143	2	Q6MCE1_PARUW	Q6mce1 parachlamyd		
888	38	42.2	2177	2	Q8BES5_9PICO	Q8bes5 human parec	961	37	41.1	144	2	Q9GZ13_CAEBR	Q9gz13 caenorhabdi		
889	38	42.2	2269	1	L_SV41	P35341 simian viru	962	37	41.1	152	2	Q8Y6E4_LISMO	Q8y6e4 listeria mo		
890	38	42.2	2516	1	CAC1D_DROME	Q24270 drosophila	963	37	41.1	152	2	Q92AR5_LISIN	Q92ar5 listeria in		
891	38	42.2	2519	2	Q8IP25_DROME	Q8ip25 drosophila	964	37	41.1	152	2	Q71YS5_LISMF	Q71ys5 listeria mo		
892	38	42.2	2552	2	Q8IP24_DROME	Q8ip24 drosophila	965	37	41.1	152	2	Q66YL9_9HIV1	Q66yl9 human immun		
893	38	42.2	3131	1	ESYN_FUSEQ	Q00869 fusarium eq	966	37	41.1	154	2	Q5V480_HALMA	Q5v480 haloarcula		
894	38	42.2	6048	2	Q7JN85_CAEEL	Q7jn85 caenorhabdi	967	37	41.1	154	2	Q8QUN2_9VIRU	Q8qun2 infectious		
895	38	42.2	6260	2	Q54299_STRHY	Q54299 streptomyce	968	37	41.1	158	2	Q4J7B8_SULAC	Q4j7b8 sulfolobus		
896	38	42.2	6839	2	Q23550_CAEEL	Q23550 caenorhabdi	969	37	41.1	164	1	CY550_CYACA	Q9tlw2 cyanidium c		
897	38	42.2	7158	2	Q23551_CAEEL	Q23551 caenorhabdi	970	37	41.1	165	2	O34612_BACSU	O34612 bacillus su		
898	37.5	41.7	115	2	Q737E5_BACC1	Q737e5 bacillus ce	971	37	41.1	173	2	Q6BD34_DROTE	Q6bd34 drosophila		
899	37.5	41.7	116	2	Q7Z3Y6_HUMAN	Q7z3y6 homo sapien	972	37	41.1	173	2	Q99F32_9HIV1	Q99f32 human immun		
900	37.5	41.7	193	2	Q4XME2_PLACH	Q4xme2 plasmodium	973	37	41.1	175	1	CUPC5_CANPG	P81584 cancer pagu		
901	37.5	41.7	285	2	Q993R4_9HIV1	Q993r4 human immun	974	37	41.1	177	2	Q6A9G6_PROAC	Q6a9g6 propionibac		
902	37.5	41.7	325	2	Q4I9S7_GIBZE	Q4i9s7 gibberella	975	37	41.1	179	2	Q6BD36_DROYA	Q6bd36 drosophila		
903	37.5	41.7	351	2	Q9ZWL8_PASED	Q9zwl8 passiflora	976	37	41.1	181	2	Q9GZ14_CAEBR	Q9gz14 caenorhabdi		
904	37.5	41.7	370	1	HVC1_HETFR	P23084 heterodontu	977	37	41.1	182	2	Q6N1H8_RHOPA	Q6n1h8 rhodopseudo		
905	37.5	41.7	384	2	Q65110_9RHAB	Q65110 adelaide ri	978	37	41.1	186	2	Q4X5F4_PLACH	Q4x5f4 plasmodium		
906	37.5	41.7	392	2	Q993P9_9HIV1	Q993p9 human immun	979	37	41.1	188	2	O06368_MYCTU	O06368 mycobacteri		
907	37.5	41.7	431	2	Q9HMR3_HALSA	Q9hmr3 halobacteri	980	37	41.1	188	2	Q8BNE4_MOUSE	Q8bne4 mus musculu		

981	37	41.1	190	2	Q560K4_CRYNE	Q560k4 cryptococcu
982	37	41.1	192	2	Q9D9R6_MOUSE	Q9d9r6 mus musculu
983	37	41.1	196	2	Q6FIZ1_CANGA	Q6fiz1 candida gla
984	37	41.1	198	2	Q5U8X9_9SMEG	Q5u8x9 mugil plata
985	37	41.1	198	2	Q70QS7_9HIV1	Q70qs7 human immun
986	37	41.1	199	2	O72085_9HIV1	O72085 human immun
987	37	41.1	204	2	Q7PCS5_ANOGA	Q7pcs5 anopheles g
988	37	41.1	208	2	Q9IVT6_9HIV1	Q9ivt6 human immun
989	37	41.1	209	2	Q5WTZ9_LEGPL	Q5wtz9 legionella
990	37	41.1	209	2	Q8AJK3_9HIV1	Q8ajk3 human immun
991	37	41.1	209	2	Q66NJ0_9HIV1	Q66nj0 human immun
992	37	41.1	210	2	Q8AJR9_9HIV1	Q8ajr9 human immun
993	37	41.1	210	2	Q8AJK1_9HIV1	Q8ajk1 human immun
994	37	41.1	210	2	Q8AJG1_9HIV1	Q8ajg1 human immun
995	37	41.1	210	2	Q8AJC4_9HIV1	Q8ajc4 human immun
996	37	41.1	210	2	Q8AJ93_9HIV1	Q8aj93 human immun
997	37	41.1	212	2	Q7RAX0_PLAYO	Q7rax0 plasmodium
998	37	41.1	212	2	Q6HCP2_BACHK	Q6hcp2 bacillus th
999	37	41.1	214	2	Q4G5W8_FUGRU	Q4g5w8 fugu rubrip
1000	37	41.1	219	2	Q7SEK8_NEUCR	Q7sek8 neurospora

ALIGNMENTS

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RESULT 1
Q4V9Z4_MOUSE
ID   Q4V9Z4_MOUSE PRELIMINARY;      PRT;   476 AA.
AC   Q4V9Z4;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   LOC544903 protein.
GN   Name=LOC544903;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=FVB/N; TISSUE=Colon;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC096617; AAH96617.1; -; mRNA.
SQ   SEQUENCE   476 AA;  51468 MW;  39E55334FAFCE5DA CRC64;

  Query Match           92.2%;  Score 83;  DB 2;  Length 476;
  Best Local Similarity  94.1%;  Pred. No. 3.2e-05;
  Matches   16;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||||||||
Db         68 EINPDSSTINYAPSLKD 84


RESULT 2
HV40_MOUSE
ID   HV40_MOUSE     STANDARD;      PRT;   119 AA.
AC   P01810;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region J539.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PRELIMINARY PROTEIN SEQUENCE.
RX   MEDLINE=79223895; PubMed=111245;
RA   Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT   "Structural evidence for independent joining region gene in
RT   immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT   its potential role in generating diversity in complementarity-
RT   determining regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX   MEDLINE=88217852; PubMed=3449853; DOI=10.1002/prot.340010112;
RA   Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
RA   Davies D.R.;
RT   "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
RT   study at 2.6-A resolution.";
RL   Proteins 1:74-80(1986).
CC   -!- MISCELLANEOUS: This chain was isolated from a myeloma protein that
CC       binds galactan.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A02080; AVMSJ5.
DR   PDB; 2FBJ; X-ray; H=1-119.
DR   SMR; P01810; 1-119.
DR   Ensembl; ENSMUSG00000003483; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   NON_TER     119    119
FT   STRAND        3      7
FT   STRAND       10     12
FT   TURN         14     15
FT   STRAND       18     25
FT   HELIX        29     31
FT   STRAND       34     39
FT   TURN         41     42
FT   STRAND       45     51
FT   TURN         53     54
FT   STRAND       58     60
FT   TURN         62     67
FT   STRAND       68     72
FT   STRAND       78     83
FT   HELIX        88     90
FT   STRAND       92    100
FT   TURN        101    103
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FT   STRAND      104    108
FT   STRAND      112    116
SQ   SEQUENCE   119 AA;  13240 MW;  577B4F1DB675C1F1 CRC64;

  Query Match             91.1%;  Score 82;  DB 1;  Length 119;
  Best Local Similarity   88.2%;  Pred. No. 9.1e-06;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||| |||| |||||
Db         50 EIHPDSGTINYTPSLKD 66


RESULT 3
HV36_MOUSE
ID   HV36_MOUSE     STANDARD;      PRT;   116 AA.
AC   P01806;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region 441 precursor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=82059449; PubMed=6795591;
RA   Ollo R., Auffray C., Sikorav J.-L., Rougeon F.;
RT   "Mouse heavy chain variable regions: nucleotide sequence of a germ-
RT   line VH gene segment.";
RL   Nucleic Acids Res. 9:4099-4109(1981).
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; V00774; CAA24152.1; -; Genomic_DNA.
DR   PIR; A02076; HVMS44.
DR   HSSP; P01810; 2FBJ.
DR   SMR; P01806; 19-116.
DR   Ensembl; ENSMUSG00000003483; Mus musculus.
DR   MGI; MGI:96492; Igh-VX24.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     18
FT   CHAIN        19    116       Ig heavy chain V region 441.
FT   DOMAIN       19   >116       Ig-like.
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12911 MW;  6B4FF3EF9A95D9F3 CRC64;

  Query Match             87.8%;  Score 79;  DB 1;  Length 116;
  Best Local Similarity   88.2%;  Pred. No. 2.9e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         68 EINPDSSTINYTPSLKD 84


RESULT 4
HV37_MOUSE
ID   HV37_MOUSE     STANDARD;      PRT;   119 AA.
AC   P01807;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Ig heavy chain V region X44.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=79223895; PubMed=111245;
RA   Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT   "Structural evidence for independent joining region gene in
RT   immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT   its potential role in generating diversity in complementarity-
RT   determining regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 1-118.
RX   MEDLINE=90064531; PubMed=2555519;
RA   Miller A. III, Glasel J.A.;
RT   "Comparative sequence and immunochemical analyses of murine monoclonal
RT   anti-morphine antibodies.";
RL   J. Mol. Biol. 209:763-778(1989).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgA myeloma protein
CC       that binds galactan.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A02077; AVMSX4.
DR   HSSP; P01810; 2FBJ.
DR   SMR; P01807; 1-119.
DR   Ensembl; ENSMUSG00000003483; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    117       Ig-like.
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13246 MW;  BC34FC8F31CD41B3 CRC64;

  Query Match             87.8%;  Score 79;  DB 1;  Length 119;
  Best Local Similarity   88.2%;  Pred. No. 3e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         50 EINPDSSTINYTPSLKD 66


RESULT 5
HV38_MOUSE
ID   HV38_MOUSE     STANDARD;      PRT;   119 AA.
AC   P01808;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region T601.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=79223895; PubMed=111245;
RA   Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
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RT   "Structural evidence for independent joining region gene in
RT   immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT   its potential role in generating diversity in complementarity-
RT   determining regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgA myeloma protein
CC       that binds galactan.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A02078; AVMST6.
DR   HSSP; P01810; 2FBJ.
DR   SMR; P01808; 1-119.
DR   Ensembl; ENSMUSG00000003483; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    112       Ig-like.
FT   NON_TER     119    119
SQ   SEQUENCE   119 AA;  13169 MW;  BC38CC84E6EA00E8 CRC64;

  Query Match             87.8%;  Score 79;  DB 1;  Length 119;
  Best Local Similarity   88.2%;  Pred. No. 3e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:||||||| |||||
Db         50 EINPDSSTINYTPSLKD 66


RESULT 6
HV41_MOUSE
ID   HV41_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01811;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region UPC10.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=83021113; PubMed=6181731;
RA   Auffray C., Sikorav J.L., Ollo R., Rougeon F.;
RT   "Correlation between D region structure and antigen-binding
RT   specificity: evidences from the comparison of closely related
RT   immunoglobulin VH sequences.";
RL   Ann. Immunol. (Paris) 132D:77-88(1981).
CC   -!- MISCELLANEOUS: This chain was isolated from an Ig gamma-2a myeloma
CC       protein binding 2,6-levan.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M36631; AAA38078.1; -; mRNA.
DR   PIR; A02081; G2MSU1.
DR   HSSP; P01810; 2FBJ.
DR   SMR; P01811; 1-117.
DR   Ensembl; ENSMUSG00000003483; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region.
FT   DOMAIN        1    116       Ig-like.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13001 MW;  B20A1074F8E99E7F CRC64;

  Query Match             81.1%;  Score 73;  DB 1;  Length 117;
  Best Local Similarity   82.4%;  Pred. No. 0.00031;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:||||||| | |||
Db         50 EINPDSSTINYTPFLKD 66


RESULT 7
HV42_MOUSE
ID   HV42_MOUSE     STANDARD;      PRT;   117 AA.
AC   P01812;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region MOPC 173.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE OF 1-104.
RX   MEDLINE=72105531; PubMed=5062012;
RA   Bourgois A., Fougereau M., de Preval C.;
RT   "Sequence of amino acids of the NH 2 -terminal region of a mouse-
RT   clonal immunoglobulin heavy chain.";
RL   Eur. J. Biochem. 24:446-455(1972).
RN   [2]
RP   PROTEIN SEQUENCE OF 105-117.
RX   MEDLINE=76091933; PubMed=812695;
RA   Rocca-Serra J., Milili M., Fougereau M.;
RT   "Determination of the primary structure of a mouse IgG2a
RT   immunoglobulin. Amino-acid sequence of the H4 cyanogen-bromide
RT   fragment.";
RL   Eur. J. Biochem. 59:511-523(1975).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 96-117.
RX   MEDLINE=81223769; PubMed=6787590;
RA   Gough N.M., Bernard O.;
RT   "Sequences of the joining region genes for immunoglobulin heavy chains
RT   and their role in generation of antibody diversity.";
RL   Proc. Natl. Acad. Sci. U.S.A. 78:509-513(1981).
RN   [4]
RP   DISULFIDE BOND.
RX   PubMed=11947590;
RA   Bourgois A., Fougereau M.;
RT   "Partial amino acid sequence of the variable region of a mouse
RT   gammaG2a immunoglobulin heavy chain. Evidence for the existence of a
RT   third sub-group of variability for the heavy chain pool.";
RL   FEBS Lett. 8:265-268(1970).
CC   -!- MISCELLANEOUS: This gamma-2a chain was isolated from a myeloma
CC       protein.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A91190; G2MS73.
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DR   HSSP; P01810; 2FBJ.
DR   SMR; P01812; 1-117.
DR   Ensembl; ENSMUSG00000003483; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    116       Ig-like.
FT   DISULFID     22     96
FT   CONFLICT    105    105       N -> D (in Ref. 2).
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  13051 MW;  156DCCC259380F19 CRC64;

  Query Match             80.0%;  Score 72;  DB 1;  Length 117;
  Best Local Similarity   82.4%;  Pred. No. 0.00046;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              || |:|||||| |||||
Db         50 EIDPNSSTINYTPSLKD 66


RESULT 8
HV39_MOUSE
ID   HV39_MOUSE     STANDARD;      PRT;   118 AA.
AC   P01809;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Ig heavy chain V region X24.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=79223895; PubMed=111245;
RA   Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT   "Structural evidence for independent joining region gene in
RT   immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT   its potential role in generating diversity in complementarity-
RT   determining regions.";
RL   Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 103-117.
RX   MEDLINE=92355114; PubMed=1644448; DOI=10.1007/BF00215659;
RA   Solin M.L., Kaartinen M.;
RT   "Allelic polymorphism of mouse Igh-J locus, which encodes
RT   immunoglobulin heavy chain joining (JH) segments.";
RL   Immunogenetics 36:306-313(1992).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgA myeloma protein
CC       that binds galactan.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X63164; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR   PIR; PT0394; AVMSX2.
DR   HSSP; P01810; 2FBJ.
DR   SMR; P01809; 1-118.
DR   Ensembl; ENSMUSG00000003483; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DOMAIN        1    111       Ig-like.
FT   NON_TER     118    118
SQ   SEQUENCE   118 AA;  13105 MW;  BB16A2DB677EF17F CRC64;

  Query Match             80.0%;  Score 72;  DB 1;  Length 118;
  Best Local Similarity   82.4%;  Pred. No. 0.00046;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:| |||||| |||||
Db         49 EINPGSSTINYTPSLKD 65


RESULT 9
Q4TC19_TETNG
ID   Q4TC19_TETNG PRELIMINARY;      PRT;   594 AA.
AC   Q4TC19;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 21 SCAF7061, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00003505001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01007061; CAF89563.1; -; Genomic_DNA.
FT   NON_TER     594    594
SQ   SEQUENCE   594 AA;  63688 MW;  E5A492DD8ED32887 CRC64;

  Query Match             56.7%;  Score 51;  DB 2;  Length 594;
  Best Local Similarity   71.4%;  Pred. No. 12;
  Matches   10;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 PDSSTINYAPSLKD 17
              |||:  ||| ||||
Db         20 PDSAVSNYAASLKD 33


RESULT 10
Q600K8_MYCHY
ID   Q600K8_MYCHY PRELIMINARY;      PRT;  3969 AA.
AC   Q600K8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
```

```
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=mhp447;
OS   Mycoplasma hyopneumoniae.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2099;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=232;
RX   PubMed=15489423; DOI=10.1128/JB.186.21.7123-7133.2004;
RA   Minion F.C., Lefkowitz E.J., Madsen M.L., Cleary B.J., Swartzell S.M.,
RA   Mahairas G.G.;
RT   "The genome sequence of Mycoplasma hyopneumoniae strain 232, the agent
RT   of swine mycoplasmosis.";
RL   J. Bacteriol. 186:7123-7133(2004).
DR   EMBL; AE017332; AAV27888.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   3969 AA;  452870 MW;  D790BF956330350F CRC64;

  Query Match             54.4%;  Score 49;  DB 2;  Length 3969;
  Best Local Similarity   58.8%;  Pred. No. 2.6e+02;
  Matches   10;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |:  ||  ||:|| |||
Db       1010 ELLLDSQRINFAPKLKD 1026


RESULT 11
Q74LE0_LACJO
ID   Q74LE0_LACJO PRELIMINARY;      PRT;   281 AA.
AC   Q74LE0;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   ABC transporter ATPase component.
GN   OrderedLocusNames=LJ0245;
OS   Lactobacillus johnsonii.
OC   Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC   Lactobacillus.
OX   NCBI_TaxID=33959;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=NCC 533;
RX   PubMed=14983040; DOI=10.1073/pnas.0307327101;
RA   Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
RA   Pittet A.-C., Zwahlen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA   Mollet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M.A.;
RT   "The genome sequence of the probiotic intestinal bacterium
RT   Lactobacillus johnsonii NCC 533.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
CC   -!- SUBCELLULAR LOCATION: Membrane-associated (By similarity).
CC   -!- SIMILARITY: Belongs to the ABC transporter family.
DR   EMBL; AE017200; AAS08227.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016887; F:ATPase activity; IEA.
DR   GO; GO:0015087; F:cobalt ion transporter activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0006824; P:cobalt ion transport; IEA.
DR   GO; GO:0006811; P:ion transport; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transp_like.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   ATP-binding; Complete proteome; Membrane; Nucleotide-binding;
KW   Transport.
SQ   SEQUENCE   281 AA;  31621 MW;  60BE84153F37A3CB CRC64;

  Query Match             53.3%;  Score 48;  DB 2;  Length 281;
  Best Local Similarity   60.0%;  Pred. No. 16;
  Matches    9;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              : | | || |||:||
Db         52 LKPTSGTIKYAPNLK 66


RESULT 12
Q817S5_BACCR
ID   Q817S5_BACCR PRELIMINARY;      PRT;   450 AA.
AC   Q817S5;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Type I restriction-modification system restriction subunit
DE   (EC 3.1.21.3).
GN   OrderedLocusNames=BC4456;
OS   Bacillus cereus (strain ATCC 14579 / DSM 31).
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC   Bacillus cereus group.
OX   NCBI_TaxID=226900;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RA   Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA   Kapatral V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA   Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
RA   Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
RA   Overbeek R., Kyrpides N.C.;
RT   "Genome sequence of Bacillus cereus and comparative analysis with
RT   Bacillus anthracis.";
RL   Nature 423:87-91(2003).
DR   EMBL; AE017012; AAP11369.1; -; Genomic_DNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
KW   Complete proteome; Hydrolase.
SQ   SEQUENCE   450 AA;  52209 MW;  FF5E6BEAAAD97D8A CRC64;

  Query Match             53.3%;  Score 48;  DB 2;  Length 450;
  Best Local Similarity   46.7%;  Pred. No. 29;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              ||||:  : | | :|
Db        417 IHPDAKPLKYGPEMK 431


RESULT 13
Q6YRI1_ONYPE
ID   Q6YRI1_ONYPE PRELIMINARY;      PRT;   179 AA.
AC   Q6YRI1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=PAM034;
OS   Onion yellows phytoplasma.
OC   Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC   Acholeplasmataceae; Candidatus Phytoplasma;
OC   Candidatus Phytoplasma asteris.
OX   NCBI_TaxID=100379;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=OY-M;
RX   PubMed=14661021; DOI=10.1038/ng1277;
RA   Oshima K., Kakizawa S., Nishigawa H., Jung H.-Y., Wei W., Suzuki S.,
RA   Arashida R., Nakata D., Miyata S.-I., Ugaki M., Namba S.;
RT   "Reductive evolution suggested from the complete genome sequence of a
RT   plant-pathogenic phytoplasma.";
RL   Nat. Genet. 36:27-29(2004).
DR   EMBL; AP006628; BAD04119.1; -; Genomic_DNA.
KW   Complete proteome.
```

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SQ   SEQUENCE   179 AA;  21315 MW;  B2EAA77FDCED4B87 CRC64;

  Query Match             52.2%;  Score 47;  DB 2;  Length 179;
  Best Local Similarity   64.7%;  Pred. No. 14;
  Matches   11;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||  ||    |||||||
Db         78 EIVKDSYYYGYAPSLKD 94


RESULT 14
Q4WK85_ASPFU
ID   Q4WK85_ASPFU PRELIMINARY;      PRT;   872 AA.
AC   Q4WK85;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Alpha-1,3-glucanase, putative.
GN   ORFNames=Afu1g03350;
OS   Aspergillus fumigatus Af293.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=330879;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Af293;
RA   Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,
RA   Arroya J., Berriman M., Abe K., Archer D.B., Bermejo C., Bennett J.,
RA   Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,
RA   Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
RA   Fosker N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
RA   Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,
RA   Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
RA   Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
RA   Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,
RA   Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
RA   Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
RA   Penalva M.A., Pertea M., Price C., Pritchard B.L., Quail M.A.,
RA   Rabbinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
RA   Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
RA   Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,
RA   Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares R., Squares S.,
RA   Takeuchi M., Tekaia F., Turner G., Vazquez de Aldana C.R., Weidman J.,
RA   White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
RA   Machida M., Hall N., Barrell B., Denning D.W.;
RT   "Genomic sequence of the pathogenic and allergenic filamentous fungus
RT   Aspergillus fumigatus.";
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAHF01000007; EAL88047.1; -; Genomic_DNA.
SQ   SEQUENCE   872 AA;  95074 MW;  9E87B98FE5AA313C CRC64;

  Query Match             52.2%;  Score 47;  DB 2;  Length 872;
  Best Local Similarity   52.9%;  Pred. No. 94;
  Matches    9;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              | | |:  :|:| ||||
Db        155 EAHLDAPALNFAASLKD 171


RESULT 15
Q52US9_OMPOL
ID   Q52US9_OMPOL PRELIMINARY;      PRT;  4547 AA.
AC   Q52US9;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Putative peptide synthetase.
OS   Omphalotus olearius.
OC   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC   Agaricales; Omphalotaceae; Omphalotus.
OX   NCBI_TaxID=72120;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=TA90170;
RX   PubMed=16019163;
RA   Welzel K., Eisfeld K., Antelo L., Anke T., Anke H.;
RT   "Characterization of the ferrichrome A biosynthetic gene cluster in
RT   the homobasidiomycete Omphalotus olearius.";
RL   FEMS Microbiol. Lett. 249:157-163(2005).
CC   -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC       family.
DR   EMBL; AY929618; AAX49356.1; -; Genomic_DNA.
DR   GO; GO:0048037; F:cofactor binding; IEA.
DR   GO; GO:0016874; F:ligase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR010071; AA_adenyl_dom.
DR   InterPro; IPR009081; ACP_like.
DR   InterPro; IPR000873; AMP-bind.
DR   InterPro; IPR001242; Condensatn.
DR   InterPro; IPR006163; Phsphopanteth_bd.
DR   InterPro; IPR006162; Ppantne_S.
DR   Pfam; PF00501; AMP-binding; 3.
DR   Pfam; PF00668; Condensation; 4.
DR   Pfam; PF00550; PP-binding; 4.
DR   PRINTS; PR00154; AMPBINDING.
DR   TIGRFAMs; TIGR01733; AA-adenyl-dom; 1.
DR   PROSITE; PS50075; ACP_DOMAIN; 5.
DR   PROSITE; PS00455; AMP_BINDING; 2.
DR   PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_3.
SQ   SEQUENCE   4547 AA;  499822 MW;  769EFB27CC5A85AF CRC64;

  Query Match             52.2%;  Score 47;  DB 2;  Length 4547;
  Best Local Similarity   43.8%;  Pred. No. 6.7e+02;
  Matches    7;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLKD 17
              :|| :: :: :|||||
Db       3961 VHPTANILDQSPSLKD 3976


RESULT 16
HV03_CAICR
ID   HV03_CAICR     STANDARD;      PRT;   117 AA.
AC   P03982;
DT   23-OCT-1986 (Rel. 02, Created)
DT   23-OCT-1986 (Rel. 02, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig heavy chain V region G4 precursor.
GN   Name=G4;
OS   Caiman crocodilus (Spectacled caiman) (Caiman sclerops).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Crocodylidae; Alligatorinae; Caiman.
OX   NCBI_TaxID=8499;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=85140192; PubMed=2983316;
RA   Litman G.W., Murphy K., Berger L., Litman R., Hinds K., Erickson B.W.;
RT   "Complete nucleotide sequences of three VH genes in Caiman, a
RT   phylogenetically ancient reptile: evolutionary diversification in
RT   coding segments and variation in the structure and organization of
RT   recombination elements.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:844-848(1985).
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; M12770; AAA49194.1; -; Genomic_DNA.
DR   PIR; A02085; HVCQG4.
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DR   HSSP; P01783; 1IGC.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    117       Ig heavy chain V region G4.
FT   REGION       20     49       Framework-1.
FT   REGION       50     54       Complementarity-determining-1.
FT   REGION       55     68       Framework-2.
FT   REGION       69     85       Complementarity-determining-2.
FT   REGION       86    117       Framework-3.
FT   DISULFID     41    115       By similarity.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12994 MW;  6330D7469AAE55FC CRC64;

  Query Match             51.1%;  Score 46;  DB 1;  Length 117;
  Best Local Similarity   56.2%;  Pred. No. 13;
  Matches    9;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLK 16
              ||: :|  || ||| :|
Db         69 EINGNSETIRYAPEVK 84


RESULT 17
SOMA_SCIOC
ID   SOMA_SCIOC     STANDARD;      PRT;   204 AA.
AC   Q9IB11; O73850;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Somatotropin precursor (Growth hormone).
GN   Name=GH;
OS   Sciaenops ocellatus (Red drum).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC   Sciaenidae; Sciaenops.
OX   NCBI_TaxID=76340;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pituitary;
RA   Trant J.M.;
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pituitary;
RA   Zhu Y.;
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Growth hormone plays an important role in growth control
CC       and is involved in the regulation of several anabolic processes.
CC       Implicated as an osmoregulatory substance important for seawater
CC       adaptation.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF063834; AAC63266.1; -; mRNA.
DR   EMBL; AF065165; AAF61751.1; -; mRNA.
DR   HSSP; P01241; 1BP3.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   InterPro; IPR001400; Somatotropin.
DR   PANTHER; PTHR11417; Somatotropin; 1.
DR   Pfam; PF00103; Hormone_1; 1.
DR   PRINTS; PR00836; SOMATOTROPIN.
DR   PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR   PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW   Hormone; Pituitary; Pyrrolidone carboxylic acid; Signal.
FT   SIGNAL        1     17       By similarity.
FT   CHAIN        18    204       Somatotropin.
FT   MOD_RES      18     18       Pyrrolidone carboxylic acid (By
FT                                similarity).
FT   DISULFID     69    177       By similarity.
FT   DISULFID    194    202       By similarity.
FT   CONFLICT      2      2       D -> N (in Ref. 2).
FT   CONFLICT     23     23       S -> G (in Ref. 2).
SQ   SEQUENCE   204 AA;  23090 MW;  08A1E1E1DB0C243D CRC64;

  Query Match             51.1%;  Score 46;  DB 1;  Length 204;
  Best Local Similarity   69.2%;  Pred. No. 25;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAP 13
              || |||||:  ||
Db        142 EIFPDSSTLQLAP 154


RESULT 18
Q7ZME2_9HIV1
ID   Q7ZME2_9HIV1 PRELIMINARY;      PRT;   212 AA.
AC   Q7ZME2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Envelope glycoprotein (Fragment).
GN   Name=env;
OS   Human immunodeficiency virus 1.
OC   Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC   Lentivirus; Primate lentivirus group.
OX   NCBI_TaxID=11676;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22555816; PubMed=12667797; DOI=10.1016/S0042-6822(02)00066-1;
RA   Renjifo B., Chung M., Gilbert P., Mwakagile D., Msamanga G., Fawzi W.,
RA   Essex M.;
RT   "In-utero transmission of quasispecies among human immunodeficiency
RT   virus type 1 genotypes.";
RL   Virology 307:278-282(2003).
DR   EMBL; AY116037; AAM77934.1; -; Genomic_DNA.
DR   SMR; Q7ZME2; 1-209.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0019031; C:viral envelope; IEA.
DR   InterPro; IPR000777; GP120.
DR   Pfam; PF00516; GP120; 1.
KW   AIDS; Envelope protein; Transmembrane.
FT   NON_TER       1      1
FT   NON_TER     212    212
SQ   SEQUENCE   212 AA;  23904 MW;  C7422733BE50EC29 CRC64;

  Query Match             51.1%;  Score 46;  DB 2;  Length 212;
  Best Local Similarity   64.3%;  Pred. No. 26;
  Matches    9;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPS 14
              |  |||:|| :|||
Db         79 EHFPDSNTIKFAPS 92


RESULT 19
Q8GAV2_9RICK
ID   Q8GAV2_9RICK PRELIMINARY;      PRT;   516 AA.
AC   Q8GAV2;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   DnaX protein.
GN   Name=dnaX;
OS   Wolbachia endosymbiont of Callosobruchus chinensis.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
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OC   Rickettsiaceae; Wolbachieae; Wolbachia.
OX   NCBI_TaxID=188349;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=WBruAus;
RX   MEDLINE=22294998; PubMed=12386340; DOI=10.1073/pnas.222228199;
RA   Kondo N., Nikoh N., Ijichi N., Shimada M., Fukatsu T.;
RT   "Genome fragment of Wolbachia endosymbiont transferred to X chromosome
RT   of host insect.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:14280-14285(2002).
DR   EMBL; AB080664; BAC22717.1; -; Genomic_DNA.
DR   HSSP; P06710; 1NJF.
DR   GO; GO:0005663; C:DNA replication factor C complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0042829; P:defense response to pathogen; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003959; AAA_ATPase_centr.
DR   InterPro; IPR001270; Chaprnin_clpA/B.
DR   InterPro; IPR000767; Disease_resist.
DR   InterPro; IPR000862; RFC.
DR   Pfam; PF00004; AAA; 1.
DR   PRINTS; PR00300; CLPPROTEASEA.
DR   PRINTS; PR00364; DISEASERSIST.
DR   SMART; SM00382; AAA; 1.
SQ   SEQUENCE   516 AA;  57626 MW;  D0524B9B50BDFC79 CRC64;

  Query Match             51.1%;  Score 46;  DB 2;  Length 516;
  Best Local Similarity   50.0%;  Pred. No. 75;
  Matches    8;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLKD 17
              |: : | :||||::||
Db        484 INREVSNLNYAPAVKD 499


RESULT 20
Q73G99_WOLPM
ID   Q73G99_WOLPM PRELIMINARY;      PRT;   533 AA.
AC   Q73G99;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   DNA polymerase III, gamma and tau subunits (EC 2.7.7.7).
GN   Name=dnaX; OrderedLocusNames=WD1060;
OS   Wolbachia pipientis wMel.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC   Rickettsiaceae; Wolbachieae; Wolbachia.
OX   NCBI_TaxID=66077;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15024419; DOI=10.1371/journal.pbio.0020069;
RA   Wu M., Sun L.V., Vamathevan J.J., Riegler M., DeBoy R.T.,
RA   Brownlie J.C., McGraw E.A., Martin W., Esser C., Ahmadinejad N.,
RA   Wiegand C., Madupu R., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA   Durkin A.S., Kolonay J.F., Nelson W.C., Mohamoud Y., Lee P.,
RA   Berry K.J., Young M.B., Utterback T.R., Weidman J.F., Nierman W.C.,
RA   Paulsen I.T., Nelson K.E., Tettelin H., O'Neill S.L., Eisen J.A.;
RT   "Phylogenomics of the reproductive parasite Wolbachia pipientis wMel:
RT   a streamlined genome overrun by mobile genetic elements.";
RL   PLoS Biol. 2:327-341(2004).
DR   EMBL; AE017259; AAS14717.1; -; Genomic_DNA.
DR   TIGR; WD1060; -.
DR   GO; GO:0005663; C:DNA replication factor C complex; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR   GO; GO:0017111; F:nucleoside-triphosphatase activity; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0042829; P:defense response to pathogen; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003959; AAA_ATPase_centr.
DR   InterPro; IPR001270; Chaprnin_clpA/B.
DR   InterPro; IPR000767; Disease_resist.
DR   InterPro; IPR000862; RFC.
DR   Pfam; PF00004; AAA; 1.
DR   PRINTS; PR00300; CLPPROTEASEA.
DR   PRINTS; PR00364; DISEASERSIST.
DR   SMART; SM00382; AAA; 1.
KW   Complete proteome; Nucleotidyltransferase; Transferase.
SQ   SEQUENCE   533 AA;  59478 MW;  44D0649F642F6E72 CRC64;

  Query Match             51.1%;  Score 46;  DB 2;  Length 533;
  Best Local Similarity   50.0%;  Pred. No. 78;
  Matches    8;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLKD 17
              |: : | :||||::||
Db        501 INREVSNLNYAPAVKD 516


RESULT 21
Q65MN3_BACLD
ID   Q65MN3_BACLD PRELIMINARY;      PRT;  1052 AA.
AC   Q65MN3; Q62Y27;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein (HsdRI).
GN   Name=hsdR1; OrderedLocusNames=BL02332, BLi00746;
OS   Bacillus licheniformis (strain DSM 13 / ATCC 14580).
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=279010;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15383718; DOI=10.1159/000079829;
RA   Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,
RA   Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,
RA   Ehrenreich A., Gottschalk G.;
RT   "The complete genome sequence of Bacillus licheniformis DSM13, an
RT   organism with great industrial potential.";
RL   J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15461803; DOI=10.1186/gb-2004-5-10-r77;
RA   Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,
RA   Tang M., Lopez de Leon A., Xiang H., Gusti V., Clausen I.G.,
RA   Olsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,
RA   Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N.,
RA   Ehrlich S.D., Berka R.M.;
RT   "Complete genome sequence of the industrial bacterium Bacillus
RT   licheniformis and comparisons with closely related Bacillus species.";
RL   Genome Biol. 5:RESEARCH077.1-RESEARCH077.12(2004).
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give random
CC       double-stranded fragments with terminal 5'-phosphates; ATP is
CC       simultaneously hydrolyzed.
CC   -!- SUBUNIT: The type I restriction/modification system is composed of
CC       three polypeptides R, M and S (By similarity).
DR   EMBL; AE017333; AAU39681.1; -; Genomic_DNA.
DR   EMBL; CP000002; AAU22331.1; -; Genomic_DNA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0004386; F:helicase activity; IEA.
DR   GO; GO:0009035; F:type I site-specific deoxyribonuclease acti. . .; IEA.
DR   GO; GO:0009307; P:DNA restriction-modification system; IEA.
DR   InterPro; IPR011545; DEAD/DEAH_N.
DR   InterPro; IPR007409; DUF450.
DR   InterPro; IPR004473; HsdR.
DR   InterPro; IPR006935; ResIII.
DR   Pfam; PF04313; HSDR_N; 1.
DR   Pfam; PF04851; ResIII; 1.
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DR   SMART; SM00487; DEXDc; 1.
DR   TIGRFAMs; TIGR00348; hsdR; 1.
KW   Complete proteome; DNA-binding; Hypothetical protein;
KW   Restriction system.
SQ   SEQUENCE   1052 AA;  120806 MW;  CF3EE8F67118A70A CRC64;

  Query Match             51.1%;  Score 46;  DB 2;  Length 1052;
  Best Local Similarity   40.0%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              :|||:  : | | :|
Db       1019 VHPDAKPLKYRPEIK 1033


RESULT 22
Q4RXT1_TETNG
ID   Q4RXT1_TETNG PRELIMINARY;      PRT;  1445 AA.
AC   Q4RXT1;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 11 SCAF14979, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00027297001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01014979; CAG06801.1; -; Genomic_DNA.
FT   NON_TER       1       1
SQ   SEQUENCE   1445 AA;  160779 MW;  3F0EEC5BFFE7E640 CRC64;

  Query Match             51.1%;  Score 46;  DB 2;  Length 1445;
  Best Local Similarity   50.0%;  Pred. No. 2.5e+02;
  Matches    8;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLK 16
              :|| |:|  |: |:||
Db       1375 KIHQDTSLTNHVPALK 1390


RESULT 23
Q517J8_ENTHI
ID   Q517J8_ENTHI PRELIMINARY;      PRT;   361 AA.
AC   Q517J8;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=54.t00035;
OS   Entamoeba histolytica HM-1:IMSS.
OC   Eukaryota; Entamoebidae; Entamoeba.
OX   NCBI_TaxID=294381;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=HM-1:IMSS;
RX   PubMed=15729342; DOI=10.1038/nature03291;
RA   Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA   Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA   Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA   Hofer M., Bruchhaus I., Willhoeft U., Bhattacharya A.,
RA   Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA   Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA   Quail M.A., Rabbinowitsch E., Norbertczak H., Price C., Wang Z.,
RA   Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA   Foster P.G., Sicheritz-Ponten T., Weber C., Singh U., Mukherjee C.,
RA   El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA   Fraser C.M., Hall N.;
RT   "The genome of the protist parasite Entamoeba histolytica.";
RL   Nature 433:865-868(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAFB01000217; EAL49023.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   361 AA;  42104 MW;  7F49F1E32D0AF783 CRC64;

  Query Match             50.6%;  Score 45.5;  DB 2;  Length 361;
  Best Local Similarity   57.9%;  Pred. No. 59;
  Matches   11;  Conservative    2;  Mismatches    3;  Indels    3;  Gaps    2;

Qy          2 IHPDS-STINYA--PSLKD 17
              :||||   :||   |||||
Db        119 LHPDSPQFVNYTSDPSLKD 137


RESULT 24
Q7QSK1_GIALA
ID   Q7QSK1_GIALA PRELIMINARY;      PRT;    79 AA.
AC   Q7QSK1;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   GLP_618_36275_36036.
OS   Giardia lamblia ATCC 50803.
OC   Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX   NCBI_TaxID=184922;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=WB C6;
RA   Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,
RA   Olsen G.J., Sogin M.L.;
RT   "Draft sequence of the Giardia lamblia genome.";
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AACB01000117; EAA38034.1; -; Genomic_DNA.
SQ   SEQUENCE   79 AA;  8979 MW;  18A642D01FDB3EEA CRC64;

  Query Match             50.0%;  Score 45;  DB 2;  Length 79;
  Best Local Similarity   64.3%;  Pred. No. 12;
  Matches    9;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 PDSSTINYAPSLKD 17
              | |||:|:  ||||
Db         37 PHSSTLNWIVSLKD 50
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RESULT 25
Q9RB46_9CLOT
ID   Q9RB46_9CLOT PRELIMINARY;      PRT;   249 AA.
AC   Q9RB46;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   3a-hydroxysteroid dehydrogenase.
GN   Name=baiA;
OS   Clostridium sp. TO-931.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=110320;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=TO-931;
RX   MEDLINE=20164011; PubMed=10698778;
RX   DOI=10.1128/AEM.66.3.1107-1113.2000;
RA   Wells J.E., Hylemon P.B.;
RT   "Identification and characterization of a bile acid 7alpha-
RT   dehydroxylation operon in Clostridium sp. strain TO-931, a highly
RT   active 7alpha-dehydroxylating strain isolated from human feces.";
RL   Appl. Environ. Microbiol. 66:1107-1113(2000).
CC   -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC       (SDR) family.
DR   EMBL; AF210152; AAF22845.1; -; Genomic_DNA.
DR   HSSP; P25716; 1Q7B.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR002198; ADH_short.
DR   InterPro; IPR002347; Adh_short_C2.
DR   InterPro; IPR002424; Insect_adh_fam.
DR   Pfam; PF00106; adh_short; 1.
DR   PRINTS; PR00081; GDHRDH.
DR   PRINTS; PR01167; INSADHFAMILY.
DR   PRINTS; PR00080; SDRFAMILY.
DR   PROSITE; PS00061; ADH_SHORT; 1.
KW   Oxidoreductase.
SQ   SEQUENCE   249 AA;  26404 MW;  C4E258DD101BED40 CRC64;

  Query Match             50.0%;  Score 45;  DB 2;  Length 249;
  Best Local Similarity   46.7%;  Pred. No. 46;
  Matches    7;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSL 15
              | |||    : :|| |
Db         52 ETHPDKEVLGFAPDL 66


RESULT 26
Q4S517_TETNG
ID   Q4S517_TETNG PRELIMINARY;      PRT;   378 AA.
AC   Q4S517;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 6 SCAF14737, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00023931001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01014737; CAG04265.1; -; Genomic_DNA.
FT   NON_TER       1       1
SQ   SEQUENCE   378 AA;  41488 MW;  5EFCD66DD858B623 CRC64;

  Query Match             50.0%;  Score 45;  DB 2;  Length 378;
  Best Local Similarity   32.3%;  Pred. No. 76;
  Matches   10;  Conservative    4;  Mismatches    3;  Indels   14;  Gaps    1;

Qy          1 EIHPDSSTINY--------------APSLKD 17
              :||||: |: |                ||| :|
Db         14 KIHPDTVTVKYATHCLQPGDEGYDDAPSFED 44


RESULT 27
Q7MZB1_PHOLL
ID   Q7MZB1_PHOLL PRELIMINARY;      PRT;   400 AA.
AC   Q7MZB1;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   DltD protein for D-alanine esterification of lipoteichoic acid and
DE   wall teichoic acid.
GN   Name=dltD; OrderedLocusNames=plu4382;
OS   Photorhabdus luminescens (subsp. laumondii).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Photorhabdus.
OX   NCBI_TaxID=141679;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=TT01;
RX   MEDLINE=22957627; PubMed=14528314; DOI=10.1038/nbt886;
RA   Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA   Taourit S., Bocs S., Boursaux-Eude C., Chandler M., Charles J.-F.,
RA   Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA   Medigue C., Lanois A., Powell K., Siguier P., Vincent R., Wingate V.,
RA   Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT   "The genome sequence of the entomopathogenic bacterium Photorhabdus
RT   luminescens.";
RL   Nat. Biotechnol. 21:1307-1313(2003).
DR   EMBL; BX571873; CAE16754.1; -; Genomic_DNA.
DR   PhotoList; plu4382; -.
KW   Complete proteome.
SQ   SEQUENCE   400 AA;  46368 MW;  70054A4F52B0B5B5 CRC64;

  Query Match             50.0%;  Score 45;  DB 2;  Length 400;
  Best Local Similarity   50.0%;  Pred. No. 82;
  Matches    8;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLKD 17
              |  || :||| |:: |
Db         40 IEDDSKSINYIPTITD 55


RESULT 28
Q6T7E8_TOBAC
ID   Q6T7E8_TOBAC PRELIMINARY;      PRT;   505 AA.
AC   Q6T7E8;
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DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Adenylosuccinate synthase (EC 6.3.4.4).
GN   Name=purA;
OS   Nicotiana tabacum (Common tobacco).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   asterids; lamiids; Solanales; Solanaceae; Nicotiana.
OX   NCBI_TaxID=4097;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Boldt R., Lerchl J., Sonnewald U.;
RL   Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the adenylosuccinate synthetase family.
DR   EMBL; AY429425; AAR06294.1; -; mRNA.
DR   HSSP; P12283; 1ADE.
DR   SMR; Q6T7E8; 77-505.
DR   GO; GO:0004019; F:adenylosuccinate synthase activity; IEA.
DR   GO; GO:0005525; F:GTP binding; IEA.
DR   GO; GO:0016874; F:ligase activity; IEA.
DR   GO; GO:0006164; P:purine nucleotide biosynthesis; IEA.
DR   InterPro; IPR001114; Asucc_synthtase.
DR   Pfam; PF00709; Adenylsucc_synt; 1.
DR   ProDom; PD001188; Asucc_synthtase; 1.
DR   TIGRFAMs; TIGR00184; purA; 1.
DR   PROSITE; PS01266; ADENYLOSUCCIN_SYN_1; 1.
DR   PROSITE; PS00513; ADENYLOSUCCIN_SYN_2; UNKNOWN_1.
KW   GTP-binding; Ligase; Magnesium; Metal-binding; Nucleotide-binding;
KW   Purine biosynthesis.
SQ   SEQUENCE   505 AA;  55218 MW;  3CBE0D8FB1DB568C CRC64;

  Query Match             50.0%;  Score 45;  DB 2;  Length 505;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 HPDSSTINYAPS 14
              ||| ||:|  ||
Db        429 HPDGSTLNSFPS 440


RESULT 29
Q9V8D9_DROME
ID   Q9V8D9_DROME PRELIMINARY;      PRT;   513 AA.
AC   Q9V8D9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   CG5719-PA.
GN   Name=CG5719; ORFNames=CG5719;
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426065; PubMed=12537568;
RA   Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA   Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA   George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA   Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA   Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA   Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT   "Finishing a whole-genome shotgun: release 3 of the Drosophila
RT   melanogaster euchromatic genome sequence.";
RL   Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426070; PubMed=12537573;
RA   Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J.W., Svirskas R.,
RA   Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA   Ashburner M., Celniker S.E.;
RT   "The transposable elements of the Drosophila melanogaster euchromatin:
RT   a genomics perspective.";
RL   Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22426069; PubMed=12537572;
RA   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA   Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA   Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA   Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA   Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA   Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA   Lewis S.E.;
RT   "Annotation of the Drosophila melanogaster euchromatic genome: a
RT   systematic review.";
RL   Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RG   Berkeley Drosophila Genome Project;
RA   Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA   Hoskins R., Stapleton M., Pacleb J., Park S., Svirskas R., Smith E.,
RA   Yu C., Rubin G.;
RT   "Drosophila melanogaster release 4 sequence.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RG   FlyBase;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003800; AAF57728.2; -; Genomic_DNA.
DR   HSSP; P26769; 1AZS.
DR   Ensembl; CG5719; Drosophila melanogaster.
DR   FlyBase; FBgn0034316; CG5719.
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DR   GO; GO:0016849; F:phosphorus-oxygen lyase activity; IEA.
DR   GO; GO:0009190; P:cyclic nucleotide biosynthesis; IEA.
DR   GO; GO:0007242; P:intracellular signaling cascade; IEA.
DR   InterPro; IPR001054; G_cyclase.
DR   Pfam; PF00211; Guanylate_cyc; 1.
DR   SMART; SM00044; CYCc; 1.
DR   PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
DR   PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
KW   Lyase.
SQ   SEQUENCE   513 AA;  58688 MW;  CA86CE966688FB40 CRC64;

  Query Match            50.0%;  Score 45;  DB 2;  Length 513;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    8;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 SSTINYAPSLKD 17
              :||:|||| ||:
Db        132 NSTLNYAPMLKN 143


RESULT 30
Q55EX4_DICDI
ID   Q55EX4_DICDI PRELIMINARY;      PRT;   746 AA.
AC   Q55EX4;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=DDB0189978;
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=AX4;
RA   Eichinger L., Pachebat J.A., Gloeckner G., Rajandream M.-A.,
RA   Sucgang R., Berriman M., Song J., Olsen R., Szafranski K., Xu Q.,
RA   Tunggal B., Kummerfeld S., Madera M., Konfortov B.A., Rivero F.,
RA   Bankier A.T., Lehmann R., Hamlin N., Davies R., Gaudet P., Fey P.,
RA   Pilcher K., Chen G., Saunders D., Sodergren E., Davis P.,
RA   Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.,
RA   Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher C.,
RA   Cooper J., Haydock S., van Driessche N., Cronin A., Goodhead I.,
RA   Muzny D., Mourier T., Pain A., Lu M., Harper D., Lindsay R.,
RA   Hauser H., James K., Quiles M., Mohan M.B., Saito T., Buchrieser C.,
RA   Wardroper A., Felder M., Thangavelu M., Johnson D., Knights A.,
RA   Loulseged H., Mungall K., Oliver K., Price C., Quail M.A.,
RA   Urushihara H., Hernandez J., Rabbinowitsch E., Steffen D., Sanders M.,
RA   Ma J., Kohara Y., Sharp S., Simmonds M., Spiegler S., Tivey A.,
RA   Sugano S., White B., Walker D., Woodward J., Winckler T., Tanaka Y.,
RA   Shaulsky G., Schleicher M., Weinstock G., Rosenthal A., Cox E.C.,
RA   Chisholm R.L., Gibbs R., Loomis W.F., Platzer M., Kay R.R.,
RA   Williams J., Dear P.H., Noegel A.A., Barrell B., Kuspa A.;
RT   "The genome of the social amoeba Dictyostelium discoideum.";
RL   Nature 0:0-0(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAFI01000010; EAL72948.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   746 AA;  84523 MW;  C05C253A74AF2F55 CRC64;

  Query Match            50.0%;  Score 45;  DB 2;  Length 746;
  Best Local Similarity   72.7%;  Pred. No. 1.7e+02;
  Matches    8;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINY 11
              ||:|||:|| |
Db        376 EIYPDSTTIEY 386


RESULT 31
Q601N7_MYCHY
ID   Q601N7_MYCHY PRELIMINARY;      PRT;  2047 AA.
AC   Q601N7;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=mhp165;
OS   Mycoplasma hyopneumoniae.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2099;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=232;
RX   PubMed=15489423; DOI=10.1128/JB.186.21.7123-7133.2004;
RA   Minion F.C., Lefkowitz E.J., Madsen M.L., Cleary B.J., Swartzell S.M.,
RA   Mahairas G.G.;
RT   "The genome sequence of Mycoplasma hyopneumoniae strain 232, the agent
RT   of swine mycoplasmosis.";
RL   J. Bacteriol. 186:7123-7133(2004).
DR   EMBL; AE017332; AAV27748.1; -; Genomic_DNA.
DR   InterPro; IPR006025; Pept_M_Zn_BS.
DR   PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   2047 AA;  235630 MW;  CD959D13B7D8EF77 CRC64;

  Query Match            50.0%;  Score 45;  DB 2;  Length 2047;
  Best Local Similarity   62.5%;  Pred. No. 5.7e+02;
  Matches   10;  Conservative    3;  Mismatches    1;  Indels    2;  Gaps    1;

Qy          2 IHPDSSTINYAPSLKD 17
              | |:|:|||  ||:||
Db        815 IDPESATIN--PSIKD 828


RESULT 32
YBGS_SALTI
ID   YBGS_SALTI     STANDARD;      PRT;   128 AA.
AC   P64438; Q8XG68;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Hypothetical protein ybgS precursor.
GN   Name=ybgS; OrderedLocusNames=STY0800, t2119;
OS   Salmonella typhi.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=601;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=CT18;
RX   MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA   Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA   Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA   Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA   Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA   Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA   Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA   Whitehead S., Barrell B.G.;
RT   "Complete genome sequence of a multiple drug resistant Salmonella
RT   enterica serovar Typhi CT18.";
RL   Nature 413:848-852(2001).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Ty2 / ATCC 700931;
RX   MEDLINE=22531367; PubMed=12644504;
RX   DOI=10.1128/JB.185.7.2330-2337.2003;
RA   Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA   Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT   "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT   and CT18.";
RL   J. Bacteriol. 185:2330-2337(2003).
CC   ----------------------------------------------------------------------
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CC   use as long as its content is in no way modified and this statement is not
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CC   --------------------------------------------------------------------------
DR   EMBL; AL627268; CAD05216.1; -; Genomic_DNA.
DR   EMBL; AE016841; AAO69736.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein; Signal.
FT   SIGNAL        1     24       Potential.
FT   CHAIN        25    128       Hypothetical protein ybgS.
SQ   SEQUENCE   128 AA;  13330 MW;  5C3CC882D3401205 CRC64;

  Query Match             48.9%;  Score 44;  DB 1;  Length 128;
  Best Local Similarity   53.3%;  Pred. No. 31;
  Matches    8;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 HPDSSTINYAPSLKD 17
              ||| ||:|:    ||
Db         75 HPDGSTMNHDGMTKD 89


RESULT 33
YBGS_SALTY
ID   YBGS_SALTY     STANDARD;      PRT;   128 AA.
AC   P64437; Q8XG68;
DT   10-OCT-2003 (Rel. 42, Created)
DT   25-OCT-2004 (Rel. 45, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Hypothetical protein ybgS precursor.
GN   Name=ybgS; OrderedLocusNames=STM0759;
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
CC   --------------------------------------------------------------------------
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CC   removed.
CC   --------------------------------------------------------------------------
DR   EMBL; AE008731; AAL19698.1; -; Genomic_DNA.
DR   StyGene; SG?????; ybgS.
KW   Complete proteome; Hypothetical protein; Signal.
FT   SIGNAL        1     24       Potential.
FT   CHAIN        25    128       Hypothetical protein ybgS.
SQ   SEQUENCE   128 AA;  13330 MW;  5C3CC882D3401205 CRC64;

  Query Match             48.9%;  Score 44;  DB 1;  Length 128;
  Best Local Similarity   53.3%;  Pred. No. 31;
  Matches    8;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 HPDSSTINYAPSLKD 17
              ||| ||:|:    ||
Db         75 HPDGSTMNHDGMTKD 89


RESULT 34
Q57RJ7_SALCH
ID   Q57RJ7_SALCH PRELIMINARY;      PRT;   128 AA.
AC   Q57RJ7;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Putative homeobox protein.
GN   Name=ybgS; OrderedLocusNames=SC0758;
OS   Salmonella cholerae-suis (Salmonella enterica).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=591;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=SC-B67;
RX   PubMed=15781495;
RA   Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
RA   Wang H.-S., Lee Y.-S.;
RT   "The genome sequence of Salmonella enterica serovar Choleraesuis, a
RT   highly invasive and resistant zoonotic pathogen.";
RL   Nucleic Acids Res. 33:1690-1698(2005).
DR   EMBL; AE017220; AAX64664.1; -; Genomic_DNA.
KW   Complete proteome; Nuclear protein.
SQ   SEQUENCE   128 AA;  13272 MW;  5C3CCA500342C0D5 CRC64;

  Query Match             48.9%;  Score 44;  DB 2;  Length 128;
  Best Local Similarity   53.3%;  Pred. No. 31;
  Matches    8;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 HPDSSTINYAPSLKD 17
              ||| ||:|:    ||
Db         75 HPDGSTMNHDGMTKD 89


RESULT 35
Q5PG71_SALPA
ID   Q5PG71_SALPA PRELIMINARY;      PRT;   128 AA.
AC   Q5PG71;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Probable secreted protein.
GN   Name=ybgS; OrderedLocusNames=SPA1984;
OS   Salmonella paratyphi-a.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=54388;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ATCC 9150;
RX   PubMed=15531882; DOI=10.1038/ng1470;
RA   McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA   Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M.,
RA   Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA   Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA   Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
RA   Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA   Spieth J., Wilson R.K.;
RT   "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT   restricted serovars of Salmonella enterica that cause typhoid.";
RL   Nat. Genet. 36:1268-1274(2004).
DR   EMBL; CP000026; AAV77892.1; -; Genomic_DNA.
KW   Complete proteome.
SQ   SEQUENCE   128 AA;  13330 MW;  5C3CC882D3401205 CRC64;

  Query Match             48.9%;  Score 44;  DB 2;  Length 128;
  Best Local Similarity   53.3%;  Pred. No. 31;
  Matches    8;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 HPDSSTINYAPSLKD 17
              ||| ||:|:    ||
Db         75 HPDGSTMNHDGMTKD 89


RESULT 36
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Q9S2Z1_STRCO
ID   Q9S2Z1_STRCO PRELIMINARY;      PRT;   305 AA.
AC   Q9S2Z1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Putative chitosanase (Putative secreted protein).
GN   OrderedLocusNames=SCO2024; ORFNames=SC3A3.02;
OS   Streptomyces coelicolor.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=A3(2) / M145;
RX   MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA   Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA   Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA   Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA   Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
RA   Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA   Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA   Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA   Hopwood D.A.;
RT   "Complete genome sequence of the model actinomycete Streptomyces
RT   coelicolor A3(2).";
RL   Nature 417:141-147(2002).
DR   EMBL; AL939111; CAB52859.1; -; Genomic_DNA.
DR   PIR; T34867; T34867.
DR   HSSP; P33665; 1CHK.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0016977; F:chitosanase activity; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   InterPro; IPR000400; Glyco_hydro_46.
DR   Pfam; PF01374; Glyco_hydro_46; 1.
DR   PIRSF; PIRSF036551; Chitosanase; 1.
DR   PROSITE; PS60000; CHITOSANASE_46_80; UNKNOWN_1.
KW   Complete proteome.
SQ   SEQUENCE   305 AA;  32919 MW;  09AA4A616713471C CRC64;

  Query Match             48.9%;  Score 44;  DB 2;  Length 305;
  Best Local Similarity   41.2%;  Pred. No. 88;
  Matches    7;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              | |||:    | |:|::
Db        135 EDHPDNGLAEYLPALRE 151


RESULT 37
Q60LS4_CAEBR
ID   Q60LS4_CAEBR PRELIMINARY;      PRT;   967 AA.
AC   Q60LS4;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein CBG23448.
GN   Name=CBG23448;
OS   Caenorhabditis briggsae.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6238;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RG   The C.briggsae Sequencing Consortium;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAC01000141; CAE75453.1; -; Genomic_DNA.
DR   GO; GO:0005856; C:cytoskeleton; IEA.
DR   InterPro; IPR000299; Band_4.1.
DR   SMART; SM00295; B41; 1.
DR   PROSITE; PS50057; FERM_3; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   967 AA;  106679 MW;  C8F95B9AE1BC094B CRC64;

  Query Match             48.9%;  Score 44;  DB 2;  Length 967;
  Best Local Similarity   43.8%;  Pred. No. 3.5e+02;
  Matches    7;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLK 16
              ::|| |  :||  |:|
Db        916 QLHPPSQQLNYQQSVK 931


RESULT 38
Q4SEC3_TETNG
ID   Q4SEC3_TETNG PRELIMINARY;      PRT;  1066 AA.
AC   Q4SEC3;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 3 SCAF14622, whole genome shotgun sequence.
GN   ORFNames=GSTENG00019622001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01014622; CAG01009.1; -; Genomic_DNA.
SQ   SEQUENCE   1066 AA;  115584 MW;  69C51047311188CD CRC64;

  Query Match             48.9%;  Score 44;  DB 2;  Length 1066;
  Best Local Similarity   53.8%;  Pred. No. 3.9e+02;
  Matches    7;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPS 14
              |||| | : | |:
Db        661 IHPDGSAVVYGPT 673


RESULT 39
Q5TWD0_ANOGA
ID   Q5TWD0_ANOGA PRELIMINARY;      PRT;  1122 AA.
AC   Q5TWD0;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   ENSANGP00000026439.
```

```
GN   ORFNames=ENSANGG00000024344;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC   Anophelinae; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RT   "Anopheles gambiae re-annotation.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=PEST;
RG   The Anopheles gambiae Sequence Committee;
RL   Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008810; EAL41696.1; -; Genomic_DNA.
DR   GO; GO:0005634; C:nucleus; IEA.
DR   GO; GO:0046872; F:metal ion binding; IEA.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   InterPro; IPR012934; Znf_AD.
DR   InterPro; IPR007087; Znf_C2H2.
DR   Pfam; PF07776; zf-AD; 1.
DR   Pfam; PF00096; zf-C2H2; 3.
DR   SMART; SM00355; ZnF_C2H2; 4.
DR   PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
DR   PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
KW   Metal-binding; Zinc; Zinc-finger.
SQ   SEQUENCE   1122 AA;  121911 MW;  E76A37BD809F6391 CRC64;

  Query Match             48.9%;  Score 44;  DB 2;  Length 1122;
  Best Local Similarity   50.0%;  Pred. No. 4.1e+02;
  Matches    8;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLK 16
              |: ||  |::  ||||
Db        121 ELPPDEDTVDTKPSLK 136


RESULT 40
Q963L7_SCHMA
ID   Q963L7_SCHMA PRELIMINARY;      PRT;  1776 AA.
AC   Q963L7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   High voltage-activated calcium channel Cav1.
OS   Schistosoma mansoni (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC   Schistosomatoidea; Schistosomatidae; Schistosoma.
OX   NCBI_TaxID=6183;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21576983; PubMed=11719960;
RA   Kohn A.B., Lea J., Roberts-Misterly J.M., Anderson P.A.V.,
RA   Greenberg R.M.;
RT   "Structure of three high voltage-activated calcium channel alpha1
RT   subunits from Schistosoma mansoni.";
RL   Parasitology 123:489-497(2001).
DR   EMBL; AF361884; AAK84312.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005891; C:voltage-gated calcium channel complex; IEA.
DR   GO; GO:0005509; F:calcium ion binding; IEA.
DR   GO; GO:0005245; F:voltage-gated calcium channel activity; IEA.
DR   GO; GO:0006816; P:calcium ion transport; IEA.
DR   GO; GO:0006812; P:cation transport; IEA.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR002077; Ca_channel_alpha.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005446; LVDCCAlpha1.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR005829; Sug_transporter.
DR   Pfam; PF00520; Ion_trans; 4.
DR   PRINTS; PR00167; CACHANNEL.
DR   PRINTS; PR01630; LVDCCALPHA1.
DR   PROSITE; PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
SQ   SEQUENCE   1776 AA;  203507 MW;  5F80896D4460395B CRC64;

  Query Match             48.9%;  Score 44;  DB 2;  Length 1776;
  Best Local Similarity   53.8%;  Pred. No. 7.2e+02;
  Matches    7;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAP 13
              ::| ||| :|| |
Db       1690 DVHNDSSKLNYDP 1702


RESULT 41
Q4SMH7_TETNG
ID   Q4SMH7_TETNG PRELIMINARY;      PRT;  2324 AA.
AC   Q4SMH7;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 18 SCAF14547, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00015752001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01014547; CAF98155.1; -; Genomic_DNA.
FT   NON_TER       1      1
FT   NON_TER    2324   2324
SQ   SEQUENCE   2324 AA;  263261 MW;  771CBE536F09CEEE CRC64;

  Query Match             48.9%;  Score 44;  DB 2;  Length 2324;
  Best Local Similarity   64.3%;  Pred. No. 9.9e+02;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSL 15
              ||  |||  ||||:
Db       2215 IHSSSSTTFYAPSI 2228
```

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RESULT 42
Q6LJK3_PHOPR
ID   Q6LJK3_PHOPR PRELIMINARY;      PRT;   108 AA.
AC   Q6LJK3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein TNP.
GN   Name=TNP; OrderedLocusNames=PBPRB0654;
OS   Photobacterium profundum (Photobacterium sp. (strain SS9)).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC   Vibrionaceae; Photobacterium.
OX   NCBI_TaxID=74109;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15746425; DOI=10.1126/science.1103341;
RA   Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N.,
RA   Lauro F.M., Cestaro A., Malacrida G., Simionati B., Cannata N.,
RA   Romualdi C., Bartlett D.H., Valle G.;
RT   "Life at depth: Photobacterium profundum genome sequence and
RT   expression analysis.";
RL   Science 307:1459-1461(2005).
DR   EMBL; CR378677; CAG22527.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   108 AA;  12754 MW;  408F0DBA06072798 CRC64;

  Query Match             48.3%;  Score 43.5;  DB 2;  Length 108;
  Best Local Similarity   55.0%;  Pred. No. 31;
  Matches   11;  Conservative    1;  Mismatches    3;  Indels    5;  Gaps    1;

Qy          2 IHPDSSTIN-----YAPSLK 16
              || | ||||     ||| |:
Db         52 IHADHSTINRWVIKYAPLLE 71


RESULT 43
Q63656_RAT
ID   Q63656_RAT  PRELIMINARY;      PRT;   117 AA.
AC   Q63656;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Pre-sialomucin complex (Fragment).
GN   Name=pSMC;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Fisher 344;
RX   MEDLINE=94216302; PubMed=8163496;
RA   Wu K., Fregien N., Carraway K.L.;
RT   "Molecular cloning and sequencing of the mucin subunit of a
RT   heterodimeric, bifunctional cell surface glycoprotein complex of
RT   ascites rat mammary adenocarcinoma cells.";
RL   J. Biol. Chem. 269:11950-11955(1994).
DR   EMBL; U06747; AAA85518.1; -; mRNA.
DR   Ensembl; ENSRNOG00000001777; Rattus norvegicus.
FT   CHAIN        <1    >117       ascites sialoglycoprotein-1.
FT   NON_TER       1      1
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  11837 MW;  E2D5CCCF5C7C0F01 CRC64;

  Query Match             47.8%;  Score 43;  DB 2;  Length 117;
  Best Local Similarity   53.8%;  Pred. No. 41;
  Matches    7;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 PDSSTINYAPSLK 16
              |||:| ::|||::
Db         50 PDSTTTSHAPSVR 62


RESULT 44
Q63658_RAT
ID   Q63658_RAT  PRELIMINARY;      PRT;   117 AA.
AC   Q63658;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Pre-sialomucin complex (Fragment).
GN   Name=pSMC;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Fisher 344;
RX   MEDLINE=94216302; PubMed=8163496;
RA   Wu K., Fregien N., Carraway K.L.;
RT   "Molecular cloning and sequencing of the mucin subunit of a
RT   heterodimeric, bifunctional cell surface glycoprotein complex of
RT   ascites rat mammary adenocarcinoma cells.";
RL   J. Biol. Chem. 269:11950-11955(1994).
DR   EMBL; U06749; AAA85520.1; -; mRNA.
DR   Ensembl; ENSRNOG00000001777; Rattus norvegicus.
FT   CHAIN        <1    >117       ascites sialoglycoprotein-1.
FT   NON_TER       1      1
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  11930 MW;  5ECB11F6451C452E CRC64;

  Query Match             47.8%;  Score 43;  DB 2;  Length 117;
  Best Local Similarity   53.8%;  Pred. No. 41;
  Matches    7;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 PDSSTINYAPSLK 16
              |||:| ::|||::
Db         50 PDSTTTSHAPSVR 62


RESULT 45
SOMA_DICLA
ID   SOMA_DICLA     STANDARD;      PRT;   204 AA.
AC   Q05163;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Somatotropin precursor (Growth hormone).
GN   Name=GH;
OS   Dicentrarchus labrax (European sea bass).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC   Moronidae; Dicentrarchus.
OX   NCBI_TaxID=13489;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93113000; PubMed=1472711;
RA   Doliana R., Bortolussi M., Colombo L.;
RT   "Cloning and sequencing of European sea bass (Dicentrarchus labrax L.)
RT   growth hormone cDNA using polymerase chain reaction and degenerate
RT   oligonucleotides.";
RL   DNA Seq. 3:185-189(1992).
CC   -!- FUNCTION: Growth hormone plays an important role in growth control
CC       and is involved in the regulation of several anabolic processes.
CC       Implicated as an osmoregulatory substance important for seawater
CC       adaptation.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------------
DR   EMBL; X65716; CAA46632.1; -; mRNA.
DR   HSSP; P01241; 1BP3.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   InterPro; IPR001400; Somatotropin.
DR   PANTHER; PTHR11417; Somatotropin; 1.
DR   Pfam; PF00103; Hormone_1; 1.
DR   PRINTS; PR00836; SOMATOTROPIN.
DR   PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR   PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW   Hormone; Pituitary; Pyrrolidone carboxylic acid; Signal.
FT   SIGNAL        1     17       By similarity.
FT   CHAIN        18    204       Somatotropin.
FT   MOD_RES      18     18       Pyrrolidone carboxylic acid (By
FT                                similarity).
FT   DISULFID     69    177       By similarity.
FT   DISULFID    194    202       By similarity.
SQ   SEQUENCE   204 AA;  23017 MW;  62480D8015592A62 CRC64;

  Query Match             47.8%;  Score 43;  DB 1;  Length 204;
  Best Local Similarity   61.5%;  Pred. No. 80;
  Matches    8;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAP 13
              |: |||||:  ||
Db        142 EMFPDSSTLQLAP 154


RESULT 46
SOMA_MORSA
ID   SOMA_MORSA     STANDARD;      PRT;   204 AA.
AC   P48248;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Somatotropin precursor (Growth hormone).
GN   Name=GH;
OS   Morone saxatilis (Striped bass).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC   Moronidae; Morone.
OX   NCBI_TaxID=34816;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Pituitary;
RX   MEDLINE=95278623; PubMed=7758842; DOI=10.1016/0303-7207(94)03458-6;
RA   Cheng C.M., Lin C.M., Shamblott M., Gonzalez-Villasenor L.I.,
RA   Powers D.A., Woods C., Chen T.T.;
RT   "Production of a biologically active recombinant teleostean growth
RT   hormone in E. coli cells.";
RL   Mol. Cell. Endocrinol. 108:75-85(1995).
CC   -!- FUNCTION: Growth hormone plays an important role in growth control
CC       and is involved in the regulation of several anabolic processes.
CC       Implicated as an osmoregulatory substance important for seawater
CC       adaptation.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC   ---------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------------
DR   EMBL; S78253; AAB34389.1; -; mRNA.
DR   PIR; I51289; I51289.
DR   HSSP; P01241; 1BP3.
DR   InterPro; IPR012351; Cytokine_4_hlx.
DR   InterPro; IPR001400; Somatotropin.
DR   PANTHER; PTHR11417; Somatotropin; 1.
DR   Pfam; PF00103; Hormone_1; 1.
DR   PRINTS; PR00836; SOMATOTROPIN.
DR   PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR   PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW   Hormone; Pituitary; Pyrrolidone carboxylic acid; Signal.
FT   SIGNAL        1     17       By similarity.
FT   CHAIN        18    204       Somatotropin.
FT   MOD_RES      18     18       Pyrrolidone carboxylic acid (By
FT                                similarity).
FT   DISULFID     69    177       By similarity.
FT   DISULFID    194    202       By similarity.
SQ   SEQUENCE   204 AA;  23045 MW;  F4186DC5FF696115 CRC64;

  Query Match             47.8%;  Score 43;  DB 1;  Length 204;
  Best Local Similarity   61.5%;  Pred. No. 80;
  Matches    8;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAP 13
              |: |||||:  ||
Db        142 EMFPDSSTLQLAP 154


RESULT 47
Q9ERB8_MOUSE
ID   Q9ERB8_MOUSE PRELIMINARY;      PRT;   232 AA.
AC   Q9ERB8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Mucin (Fragment).
GN   Name=Muc4;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CD-1;
RA   Bartman A.E., Shekels L.L., Anway R.E., Moccia R., Gipson I.K.,
RA   Ho S.B.;
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY007202; AAG02256.1; -; mRNA.
FT   NON_TER     232    232
SQ   SEQUENCE   232 AA;  24363 MW;  C59B55AD7A1A1FF3 CRC64;

  Query Match             47.8%;  Score 43;  DB 2;  Length 232;
  Best Local Similarity   46.7%;  Pred. No. 94;
  Matches    7;  Conservative    5;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              | || :| ::|||::
Db        126 ISPDGTTTSHAPSIR 140


RESULT 48
Q6N2Q7_RHOPA
ID   Q6N2Q7_RHOPA PRELIMINARY;      PRT;   233 AA.
AC   Q6N2Q7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Fumarylacetoacetate (FAA) hydrolase.
GN   OrderedLocusNames=RPA3992;
OS   Rhodopseudomonas palustris.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Bradyrhizobiaceae; Rhodopseudomonas.
OX   NCBI_TaxID=1076;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=CGA009 / ATCC BAA-98;
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RX   PubMed=14704707; DOI=10.1038/nbt923;
RA   Larimer F.W., Chain P., Hauser L., Lamerdin J.E., Malfatti S., Do L.,
RA   Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
RA   Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L., Peres C.,
RA   Harrison F.H., Gibson J., Harwood C.S.;
RT   "Complete genome sequence of the metabolically versatile
RT   photosynthetic bacterium Rhodopseudomonas palustris.";
RL   Nat. Biotechnol. 22:55-61(2004).
DR   EMBL; BX572605; CAE29433.1; -; Genomic_DNA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR002529; FAA_hydrolase.
DR   Pfam; PF01557; FAA_hydrolase; 1.
KW   Complete proteome; Hydrolase.
SQ   SEQUENCE   233 AA;  24984 MW;  7AAB66D26E20A1D3 CRC64;

  Query Match             47.8%;  Score 43;  DB 2;  Length 233;
  Best Local Similarity   50.0%;  Pred. No. 94;
  Matches    8;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLKD 17
              : || :|| | |  ||
Db         62 VTPDGATIPYPPLTKD 77


RESULT 49
Q503N3_BRARE
ID   Q503N3_BRARE PRELIMINARY;      PRT;   341 AA.
AC   Q503N3;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   LOC445375 protein (Fragment).
GN   Name=LOC445375;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryo;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC095250; AAH95250.1; -; mRNA.
FT   NON_TER       1       1
SQ   SEQUENCE   341 AA;  37512 MW;  05C85EF1ED01BE96 CRC64;

  Query Match             47.8%;  Score 43;  DB 2;  Length 341;
  Best Local Similarity   70.0%;  Pred. No. 1.5e+02;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TINYAPSLKD 17
              |:|||||: |
Db        216 TVNYAPSVSD 225


RESULT 50
Q9GNR4_LEIMA
ID   Q9GNR4_LEIMA PRELIMINARY;      PRT;   371 AA.
AC   Q9GNR4;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein LmPKAC2b (EC 2.7.1.37) (Protein kinase A
DE   catalytic subunit isoform 1).
GN   Name=LmPKAC2b; ORFNames=LMJ_1331;
OS   Leishmania major.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX   NCBI_TaxID=5664;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Friedlin;
RX   MEDLINE=96408659; PubMed=8813666; DOI=10.1016/0166-6851(96)02601-1;
RA   Siman-Tov M.M., Aly R., Shapira M., Jaffe C.L.;
RT   "Cloning from Leishmania major of a developmentally regulated gene, c-
RT   lpk2, for the catalytic subunit of the cAMP-dependent protein
RT   kinase.";
RL   Mol. Biochem. Parasitol. 77:201-215(1996).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Friedlin;
RX   MEDLINE=22030454; PubMed=12034495; DOI=10.1016/S0378-1119(02)00403-1;
RA   Siman-Tov M.M., Ivens A.C., Jaffe C.L.;
RT   "Molecular cloning and characterization of two new isoforms of the
RT   protein kinase A catalytic subunit from the human parasite
RT   Leishmania.";
RL   Gene 288:65-75(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Friedlin;
RX   PubMed=16020728; DOI=10.1126/science.1112680;
RA   Ivens A.C., Peacock C.S., Worthey E.A., Murphy L., Aggarwal G.,
RA   Berriman M., Sisk E., Rajandream M.A., Adlem E., Aert R., Anupama A.,
RA   Apostolou Z., Attipoe P., Bason N., Bauser C., Beck A., Beverley S.M.,
RA   Bianchettin G., Borzym K., Bothe G., Bruschi C.V., Collins M.,
RA   Cadag E., Ciarloni L., Clayton C., Coulson R.M., Cronin A., Cruz A.K.,
RA   Davies R.M., De Gaudenzi J., Dobson D.E., Duesterhoeft A.,
RA   Fazelina G., Fosker N., Frasch A.C., Fraser A., Fuchs M., Gabel C.,
RA   Goble A., Goffeau A., Harris D., Hertz-Fowler C., Hilbert H., Horn D.,
RA   Huang Y., Klages S., Knights A., Kube M., Larke N., Litvin L.,
RA   Lord A., Louie T., Marra M., Masuy D., Matthews K., Michaeli S.,
RA   Mottram J.C., Muller-Auer S., Munden H., Nelson S., Norbertczak H.,
RA   Oliver K., O'Neil S., Pentony M., Pohl T.M., Price C., Purnelle B.,
RA   Quail M.A., Rabbinowitsch E., Reinhardt R., Rieger M., Rinta J.,
RA   Robben J., Robertson L., Ruiz J.C., Rutter S., Saunders D.,
RA   Schafer M., Schein J., Schwartz D.C., Seeger K., Seyler A., Sharp S.,
RA   Shin H., Sivam D., Squares R., Squares S., Tosato V., Vogt C.,
RA   Volckaert G., Wambutt R., Warren T., Wedler H., Woodward J., Zhou S.,
RA   Zimmermann W., Smith D.F., Blackwell J.M., Stuart K.D., Barrell B.,
RA   Myler P.J.;
RT   "The Genome of the Kinetoplastid Parasite, Leishmania major.";
RL   Science 309:436-442(2005).
CC   -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC   -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR   EMBL; U91743; AAD00706.3; -; Genomic_DNA.
DR   EMBL; CP000081; AAZ14625.1; -; Genomic_DNA.
DR   HSSP; P05132; 1J3H.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
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DR   InterPro; IPR000961; Pkinase_C.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   Pfam; PF00069; Pkinase; 1.
DR   Pfam; PF00433; Pkinase_C; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00133; S_TK_X; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Hypothetical protein; Kinase; Nucleotide-binding;
KW   Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   371 AA;  42255 MW;  A6D2AF4BF7866EA7 CRC64;

  Query Match             47.8%;  Score 43;  DB 2;  Length 371;
  Best Local Similarity   50.0%;  Pred. No. 1.6e+02;
  Matches    7;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 HPDSSTINYAPSLK 16
              ||| | :  ||::|
Db         31 HPDPSKVTVAPNVK 44


Search completed: March 23, 2006, 02:04:38
Job time : 179.389 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:05:22 ; Search time 36.7945 Seconds
(without alignments)
38.198 Million cell updates/sec

Title: US-10-755-382-24
Perfect score: 90
Sequence: 1 EIHPDSSTINYAPSLKD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	90	100.0	17	1	US-08-318-157B-24	Sequence 24, Appl
2	90	100.0	17	2	US-09-253-794-24	Sequence 24, Appl
3	90	100.0	119	1	US-08-318-157B-2	Sequence 2, Appli
4	90	100.0	119	1	US-08-318-157B-8	Sequence 8, Appli
5	90	100.0	119	1	US-08-318-157B-9	Sequence 9, Appli
6	90	100.0	119	1	US-08-318-157B-10	Sequence 10, Appl
7	90	100.0	119	1	US-08-318-157B-11	Sequence 11, Appl
8	90	100.0	119	1	US-08-318-157B-12	Sequence 12, Appl
9	90	100.0	119	1	US-08-318-157B-13	Sequence 13, Appl
10	90	100.0	119	1	US-08-318-157B-14	Sequence 14, Appl
11	90	100.0	119	1	US-08-318-157B-15	Sequence 15, Appl
12	90	100.0	119	1	US-08-318-157B-17	Sequence 17, Appl
13	90	100.0	119	1	US-08-318-157B-57	Sequence 57, Appl
14	90	100.0	119	1	US-08-318-157B-58	Sequence 58, Appl
15	90	100.0	119	2	US-09-253-794-2	Sequence 2, Appli
16	90	100.0	119	2	US-09-253-794-8	Sequence 8, Appli
17	90	100.0	119	2	US-09-253-794-9	Sequence 9, Appli
18	90	100.0	119	2	US-09-253-794-10	Sequence 10, Appl
19	90	100.0	119	2	US-09-253-794-11	Sequence 11, Appl
20	90	100.0	119	2	US-09-253-794-12	Sequence 12, Appl
21	90	100.0	119	2	US-09-253-794-13	Sequence 13, Appl
22	90	100.0	119	2	US-09-253-794-14	Sequence 14, Appl
23	90	100.0	119	2	US-09-253-794-15	Sequence 15, Appl
24	90	100.0	119	2	US-09-253-794-17	Sequence 17, Appl
25	90	100.0	119	2	US-09-253-794-57	Sequence 57, Appl
26	90	100.0	119	2	US-09-253-794-58	Sequence 58, Appl
27	82	91.1	33	2	US-08-525-539A-28	Sequence 28, Appl
28	82	91.1	109	1	US-07-942-245-17	Sequence 17, Appl
29	82	91.1	118	2	US-09-232-290-53	Sequence 53, Appl
30	79	87.8	17	2	US-10-226-795-24	Sequence 24, Appl
31	79	87.8	98	2	US-09-840-459-47	Sequence 47, Appl
32	79	87.8	98	2	US-09-497-625A-47	Sequence 47, Appl
33	79	87.8	116	2	US-08-483-749A-18	Sequence 18, Appl
34	79	87.8	117	1	US-07-958-140-3	Sequence 3, Appli
35	79	87.8	117	4	PCT-US93-09166-3	Sequence 3, Appli
36	79	87.8	150	2	US-10-226-795-22	Sequence 22, Appl
37	79	87.8	243	1	US-07-958-140-2	Sequence 2, Appli
38	79	87.8	243	4	PCT-US93-09166-2	Sequence 2, Appli
39	77	85.6	122	1	US-08-335-573-7	Sequence 7, Appli
40	72	80.0	98	2	US-09-840-459-52	Sequence 52, Appl
41	72	80.0	98	2	US-09-497-625A-52	Sequence 52, Appl
42	70	77.8	124	1	US-07-958-140-4	Sequence 4, Appli
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44	69	76.7	139	2	US-09-136-315-2	Sequence 2, Appli
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46	69	76.7	139	2	US-09-767-888-2	Sequence 2, Appli
47	69	76.7	139	2	US-09-767-888-6	Sequence 6, Appli
48	68	75.6	19	1	US-08-480-434-34	Sequence 34, Appl
49	68	75.6	19	1	US-08-053-451B-34	Sequence 34, Appl
50	68	75.6	120	1	US-08-480-434-30	Sequence 30, Appl
51	68	75.6	120	1	US-08-053-451B-30	Sequence 30, Appl
52	68	75.6	120	1	US-08-053-451B-127	Sequence 127, App
53	61	67.8	17	1	US-08-480-434-25	Sequence 25, Appl
54	61	67.8	17	1	US-08-480-434-33	Sequence 33, Appl
55	61	67.8	17	1	US-08-053-451B-25	Sequence 25, Appl
56	61	67.8	17	1	US-08-053-451B-33	Sequence 33, Appl
57	61	67.8	119	1	US-08-053-451B-125	Sequence 125, App
58	61	67.8	121	1	US-08-480-434-29	Sequence 29, Appl
59	61	67.8	121	1	US-08-053-451B-29	Sequence 29, Appl
60	61	67.8	126	1	US-08-480-434-18	Sequence 18, Appl
61	61	67.8	126	1	US-08-480-434-19	Sequence 19, Appl
62	61	67.8	126	1	US-08-053-451B-18	Sequence 18, Appl
63	61	67.8	126	1	US-08-053-451B-19	Sequence 19, Appl
64	61	67.8	265	1	US-08-403-853-16	Sequence 16, Appl
65	47	52.2	17	1	US-08-244-626-14	Sequence 14, Appl
66	47	52.2	99	1	US-08-244-626-10	Sequence 10, Appl
67	45	50.0	122	2	US-08-957-001B-26	Sequence 26, Appl
68	45	50.0	122	2	US-09-496-301-26	Sequence 26, Appl
69	43	47.8	118	1	US-08-888-366-4	Sequence 4, Appli
70	43	47.8	421	2	US-09-000-040-1	Sequence 1, Appli
71	42	46.7	103	2	US-10-630-406-2	Sequence 2, Appli
72	42	46.7	123	2	US-09-270-767-62369	Sequence 62369, A
73	42	46.7	460	2	US-10-630-406-5	Sequence 5, Appli
74	42	46.7	804	2	US-09-270-767-46750	Sequence 46750, A
75	42	46.7	811	2	US-08-983-275-2	Sequence 2, Appli
76	42	46.7	1884	2	US-09-538-092-1329	Sequence 1329, Ap
77	41	45.6	88	2	US-09-726-219A-172	Sequence 172, App
78	41	45.6	88	2	US-09-196-522-172	Sequence 172, App
79	41	45.6	96	2	US-09-905-243-15	Sequence 15, Appl
80	41	45.6	116	2	US-09-027-449-50	Sequence 50, Appl
81	41	45.6	116	2	US-08-804-444A-50	Sequence 50, Appl
82	41	45.6	116	2	US-09-026-985-50	Sequence 50, Appl
83	41	45.6	116	2	US-09-121-952A-50	Sequence 50, Appl
84	41	45.6	116	2	US-09-234-340A-50	Sequence 50, Appl
85	41	45.6	116	2	US-09-355-014-50	Sequence 50, Appl
86	41	45.6	141	2	US-08-957-001B-7	Sequence 7, Appli
87	41	45.6	141	2	US-09-496-301-7	Sequence 7, Appli
88	41	45.6	320	2	US-09-198-452A-1208	Sequence 1208, Ap
89	41	45.6	326	2	US-09-438-185A-580	Sequence 580, App
90	41	45.6	333	2	US-09-270-767-43209	Sequence 43209, A
91	41	45.6	464	2	US-09-198-452A-649	Sequence 649, App
92	41	45.6	474	2	US-09-438-185A-612	Sequence 612, App
93	41	45.6	476	2	US-08-487-550-4	Sequence 4, Appli
94	41	45.6	476	2	US-09-526-098-4	Sequence 4, Appli
95	41	45.6	476	2	US-09-383-916-4	Sequence 4, Appli
96	41	45.6	476	2	US-09-758-173-4	Sequence 4, Appli
97	41	45.6	476	2	US-09-576-424-4	Sequence 4, Appli
98	41	45.6	499	2	US-09-090-793-11	Sequence 11, Appl
99	41	45.6	499	2	US-09-231-899-11	Sequence 11, Appl
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102	41	45.6	525	1	US-08-752-929-19	Sequence 19, Appl
103	41	45.6	806	2	US-09-949-016-10478	Sequence 10478, A
104	41	45.6	846	2	US-09-949-016-6683	Sequence 6683, Ap
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106	40	44.4	400	2	US-09-902-540-13370	Sequence 13370, A
107	40	44.4	409	2	US-09-949-016-11141	Sequence 11141, A
108	40	44.4	475	2	US-09-248-796A-14607	Sequence 14607, A
109	40	44.4	712	2	US-09-248-796A-18407	Sequence 18407, A
110	39.5	43.9	134	2	US-09-471-276-845	Sequence 845, App
111	39	43.3	17	2	US-09-424-840B-114	Sequence 114, App
112	39	43.3	72	2	US-08-338-579A-101	Sequence 101, App
113	39	43.3	100	2	US-09-905-243-50	Sequence 50, Appl
114	39	43.3	115	2	US-09-513-999C-4117	Sequence 4117, Ap
115	39	43.3	117	1	US-07-942-245-24	Sequence 24, Appl
116	39	43.3	124	2	US-09-424-840B-18	Sequence 18, Appl
117	39	43.3	126	2	US-09-232-290-35	Sequence 35, Appl
118	39	43.3	128	2	US-09-134-000C-3995	Sequence 3995, Ap
119	39	43.3	132	2	US-09-248-796A-16572	Sequence 16572, A
120	39	43.3	138	2	US-09-513-999C-7603	Sequence 7603, Ap
121	39	43.3	149	2	US-08-338-579A-95	Sequence 95, Appl
122	39	43.3	197	2	US-09-248-796A-20880	Sequence 20880, A
123	39	43.3	204	2	US-09-549-831-6	Sequence 6, Appli
124	39	43.3	224	2	US-09-248-796A-17090	Sequence 17090, A
125	39	43.3	255	2	US-08-906-769-83	Sequence 83, Appl
126	39	43.3	255	2	US-08-906-616-83	Sequence 83, Appl
127	39	43.3	255	2	US-08-817-795-83	Sequence 83, Appl
128	39	43.3	255	2	US-08-639-075A-83	Sequence 83, Appl
129	39	43.3	255	2	US-09-012-431-83	Sequence 83, Appl
130	39	43.3	255	2	US-09-012-692-83	Sequence 83, Appl
131	39	43.3	255	2	US-08-906-613-83	Sequence 83, Appl
132	39	43.3	255	4	PCT-US95-14442A-83	Sequence 83, Appl
133	39	43.3	256	2	US-09-032-215-27	Sequence 27, Appl
134	39	43.3	358	2	US-09-328-352-6447	Sequence 6447, Ap
135	39	43.3	359	2	US-09-984-292-15	Sequence 15, Appl
136	39	43.3	359	2	US-09-984-292-23	Sequence 23, Appl
137	39	43.3	359	2	US-09-984-292-37	Sequence 37, Appl
138	39	43.3	367	1	US-08-990-379-6	Sequence 6, Appli
139	39	43.3	374	2	US-09-252-991A-23377	Sequence 23377, A
140	39	43.3	400	2	US-09-134-000C-4389	Sequence 4389, Ap
141	39	43.3	626	2	US-09-252-991A-20268	Sequence 20268, A
142	39	43.3	626	2	US-09-712-363-151	Sequence 151, App
143	39	43.3	825	2	US-09-248-796A-16538	Sequence 16538, A
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145	38.5	42.8	118	2	US-09-025-769B-25	Sequence 25, Appl
146	38.5	42.8	118	2	US-09-490-070A-25	Sequence 25, Appl
147	38.5	42.8	118	2	US-09-490-153-25	Sequence 25, Appl
148	38.5	42.8	118	2	US-09-490-324-25	Sequence 25, Appl
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150	38.5	42.8	137	2	US-08-466-163B-7	Sequence 7, Appli
151	38.5	42.8	137	2	US-09-802-096-7	Sequence 7, Appli
152	38.5	42.8	137	2	US-09-802-077-7	Sequence 7, Appli
153	38.5	42.8	137	2	US-09-925-179-7	Sequence 7, Appli
154	38	42.2	117	2	US-10-432-006-5	Sequence 5, Appli
155	38	42.2	142	1	US-08-480-774A-2	Sequence 2, Appli
156	38	42.2	179	2	US-09-270-767-45711	Sequence 45711, A
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158	38	42.2	199	2	US-09-270-767-32537	Sequence 32537, A
159	38	42.2	226	2	US-09-134-000C-3747	Sequence 3747, Ap
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161	38	42.2	328	2	US-09-270-767-45597	Sequence 45597, A
162	38	42.2	433	2	US-09-248-796A-15383	Sequence 15383, A
163	38	42.2	452	2	US-09-248-796A-16219	Sequence 16219, A
164	38	42.2	478	2	US-08-487-550-8	Sequence 8, Appli
165	38	42.2	478	2	US-09-526-098-8	Sequence 8, Appli
166	38	42.2	478	2	US-09-383-916-8	Sequence 8, Appli
167	38	42.2	478	2	US-09-758-173-8	Sequence 8, Appli
168	38	42.2	478	2	US-09-576-424-8	Sequence 8, Appli
169	38	42.2	481	2	US-09-489-039A-12322	Sequence 12322, A
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171	38	42.2	876	2	US-09-134-001C-3943	Sequence 3943, Ap
172	38	42.2	1162	2	US-09-252-991A-32764	Sequence 32764, A
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174	38	42.2	1222	2	US-09-593-828-15	Sequence 15, Appl
175	38	42.2	2516	2	US-08-374-077C-2	Sequence 2, Appli
176	38	42.2	2516	2	US-08-895-590-2	Sequence 2, Appli
177	38	42.2	2516	2	US-09-539-879A-2	Sequence 2, Appli
178	38	42.2	3129	2	US-09-482-788-2	Sequence 2, Appli
179	37.5	41.7	97	2	US-10-194-975-40	Sequence 40, Appl
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181	37.5	41.7	116	2	US-08-545-809A-118	Sequence 118, App
182	37.5	41.7	116	2	US-09-515-697-118	Sequence 118, App
183	37.5	41.7	120	2	US-08-545-809A-137	Sequence 137, App
184	37.5	41.7	120	2	US-09-515-697-137	Sequence 137, App
185	37.5	41.7	123	2	US-08-793-450-4	Sequence 4, Appli
186	37.5	41.7	139	2	US-09-203-768A-2	Sequence 2, Appli
187	37.5	41.7	472	2	US-08-793-450-8	Sequence 8, Appli
188	37.5	41.7	718	2	US-09-107-532A-5234	Sequence 5234, Ap
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191	37	41.1	20	1	US-08-053-451B-116	Sequence 116, App
192	37	41.1	98	1	US-08-211-202-116	Sequence 116, App
193	37	41.1	98	1	US-08-428-197-17	Sequence 17, Appl
194	37	41.1	98	2	US-10-194-975-28	Sequence 28, Appl
195	37	41.1	98	2	US-09-534-717-656	Sequence 656, App
196	37	41.1	98	2	US-09-534-717-660	Sequence 660, App
197	37	41.1	98	4	PCT-US93-10555-17	Sequence 17, Appl
198	37	41.1	110	1	US-08-211-202-117	Sequence 117, App
199	37	41.1	111	1	US-08-211-202-134	Sequence 134, App
200	37	41.1	117	2	US-08-545-809A-130	Sequence 130, App
201	37	41.1	117	2	US-09-515-697-130	Sequence 130, App
202	37	41.1	119	2	US-09-406-535-2	Sequence 2, Appli
203	37	41.1	126	2	US-08-983-607-48	Sequence 48, Appl
204	37	41.1	129	2	US-09-240-274-143	Sequence 143, App
205	37	41.1	129	2	US-09-848-798-143	Sequence 143, App
206	37	41.1	130	2	US-09-248-796A-25748	Sequence 25748, A
207	37	41.1	141	2	US-09-069-628-29	Sequence 29, Appl
208	37	41.1	163	2	US-09-270-767-46943	Sequence 46943, A
209	37	41.1	164	2	US-09-602-787A-218	Sequence 218, App
210	37	41.1	170	2	US-09-489-039A-10503	Sequence 10503, A
211	37	41.1	171	2	US-09-489-039A-13586	Sequence 13586, A
212	37	41.1	239	2	US-09-543-681A-6731	Sequence 6731, Ap
213	37	41.1	247	2	US-09-252-991A-24916	Sequence 24916, A
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216	37	41.1	305	1	US-08-319-622A-2	Sequence 2, Appli
217	37	41.1	305	1	US-08-471-564-2	Sequence 2, Appli
218	37	41.1	307	2	US-09-173-300-15	Sequence 15, Appl
219	37	41.1	307	2	US-10-027-450-15	Sequence 15, Appl
220	37	41.1	323	2	US-09-248-796A-16307	Sequence 16307, A
221	37	41.1	323	2	US-10-033-269-4	Sequence 4, Appli
222	37	41.1	325	2	US-10-033-269-2	Sequence 2, Appli
223	37	41.1	381	2	US-09-540-236-3321	Sequence 3321, Ap
224	37	41.1	434	2	US-09-248-796A-20199	Sequence 20199, A
225	37	41.1	479	2	US-09-248-796A-20464	Sequence 20464, A
226	37	41.1	489	2	US-09-538-092-699	Sequence 699, App
227	37	41.1	521	2	US-10-037-927B-12	Sequence 12, Appl
228	37	41.1	543	1	US-08-776-597A-2	Sequence 2, Appli
229	37	41.1	543	1	US-08-693-228-2	Sequence 2, Appli
230	37	41.1	543	2	US-09-602-787A-212	Sequence 212, App
231	37	41.1	549	2	US-09-345-473E-32	Sequence 32, Appl
232	37	41.1	549	2	US-09-862-027-32	Sequence 32, Appl
233	37	41.1	1518	2	US-09-487-558B-152	Sequence 152, App
234	37	41.1	2766	2	US-09-964-956-62	Sequence 62, Appl
235	36.5	40.6	112	2	US-09-344-587-14	Sequence 14, Appl
236	36.5	40.6	804	2	US-09-328-352-5545	Sequence 5545, Ap
237	36.5	40.6	843	1	US-09-172-977-3	Sequence 3, Appli
238	36.5	40.6	843	2	US-09-404-108-3	Sequence 3, Appli
239	36.5	40.6	867	2	US-09-668-673B-2	Sequence 2, Appli
240	36.5	40.6	867	2	US-10-389-532-2	Sequence 2, Appli
241	36.5	40.6	1002	2	US-10-290-579A-189	Sequence 189, App
242	36.5	40.6	1839	1	US-09-172-977-4	Sequence 4, Appli
243	36.5	40.6	1839	2	US-09-404-108-4	Sequence 4, Appli
244	36.5	40.6	2753	2	US-09-949-016-7659	Sequence 7659, Ap
245	36.5	40.6	2753	2	US-09-949-016-7660	Sequence 7660, Ap
246	36.5	40.6	3924	2	US-09-538-092-1246	Sequence 1246, Ap

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248	36	40.0	17	2	US-09-795-798-11	Sequence 11, Appl
249	36	40.0	17	2	US-09-424-840B-70	Sequence 70, Appl
250	36	40.0	17	2	US-09-424-840B-78	Sequence 78, Appl
251	36	40.0	61	2	US-09-973-278-168	Sequence 168, App
252	36	40.0	62	2	US-09-227-357-231	Sequence 231, App
253	36	40.0	70	2	US-09-270-767-39559	Sequence 39559, A
254	36	40.0	70	2	US-09-270-767-54776	Sequence 54776, A
255	36	40.0	97	2	US-10-194-975-49	Sequence 49, Appl
256	36	40.0	98	2	US-09-621-976-4473	Sequence 4473, Ap
257	36	40.0	98	2	US-09-534-717-665	Sequence 665, App
258	36	40.0	107	2	US-09-899-896-11	Sequence 11, Appl
259	36	40.0	117	1	US-08-652-558-3	Sequence 3, Appli
260	36	40.0	117	1	US-08-652-558-44	Sequence 44, Appl
261	36	40.0	117	1	US-08-652-558-45	Sequence 45, Appl
262	36	40.0	117	1	US-08-652-558-46	Sequence 46, Appl
263	36	40.0	117	1	US-08-652-558-51	Sequence 51, Appl
264	36	40.0	121	2	US-08-974-899-5	Sequence 5, Appli
265	36	40.0	121	2	US-09-795-798-5	Sequence 5, Appli
266	36	40.0	124	2	US-09-424-840B-123	Sequence 123, App
267	36	40.0	128	1	US-08-478-039-63	Sequence 63, Appl
268	36	40.0	128	1	US-08-476-349A-63	Sequence 63, Appl
269	36	40.0	140	2	US-09-270-767-34254	Sequence 34254, A
270	36	40.0	140	2	US-09-270-767-49471	Sequence 49471, A
271	36	40.0	142	2	US-09-564-329A-13	Sequence 13, Appl
272	36	40.0	142	2	US-09-963-620-13	Sequence 13, Appl
273	36	40.0	142	2	US-09-855-632-13	Sequence 13, Appl
274	36	40.0	142	2	US-09-934-773-13	Sequence 13, Appl
275	36	40.0	142	2	US-09-855-153-13	Sequence 13, Appl
276	36	40.0	142	2	US-10-224-720-13	Sequence 13, Appl
277	36	40.0	170	1	US-08-652-558-40	Sequence 40, Appl
278	36	40.0	197	2	US-09-543-681A-4775	Sequence 4775, Ap
279	36	40.0	225	2	US-09-465-901-18	Sequence 18, Appl
280	36	40.0	262	2	US-09-270-767-61644	Sequence 61644, A
281	36	40.0	299	2	US-09-107-532A-5981	Sequence 5981, Ap
282	36	40.0	341	2	US-09-543-681A-5975	Sequence 5975, Ap
283	36	40.0	358	2	US-09-270-767-46092	Sequence 46092, A
284	36	40.0	362	2	US-09-949-016-7725	Sequence 7725, Ap
285	36	40.0	372	2	US-09-134-001C-5163	Sequence 5163, Ap
286	36	40.0	376	2	US-09-538-092-1109	Sequence 1109, Ap
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288	36	40.0	387	1	US-08-329-560-2	Sequence 2, Appli
289	36	40.0	392	1	US-08-904-031-1	Sequence 1, Appli
290	36	40.0	393	1	US-08-904-031-3	Sequence 3, Appli
291	36	40.0	394	2	US-09-949-016-10437	Sequence 10437, A
292	36	40.0	401	2	US-09-270-767-45952	Sequence 45952, A
293	36	40.0	443	2	US-09-949-016-11352	Sequence 11352, A
294	36	40.0	450	2	US-09-107-532A-7055	Sequence 7055, Ap
295	36	40.0	480	2	US-09-248-796A-23564	Sequence 23564, A
296	36	40.0	504	2	US-09-487-558B-208	Sequence 208, App
297	36	40.0	525	2	US-09-248-796A-19906	Sequence 19906, A
298	36	40.0	550	2	US-09-198-452A-225	Sequence 225, App
299	36	40.0	552	2	US-09-460-295B-8	Sequence 8, Appli
300	36	40.0	556	2	US-09-438-185A-210	Sequence 210, App
301	36	40.0	579	2	US-09-252-991A-27970	Sequence 27970, A
302	36	40.0	599	2	US-09-248-796A-19578	Sequence 19578, A
303	36	40.0	629	2	US-09-248-796A-19860	Sequence 19860, A
304	36	40.0	654	2	US-09-437-687A-2	Sequence 2, Appli
305	36	40.0	654	2	US-10-263-250-2	Sequence 2, Appli
306	36	40.0	737	2	US-09-949-016-11607	Sequence 11607, A
307	36	40.0	803	2	US-09-543-681A-6767	Sequence 6767, Ap
308	36	40.0	898	2	US-09-688-188B-22	Sequence 22, Appl
309	36	40.0	898	2	US-09-291-417D-22	Sequence 22, Appl
310	36	40.0	898	2	US-09-771-161A-260	Sequence 260, App
311	36	40.0	1037	2	US-09-949-016-6723	Sequence 6723, Ap
312	36	40.0	1061	2	US-09-949-016-10165	Sequence 10165, A
313	36	40.0	1318	2	US-09-540-236-3623	Sequence 3623, Ap
314	36	40.0	1683	2	US-08-755-587-183	Sequence 183, App
315	36	40.0	5532	2	US-09-914-286-6	Sequence 6, Appli
316	35.5	39.4	194	2	US-09-248-796A-25232	Sequence 25232, A
317	35.5	39.4	236	2	US-09-328-352-4344	Sequence 4344, Ap
318	35.5	39.4	317	1	US-08-463-090B-9	Sequence 9, Appli
319	35.5	39.4	317	1	US-08-874-347-18	Sequence 18, Appl
320	35.5	39.4	317	2	US-09-093-522-18	Sequence 18, Appl
321	35.5	39.4	330	2	US-09-248-796A-18426	Sequence 18426, A
322	35.5	39.4	421	2	US-09-362-473-14	Sequence 14, Appl
323	35.5	39.4	429	2	US-09-372-425A-6	Sequence 6, Appli
324	35.5	39.4	447	2	US-09-372-425A-2	Sequence 2, Appli
325	35.5	39.4	451	2	US-09-925-179-66	Sequence 66, Appl
326	35	38.9	16	2	US-09-424-840B-110	Sequence 110, App
327	35	38.9	17	1	US-08-650-262-14	Sequence 14, Appl
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329	35	38.9	19	2	US-09-424-712-18	Sequence 18, Appl
330	35	38.9	21	2	US-08-918-148-45	Sequence 45, Appl
331	35	38.9	21	2	US-09-138-091A-45	Sequence 45, Appl
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333	35	38.9	43	2	US-09-902-540-13610	Sequence 13610, A
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335	35	38.9	60	2	US-09-248-796A-15981	Sequence 15981, A
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339	35	38.9	96	2	US-10-330-613A-42	Sequence 42, Appl
340	35	38.9	97	2	US-10-194-975-42	Sequence 42, Appl
341	35	38.9	97	2	US-10-194-975-51	Sequence 51, Appl
342	35	38.9	97	2	US-10-194-975-52	Sequence 52, Appl
343	35	38.9	97	2	US-10-194-975-53	Sequence 53, Appl
344	35	38.9	97	2	US-10-330-613A-41	Sequence 41, Appl
345	35	38.9	97	2	US-10-330-613A-49	Sequence 49, Appl
346	35	38.9	97	2	US-10-330-613A-69	Sequence 69, Appl
347	35	38.9	98	2	US-10-194-975-33	Sequence 33, Appl
348	35	38.9	98	2	US-09-534-717-662	Sequence 662, App
349	35	38.9	98	2	US-09-534-717-663	Sequence 663, App
350	35	38.9	99	2	US-10-194-975-43	Sequence 43, Appl
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352	35	38.9	116	2	US-08-545-809A-140	Sequence 140, App
353	35	38.9	116	2	US-09-515-697-92	Sequence 92, Appl
354	35	38.9	116	2	US-09-515-697-140	Sequence 140, App
355	35	38.9	117	1	US-08-650-262-4	Sequence 4, Appli
356	35	38.9	117	2	US-08-851-362D-48	Sequence 48, Appl
357	35	38.9	118	2	US-08-545-809A-142	Sequence 142, App
358	35	38.9	118	2	US-09-515-697-142	Sequence 142, App
359	35	38.9	119	2	US-09-025-769B-39	Sequence 39, Appl
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361	35	38.9	119	2	US-09-490-070A-39	Sequence 39, Appl
362	35	38.9	119	2	US-09-490-070A-65	Sequence 65, Appl
363	35	38.9	119	2	US-09-490-153-39	Sequence 39, Appl
364	35	38.9	119	2	US-09-490-153-65	Sequence 65, Appl
365	35	38.9	119	2	US-09-490-324-39	Sequence 39, Appl
366	35	38.9	119	2	US-09-490-324-65	Sequence 65, Appl
367	35	38.9	120	2	US-09-513-999C-7802	Sequence 7802, Ap
368	35	38.9	120	2	US-10-014-012-230	Sequence 230, App
369	35	38.9	121	2	US-10-330-613A-9	Sequence 9, Appli
370	35	38.9	125	2	US-10-432-006-1	Sequence 1, Appli
371	35	38.9	128	2	US-09-248-796A-28119	Sequence 28119, A
372	35	38.9	129	2	US-09-471-276-864	Sequence 864, App
373	35	38.9	139	2	US-09-471-276-837	Sequence 837, App
374	35	38.9	156	2	US-09-902-540-13352	Sequence 13352, A
375	35	38.9	164	2	US-09-585-173B-32	Sequence 32, Appl
376	35	38.9	169	2	US-09-540-236-3364	Sequence 3364, Ap
377	35	38.9	169	2	US-09-248-796A-27859	Sequence 27859, A
378	35	38.9	189	2	US-09-248-796A-16820	Sequence 16820, A
379	35	38.9	213	2	US-09-270-767-33720	Sequence 33720, A
380	35	38.9	213	2	US-09-270-767-48937	Sequence 48937, A
381	35	38.9	230	2	US-09-270-767-57718	Sequence 57718, A
382	35	38.9	243	2	US-09-252-991A-17532	Sequence 17532, A
383	35	38.9	244	2	US-08-918-148-79	Sequence 79, Appl
384	35	38.9	244	2	US-09-138-091A-77	Sequence 77, Appl
385	35	38.9	252	2	US-09-949-016-6472	Sequence 6472, Ap
386	35	38.9	253	2	US-09-949-016-9375	Sequence 9375, Ap
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388	35	38.9	259	1	US-08-448-164-5	Sequence 5, Appli
389	35	38.9	259	2	US-08-081-929-5	Sequence 5, Appli
390	35	38.9	259	2	US-10-000-954-5	Sequence 5, Appli
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392	35	38.9	260	1	US-08-446-363-9	Sequence 9, Appli

393	35	38.9	260	2	US-08-927-128-4	Sequence 4, Appli
394	35	38.9	260	2	US-09-976-594-644	Sequence 644, App
395	35	38.9	270	2	US-09-252-991A-28787	Sequence 28787, A
396	35	38.9	287	2	US-09-248-796A-19104	Sequence 19104, A
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399	35	38.9	288	2	US-09-139-819A-12	Sequence 12, Appl
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404	35	38.9	324	2	US-09-328-352-7458	Sequence 7458, Ap
405	35	38.9	333	2	US-09-583-110-4020	Sequence 4020, Ap
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407	35	38.9	346	1	US-08-702-153-2	Sequence 2, Appli
408	35	38.9	346	1	US-08-702-153-4	Sequence 4, Appli
409	35	38.9	361	2	US-09-107-433-5205	Sequence 5205, Ap
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412	35	38.9	384	2	US-09-949-002-422	Sequence 422, App
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423	35	38.9	428	2	US-10-239-333B-7	Sequence 7, Appli
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435	35	38.9	450	2	US-09-906-618-320	Sequence 320, App
436	35	38.9	450	2	US-09-906-646-320	Sequence 320, App
437	35	38.9	450	2	US-09-904-462-320	Sequence 320, App
438	35	38.9	450	2	US-09-902-736A-320	Sequence 320, App
439	35	38.9	450	2	US-09-906-722A-320	Sequence 320, App
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448	35	38.9	627	2	US-10-206-576-452	Sequence 452, App
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458	35	38.9	898	2	US-08-863-102-4	Sequence 4, Appli
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482	35	38.9	1313	2	US-10-206-576-450	Sequence 450, App
483	35	38.9	1313	2	US-10-206-576-454	Sequence 454, App
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486	35	38.9	1495	2	US-09-337-384-1	Sequence 1, Appli
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489	35	38.9	1791	2	US-09-827-998-3	Sequence 3, Appli
490	35	38.9	1792	1	US-08-962-284-4	Sequence 4, Appli
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496	34.5	38.3	208	2	US-09-538-092-1018	Sequence 1018, Ap
497	34.5	38.3	208	2	US-09-214-881A-2	Sequence 2, Appli
498	34.5	38.3	209	2	US-09-214-881A-6	Sequence 6, Appli
499	34.5	38.3	209	2	US-09-214-881A-8	Sequence 8, Appli
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508	34.5	38.3	1221	2	US-09-919-891-2	Sequence 2, Appli
509	34	37.8	11	1	US-07-803-623B-13	Sequence 13, Appl
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511	34	37.8	11	2	US-09-201-970A-13	Sequence 13, Appl
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513	34	37.8	17	2	US-09-534-717-348	Sequence 348, App
514	34	37.8	17	2	US-09-534-717-398	Sequence 398, App
515	34	37.8	84	2	US-09-270-767-32345	Sequence 32345, A
516	34	37.8	84	2	US-09-270-767-47562	Sequence 47562, A
517	34	37.8	85	2	US-09-107-532A-6447	Sequence 6447, Ap
518	34	37.8	87	2	US-09-248-796A-17666	Sequence 17666, A
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520	34	37.8	96	2	US-10-330-613A-50	Sequence 50, Appl
521	34	37.8	97	2	US-08-851-362D-33	Sequence 33, Appl
522	34	37.8	98	1	US-08-478-039-81	Sequence 81, Appl
523	34	37.8	98	1	US-08-476-349A-81	Sequence 81, Appl
524	34	37.8	98	1	US-08-665-202-33	Sequence 33, Appl
525	34	37.8	98	2	US-09-315-574-33	Sequence 33, Appl
526	34	37.8	98	2	US-10-194-975-45	Sequence 45, Appl
527	34	37.8	98	2	US-09-534-717-610	Sequence 610, App
528	34	37.8	102	2	US-08-477-347-9	Sequence 9, Appli
529	34	37.8	102	2	US-09-800-908-9	Sequence 9, Appli
530	34	37.8	106	2	US-09-270-767-56985	Sequence 56985, A
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533	34	37.8	111	2	US-09-196-522-171	Sequence 171, App
534	34	37.8	114	2	US-09-726-219A-214	Sequence 214, App
535	34	37.8	114	2	US-09-726-219A-223	Sequence 223, App
536	34	37.8	114	2	US-09-726-219A-227	Sequence 227, App
537	34	37.8	114	2	US-09-726-219A-231	Sequence 231, App
538	34	37.8	114	2	US-09-726-219A-233	Sequence 233, App

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540	34	37.8	114	2	US-09-196-522-223	Sequence 223, App
541	34	37.8	114	2	US-09-196-522-227	Sequence 227, App
542	34	37.8	114	2	US-09-196-522-231	Sequence 231, App
543	34	37.8	114	2	US-09-196-522-233	Sequence 233, App
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545	34	37.8	117	2	US-08-545-809A-133	Sequence 133, App
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551	34	37.8	119	2	US-09-490-070A-26	Sequence 26, Appl
552	34	37.8	119	2	US-09-490-153-26	Sequence 26, Appl
553	34	37.8	119	2	US-09-490-324-26	Sequence 26, Appl
554	34	37.8	120	2	US-09-025-769B-40	Sequence 40, Appl
555	34	37.8	120	2	US-09-025-769B-67	Sequence 67, Appl
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561	34	37.8	120	2	US-09-490-324-40	Sequence 40, Appl
562	34	37.8	120	2	US-09-490-324-67	Sequence 67, Appl
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564	34	37.8	121	2	US-10-330-613A-17	Sequence 17, Appl
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568	34	37.8	125	1	US-08-665-202-45	Sequence 45, Appl
569	34	37.8	125	1	US-08-665-202-46	Sequence 46, Appl
570	34	37.8	125	1	US-08-665-202-47	Sequence 47, Appl
571	34	37.8	125	1	US-08-665-202-48	Sequence 48, Appl
572	34	37.8	125	1	US-08-665-202-49	Sequence 49, Appl
573	34	37.8	125	1	US-08-665-202-50	Sequence 50, Appl
574	34	37.8	125	1	US-08-665-202-51	Sequence 51, Appl
575	34	37.8	125	1	US-08-665-202-52	Sequence 52, Appl
576	34	37.8	125	1	US-08-665-202-53	Sequence 53, Appl
577	34	37.8	125	1	US-08-665-202-54	Sequence 54, Appl
578	34	37.8	125	1	US-08-665-202-55	Sequence 55, Appl
579	34	37.8	125	1	US-08-665-202-57	Sequence 57, Appl
580	34	37.8	125	1	US-08-665-202-58	Sequence 58, Appl
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594	34	37.8	125	2	US-09-315-574-58	Sequence 58, Appl
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600	34	37.8	130	2	US-09-802-077-5	Sequence 5, Appli
601	34	37.8	130	2	US-09-925-179-5	Sequence 5, Appli
602	34	37.8	132	2	US-09-071-035-448	Sequence 448, App
603	34	37.8	132	2	US-10-206-576-448	Sequence 448, App
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605	34	37.8	134	1	US-08-468-671-6	Sequence 6, Appli
606	34	37.8	142	2	US-09-069-628-27	Sequence 27, Appl
607	34	37.8	157	2	US-09-071-035-446	Sequence 446, App
608	34	37.8	157	2	US-10-206-576-446	Sequence 446, App
609	34	37.8	165	2	US-09-605-703B-910	Sequence 910, App
610	34	37.8	169	2	US-09-540-236-2468	Sequence 2468, Ap
611	34	37.8	176	2	US-09-328-352-6646	Sequence 6646, Ap
612	34	37.8	182	2	US-09-270-767-62046	Sequence 62046, A
613	34	37.8	182	2	US-09-248-796A-19704	Sequence 19704, A
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615	34	37.8	237	2	US-09-248-796A-20951	Sequence 20951, A
616	34	37.8	239	2	US-09-248-796A-16742	Sequence 16742, A
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622	34	37.8	252	2	US-10-027-450-17	Sequence 17, Appl
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624	34	37.8	258	2	US-09-315-574-5	Sequence 5, Appli
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626	34	37.8	262	2	US-09-069-821-4	Sequence 4, Appli
627	34	37.8	262	2	US-09-956-086-4	Sequence 4, Appli
628	34	37.8	262	2	US-09-956-087-4	Sequence 4, Appli
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633	34	37.8	282	2	US-09-985-442-7	Sequence 7, Appli
634	34	37.8	282	2	US-09-983-580-7	Sequence 7, Appli
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640	34	37.8	298	2	US-10-314-639-52	Sequence 52, Appl
641	34	37.8	298	2	US-10-059-964A-52	Sequence 52, Appl
642	34	37.8	300	2	US-09-248-796A-16769	Sequence 16769, A
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827	33	36.7	117	2	US-09-490-153-22	Sequence 22, Appl
828	33	36.7	117	2	US-09-490-324-22	Sequence 22, Appl
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835	33	36.7	124	2	US-09-698-705-6	Sequence 6, Appli
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842	33	36.7	142	2	US-09-069-628-14	Sequence 14, Appl
843	33	36.7	143	2	US-09-069-628-7	Sequence 7, Appli
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874	33	36.7	240	1	US-08-956-047-25	Sequence 25, Appl
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877	33	36.7	245	2	US-09-710-279-1042	Sequence 1042, Ap
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894	33	36.7	261	2	US-09-610-838-9	Sequence 9, Appli
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910	33	36.7	293	2	US-10-012-542-233	Sequence 233, App
911	33	36.7	293	2	US-10-115-123-233	Sequence 233, App
912	33	36.7	296	2	US-09-489-039A-12979	Sequence 12979, A
913	33	36.7	299	4	PCT-US91-00899-6	Sequence 6, Appli
914	33	36.7	300	2	US-09-277-078-2	Sequence 2, Appli
915	33	36.7	302	1	US-08-893-853-3	Sequence 3, Appli
916	33	36.7	302	2	US-09-113-921-3	Sequence 3, Appli
917	33	36.7	302	2	US-09-451-067-3	Sequence 3, Appli
918	33	36.7	303	2	US-09-270-767-42250	Sequence 42250, A
919	33	36.7	305	2	US-09-509-738C-4	Sequence 4, Appli
920	33	36.7	307	2	US-09-461-325-331	Sequence 331, App
921	33	36.7	307	2	US-10-012-542-331	Sequence 331, App
922	33	36.7	307	2	US-10-115-123-331	Sequence 331, App
923	33	36.7	309	2	US-09-902-540-11246	Sequence 11246, A
924	33	36.7	312	2	US-09-270-767-59311	Sequence 59311, A
925	33	36.7	314	1	US-08-589-446-6	Sequence 6, Appli
926	33	36.7	314	1	US-08-444-882-6	Sequence 6, Appli
927	33	36.7	314	1	US-08-389-459A-6	Sequence 6, Appli
928	33	36.7	314	2	US-08-987-867A-6	Sequence 6, Appli
929	33	36.7	315	2	US-09-248-796A-19221	Sequence 19221, A
930	33	36.7	320	2	US-09-489-039A-11871	Sequence 11871, A
931	33	36.7	320	2	US-09-303-518D-134	Sequence 134, App
932	33	36.7	327	2	US-08-679-493A-71	Sequence 71, Appl
933	33	36.7	327	2	US-08-679-493A-72	Sequence 72, Appl
934	33	36.7	328	2	US-09-949-016-8858	Sequence 8858, Ap
935	33	36.7	329	2	US-09-248-796A-15096	Sequence 15096, A
936	33	36.7	332	2	US-09-538-092-376	Sequence 376, App
937	33	36.7	348	2	US-09-173-300-19	Sequence 19, Appl
938	33	36.7	348	2	US-10-027-450-19	Sequence 19, Appl
939	33	36.7	352	2	US-09-134-000C-6028	Sequence 6028, Ap
940	33	36.7	355	2	US-09-466-778-9	Sequence 9, Appli
941	33	36.7	358	2	US-09-248-796A-17253	Sequence 17253, A
942	33	36.7	359	2	US-09-723-806A-7	Sequence 7, Appli
943	33	36.7	361	1	US-07-914-281-2	Sequence 2, Appli
944	33	36.7	361	1	US-08-393-246-2	Sequence 2, Appli
945	33	36.7	361	1	US-08-273-411-3	Sequence 3, Appli
946	33	36.7	361	1	US-08-525-058A-2	Sequence 2, Appli
947	33	36.7	361	1	US-08-696-731-2	Sequence 2, Appli
948	33	36.7	361	2	US-09-042-531-2	Sequence 2, Appli
949	33	36.7	361	2	US-09-390-131-6	Sequence 6, Appli
950	33	36.7	361	4	PCT-US91-00899-7	Sequence 7, Appli
951	33	36.7	364	2	US-09-248-796A-16427	Sequence 16427, A
952	33	36.7	374	1	US-07-914-281-11	Sequence 11, Appl
953	33	36.7	374	1	US-08-393-246-11	Sequence 11, Appl
954	33	36.7	374	1	US-08-525-058A-11	Sequence 11, Appl
955	33	36.7	374	1	US-08-696-731-11	Sequence 11, Appl
956	33	36.7	374	2	US-09-042-531-11	Sequence 11, Appl
957	33	36.7	375	2	US-09-444-412-2	Sequence 2, Appli
958	33	36.7	375	2	US-09-660-742-12	Sequence 12, Appl
959	33	36.7	375	2	US-09-825-414-36	Sequence 36, Appl
960	33	36.7	376	2	US-09-540-236-3071	Sequence 3071, Ap
961	33	36.7	385	2	US-09-328-352-7887	Sequence 7887, Ap
962	33	36.7	388	2	US-09-949-016-10243	Sequence 10243, A
963	33	36.7	389	2	US-10-138-701-20	Sequence 20, Appl
964	33	36.7	393	2	US-09-260-843-2	Sequence 2, Appli
965	33	36.7	393	2	US-09-923-654-2	Sequence 2, Appli
966	33	36.7	394	2	US-09-198-452A-396	Sequence 396, App
967	33	36.7	397	2	US-09-252-991A-29847	Sequence 29847, A
968	33	36.7	399	2	US-09-252-991A-22529	Sequence 22529, A
969	33	36.7	400	2	US-09-252-991A-26145	Sequence 26145, A
970	33	36.7	402	2	US-09-438-185A-382	Sequence 382, App
971	33	36.7	407	2	US-09-389-956-14	Sequence 14, Appl
972	33	36.7	410	2	US-09-238-480-2	Sequence 2, Appli
973	33	36.7	410	2	US-09-489-039A-13326	Sequence 13326, A
974	33	36.7	415	1	US-08-381-936-2	Sequence 2, Appli
975	33	36.7	415	2	US-08-943-374-2	Sequence 2, Appli
976	33	36.7	415	2	US-09-469-648A-2	Sequence 2, Appli

977	33	36.7	416	2	US-09-949-016-8977	Sequence 8977, Ap
978	33	36.7	417	2	US-09-487-558B-186	Sequence 186, App
979	33	36.7	421	2	US-09-134-001C-4890	Sequence 4890, Ap
980	33	36.7	424	2	US-09-173-300-45	Sequence 45, Appl
981	33	36.7	424	2	US-10-027-450-45	Sequence 45, Appl
982	33	36.7	427	2	US-08-448-722A-4	Sequence 4, Appli
983	33	36.7	427	2	US-08-189-309B-4	Sequence 4, Appli
984	33	36.7	427	2	US-09-690-265-1	Sequence 1, Appli
985	33	36.7	427	2	US-09-205-785-1	Sequence 1, Appli
986	33	36.7	431	4	PCT-US91-00909-6	Sequence 6, Appli
987	33	36.7	440	1	US-08-483-140-27	Sequence 27, Appl
988	33	36.7	440	1	US-08-485-938A-31	Sequence 31, Appl
989	33	36.7	440	2	US-09-949-016-8606	Sequence 8606, Ap
990	33	36.7	440	2	US-09-949-016-8607	Sequence 8607, Ap
991	33	36.7	441	2	US-09-991-258-16	Sequence 16, Appl
992	33	36.7	444	1	US-08-351-981-2	Sequence 2, Appli
993	33	36.7	444	1	US-08-351-981-8	Sequence 8, Appli
994	33	36.7	448	2	US-09-520-781-32	Sequence 32, Appl
995	33	36.7	448	2	US-09-957-187-32	Sequence 32, Appl
996	33	36.7	448	2	US-09-991-053-32	Sequence 32, Appl
997	33	36.7	452	2	US-09-489-039A-12162	Sequence 12162, A
998	33	36.7	465	1	US-08-588-983-20	Sequence 20, Appl
999	33	36.7	465	1	US-08-588-983-22	Sequence 22, Appl
1000	33	36.7	465	1	US-08-588-976-20	Sequence 20, Appl

ALIGNMENTS

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RESULT 1
US-08-318-157B-24
; Sequence 24, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-24

  Query Match           100.0%;  Score 90;  DB 1;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db          1 EIHPDSSTINYAPSLKD 17


RESULT 2
US-09-253-794-24
; Sequence 24, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 24:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 17 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-253-794-24

  Query Match           100.0%;  Score 90;  DB 2;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-08;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db          1 EIHPDSSTINYAPSLKD 17


RESULT 3
US-08-318-157B-2
; Sequence 2, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
```

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;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-2

  Query Match             100.0%;  Score 90;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 4
US-08-318-157B-8
; Sequence 8, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-8

  Query Match             100.0%;  Score 90;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 5
US-08-318-157B-9
; Sequence 9, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-9

  Query Match             100.0%;  Score 90;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66
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RESULT 6
US-08-318-157B-10
; Sequence 10, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-10

  Query Match             100.0%;  Score 90;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 7
US-08-318-157B-11
; Sequence 11, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-11

  Query Match             100.0%;  Score 90;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 8
US-08-318-157B-12
; Sequence 12, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-12
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  Query Match             100.0%;  Score 90;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 9
US-08-318-157B-13
; Sequence 13, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-13

  Query Match             100.0%;  Score 90;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 10
US-08-318-157B-14
; Sequence 14, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-14

  Query Match             100.0%;  Score 90;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 11
US-08-318-157B-15
; Sequence 15, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
```

```
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-15

  Query Match             100.0%;  Score 90;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 12
US-08-318-157B-17
; Sequence 17, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-17

  Query Match             100.0%;  Score 90;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 13
US-08-318-157B-57
; Sequence 57, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-318-157B-57

  Query Match             100.0%;  Score 90;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 14
US-08-318-157B-58
; Sequence 58, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
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;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-318-157B-58

  Query Match             100.0%;  Score 90;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 15
US-09-253-794-2
; Sequence 2, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-253-794-2

  Query Match             100.0%;  Score 90;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 16
US-09-253-794-8
; Sequence 8, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-253-794-8

  Query Match             100.0%;  Score 90;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 17
US-09-253-794-9
; Sequence 9, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
```

```
;                          MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-253-794-9

  Query Match             100.0%;  Score 90;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 18
US-09-253-794-10
; Sequence 10, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 10:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-253-794-10

  Query Match             100.0%;  Score 90;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 19
US-09-253-794-11
; Sequence 11, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 11:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
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```
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-253-794-11

  Query Match            100.0%;  Score 90;  DB 2;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 20
US-09-253-794-12
; Sequence 12, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-253-794-12

  Query Match            100.0%;  Score 90;  DB 2;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 21
US-09-253-794-13
; Sequence 13, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-253-794-13

  Query Match            100.0%;  Score 90;  DB 2;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 22
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
```

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;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/253,794
;              FILING DATE: 22-Feb-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US 08/318,157
;              FILING DATE: 05-OCT-1994
;         ATTORNEY/AGENT INFORMATION:
;              NAME: SAXE, Bernhard D.
;              REGISTRATION NUMBER: 28,665
;              REFERENCE/DOCKET NUMBER: 18733/464
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (202)672-5300
;              TELEFAX: (202)672-5399
;              TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 14:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 119 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: <Unknown>
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

  Query Match             100.0%;  Score 90;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 23
US-09-253-794-15
; Sequence 15, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;         APPLICANT: HANSEN, Hans J.
;                    ARMOUR, Kathryn L.
;         TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                             MOUSE MONOCLONAL ANTIBODIES
;         NUMBER OF SEQUENCES: 58
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Foley & Lardner
;              STREET: 3000 K Street, N.W., Suite 500
;              CITY: Washington
;              STATE: D.C.
;              COUNTRY: USA
;              ZIP: 20007-5109
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/253,794
;              FILING DATE: 22-Feb-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US 08/318,157
;              FILING DATE: 05-OCT-1994
;         ATTORNEY/AGENT INFORMATION:
;              NAME: SAXE, Bernhard D.
;              REGISTRATION NUMBER: 28,665
;              REFERENCE/DOCKET NUMBER: 18733/464
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (202)672-5300
;              TELEFAX: (202)672-5399
;              TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 15:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 119 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: <Unknown>
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-253-794-15

  Query Match             100.0%;  Score 90;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 24
US-09-253-794-17
; Sequence 17, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;         APPLICANT: HANSEN, Hans J.
;                    ARMOUR, Kathryn L.
;         TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                             MOUSE MONOCLONAL ANTIBODIES
;         NUMBER OF SEQUENCES: 58
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Foley & Lardner
;              STREET: 3000 K Street, N.W., Suite 500
;              CITY: Washington
;              STATE: D.C.
;              COUNTRY: USA
;              ZIP: 20007-5109
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/253,794
;              FILING DATE: 22-Feb-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US 08/318,157
;              FILING DATE: 05-OCT-1994
;         ATTORNEY/AGENT INFORMATION:
;              NAME: SAXE, Bernhard D.
;              REGISTRATION NUMBER: 28,665
;              REFERENCE/DOCKET NUMBER: 18733/464
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (202)672-5300
;              TELEFAX: (202)672-5399
;              TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 17:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 119 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-253-794-17

  Query Match             100.0%;  Score 90;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66
```

```
RESULT 25
US-09-253-794-57
; Sequence 57, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 57:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-253-794-57

  Query Match             100.0%;  Score 90;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 26
US-09-253-794-58
; Sequence 58, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 58:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-253-794-58

  Query Match             100.0%;  Score 90;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 27
US-08-525-539A-28
; Sequence 28, Application US/08525539A
; Patent No. 6309636
;  GENERAL INFORMATION:
;    APPLICANT:  DO COUTO, FERNANDO J.R.
;    APPLICANT:  CERIANI, ROBERTO L.
;    APPLICANT:  PETERSON, JERRY A.
;    TITLE OF INVENTION:  RECOMBINANT PEPTIDES DERIVED FROM THE
;    TITLE OF INVENTION:  Mc3 ANTI-BA46 ANTIBODY, METHODS OF USE THEREOF, AND
;    TITLE OF INVENTION:  METHODS OF HUMANIZING ANTIBODY PEPTIDES
;    NUMBER OF SEQUENCES:  81
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/525,539A
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DYLAN, TYLER
;      REGISTRATION NUMBER:  37,612
;      REFERENCE/DOCKET NUMBER:  27633-20001.21
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 813-5600
;      TELEFAX:  (415) 494-0792
```

```
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  33 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-525-539A-28

  Query Match             91.1%;  Score 82;  DB 2;  Length 33;
  Best Local Similarity   88.2%;  Pred. No. 9.8e-07;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||| |||| |||||
Db          1 EIHPDSGTINYTPSLKD 17


RESULT 28
US-07-942-245-17
; Sequence 17, Application US/07942245
; Patent No. 5639641
;  GENERAL INFORMATION:
;    APPLICANT:  PEDERSEN, Jan T.
;    APPLICANT:  SEARLE,   Stephen M.J.
;    APPLICANT:  REES,     Anthony R.
;    APPLICANT:  ROGUSKA,  Michael A.
;    APPLICANT:  GUILD,    Braydon C.
;    TITLE OF INVENTION:  SURFACE RESIDUE VENEERING OF RODENT
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  522
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sughrue, Mion, Zinn, Macpeak & Seas
;      STREET:  2100 Pensylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States
;      ZIP:  20037-3202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  HP 9000/700 Workstation
;      OPERATING SYSTEM:  UNIX
;      SOFTWARE:  In house
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/942,245
;      FILING DATE:  09-SEP-1992
;      CLASSIFICATION:  530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 293-7060
;      TELEFAX:  (202) 293-7860
;      TELEX:  6491103
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  109 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-07-942-245-17

  Query Match             91.1%;  Score 82;  DB 1;  Length 109;
  Best Local Similarity   88.2%;  Pred. No. 3.9e-06;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||| |||| |||||
Db         50 EIHPDSGTINYTPSLKD 66


RESULT 29
US-09-232-290-53
; Sequence 53, Application US/09232290A
; Patent No. 6815540
; GENERAL INFORMATION:
;  APPLICANT: PLUCKTHUN, ANDREAS
;  APPLICANT: NIEBA, LARS
;  APPLICANT: HONEGGER, ANNEMARIE
;  TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH
;  TITLE OF INVENTION: INCREASED SOLUBILITY
;  FILE REFERENCE: MORPHO/7
;  CURRENT APPLICATION NUMBER: US/09/232,290A
;  CURRENT FILING DATE: 1999-01-15
;  EARLIER APPLICATION NUMBER: PCT/EP96/02230
;  EARLIER FILING DATE: 1996-05-23
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Murine
US-09-232-290-53

  Query Match             91.1%;  Score 82;  DB 2;  Length 118;
  Best Local Similarity   88.2%;  Pred. No. 4.3e-06;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||| |||| |||||
Db         50 EIHPDSGTINYTPSLKD 66


RESULT 30
US-10-226-795-24
; Sequence 24, Application US/10226795
; Patent No. 6875433
; GENERAL INFORMATION:
;  APPLICANT: HART, MARY KATE
;  APPLICANT:  WILSON, JULIE
;  TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
;  TITLE OF INVENTION:  REGIONS BINDING TO EBOLA GLYCOPROTEIN
;  FILE REFERENCE: ARMY 166
;  CURRENT APPLICATION NUMBER: US/10/226,795
;  CURRENT FILING DATE:  2002-11-18
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
;   OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence
US-10-226-795-24

  Query Match             87.8%;  Score 79;  DB 2;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.4e-06;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db          1 EINPDSSTINYTPSLKD 17


RESULT 31
US-09-840-459-47
; Sequence 47, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
;  APPLICANT: LaRosa, Gregory J.
;  APPLICANT:  Horvath, Christopher
;  APPLICANT:  Newman, Walter
;  APPLICANT:  Jones, S. Tarran
;  APPLICANT:  O'Brien, Siobhan H.
;  APPLICANT:  O'Keefe, Theresa
;  TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
;  TITLE OF INVENTION:  METHODS OF USE THEREFOR
;  FILE REFERENCE: 1855.1052-012
```

```
;  CURRENT APPLICATION NUMBER: US/09/840,459
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: PCT/US01/03537
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 09/497,625
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: 09/359,193
;  PRIOR FILING DATE: 1999-07-22
;  PRIOR APPLICATION NUMBER: 09/121,781
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 47
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-840-459-47

  Query Match             87.8%;  Score 79;  DB 2;  Length 98;
  Best Local Similarity   88.2%;  Pred. No. 1.1e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         50 EINPDSSTINYTPSLKD 66


RESULT 32
US-09-497-625A-47
; Sequence 47, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
;  APPLICANT: LaRosa, Gregory J.
;  APPLICANT:  Horvath, Christopher
;  APPLICANT:  Newman, Walter
;  APPLICANT:  Jones, S. Tarran
;  APPLICANT:  O'Brien, Siobhan H.
;  APPLICANT:  O'Keefe, Theresa
;  TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
;  TITLE OF INVENTION:  METHODS OF USE THEREFOR
;  FILE REFERENCE: 1855.1052-004
;  CURRENT APPLICATION NUMBER: US/09/497,625A
;  CURRENT FILING DATE:  2000-02-03
;  PRIOR APPLICATION NUMBER: 09/359,193
;  PRIOR FILING DATE: 1999-07-22
;  PRIOR APPLICATION NUMBER: 09/121,781
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 47
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-497-625A-47

  Query Match             87.8%;  Score 79;  DB 2;  Length 98;
  Best Local Similarity   88.2%;  Pred. No. 1.1e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         50 EINPDSSTINYTPSLKD 66


RESULT 33
US-08-483-749A-18
; Sequence 18, Application US/08483749A
; Patent No. 6054561
;  GENERAL INFORMATION:
;    APPLICANT:  RING, DAVID B.
;    TITLE OF INVENTION:  ANTIGEN-BINDING SITES OF ANTIBODY
;    TITLE OF INVENTION:  MOLECULES SPECIFIC FOR CANCER ANTIGENS
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CHIRON CORPORATION
;      STREET:  INTELLECTUAL PROPERTY - R440, PO BOX 8097
;      CITY:  EMERYVILLE
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94662-8097
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/483,749A
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAVEREIDE, PAUL B.
;      REGISTRATION NUMBER:  36,914
;      REFERENCE/DOCKET NUMBER:  0508.008
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (510) 601-2585
;      TELEFAX:  (510) 655-3542
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  116 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-483-749A-18

  Query Match             87.8%;  Score 79;  DB 2;  Length 116;
  Best Local Similarity   88.2%;  Pred. No. 1.3e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         50 EINPDSSTINYTPSLKD 66


RESULT 34
US-07-958-140-3
; Sequence 3, Application US/07958140
; Patent No. 5489525
;  GENERAL INFORMATION:
;    APPLICANT:  Pastan, Ira H.
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES TO PROSTATE CELLS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend
;      STREET:  One Market Plaza, Steuart Street Tower
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/958,140
;      FILING DATE:  19921008
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parmelee, Steven W.
;      REGISTRATION NUMBER:  31,990
;      REFERENCE/DOCKET NUMBER:  15280-77
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 467-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
```

```
;      LENGTH:  117 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-07-958-140-3

  Query Match             87.8%;  Score 79;  DB 1;  Length 117;
  Best Local Similarity   88.2%;  Pred. No. 1.3e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         50 EINPDSSTINYTPSLKD 66


RESULT 35
PCT-US93-09166-3
; Sequence 3, Application PC/TUS9309166
;  GENERAL INFORMATION:
;    APPLICANT:  Pastan, Ira H.
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES TO PROSTATE CELLS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend
;      STREET:  One Market Plaza, Steuart Street Tower
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/09166
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parmelee, Steven W.
;      REGISTRATION NUMBER:  31,990
;      REFERENCE/DOCKET NUMBER:  15280-77
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 467-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  117 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US93-09166-3

  Query Match             87.8%;  Score 79;  DB 4;  Length 117;
  Best Local Similarity   88.2%;  Pred. No. 1.3e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         50 EINPDSSTINYTPSLKD 66


RESULT 36
US-10-226-795-22
; Sequence 22, Application US/10226795
; Patent No. 6875433
; GENERAL INFORMATION:
;  APPLICANT: HART, MARY KATE
;  APPLICANT:  WILSON, JULIE
;  TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND COMPLEMENTARITY-DETERMINING
;  TITLE OF INVENTION:  REGIONS BINDING TO EBOLA GLYCOPROTEIN
;  FILE REFERENCE: ARMY 166
;  CURRENT APPLICATION NUMBER: US/10/226,795
;  CURRENT FILING DATE:  2002-11-18
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;    LENGTH: 150
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy
;    OTHER INFORMATION: chain of Mab EGP6D8-1-2 amino acid sequence
US-10-226-795-22

  Query Match             87.8%;  Score 79;  DB 2;  Length 150;
  Best Local Similarity   88.2%;  Pred. No. 1.8e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         68 EINPDSSTINYTPSLKD 84


RESULT 37
US-07-958-140-2
; Sequence 2, Application US/07958140
; Patent No. 5489525
;  GENERAL INFORMATION:
;    APPLICANT:  Pastan, Ira H.
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES TO PROSTATE CELLS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend
;      STREET:  One Market Plaza, Steuart Street Tower
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/958,140
;      FILING DATE:  19921008
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parmelee, Steven W.
;      REGISTRATION NUMBER:  31,990
;      REFERENCE/DOCKET NUMBER:  15280-77
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 467-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  243 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-958-140-2

  Query Match             87.8%;  Score 79;  DB 1;  Length 243;
  Best Local Similarity   88.2%;  Pred. No. 3.2e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         51 EINPDSSTINYTPSLKD 67


RESULT 38
PCT-US93-09166-2
```

```
; Sequence 2, Application PC/TUS9309166
;  GENERAL INFORMATION:
;    APPLICANT:  Pastan, Ira H.
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES TO PROSTATE CELLS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend
;      STREET:  One Market Plaza, Steuart Street Tower
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/09166
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parmelee, Steven W.
;      REGISTRATION NUMBER:  31,990
;      REFERENCE/DOCKET NUMBER:  15280-77
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 467-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  243 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US93-09166-2

  Query Match             87.8%;  Score 79;  DB 4;  Length 243;
  Best Local Similarity   88.2%;  Pred. No. 3.2e-05;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||||| |||||
Db         51 EINPDSSTINYTPSLKD 67


RESULT 39
US-08-335-573-7
; Sequence 7, Application US/08335573
; Patent No. 5753229
;  GENERAL INFORMATION:
;    APPLICANT:  Mordoh, Jose
;    APPLICANT:  Leis De Cerrone, Silvia
;    APPLICANT:  Podhajcer, Osvaldo L.
;    APPLICANT:  Bravo, Alicia I.
;    TITLE OF INVENTION:  A PROCEDURE FOR PRODUCING MONOCLONAL
;    TITLE OF INVENTION:  ANTIBODIES AND SAID MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Darby & Darby
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/335,573
;      FILING DATE:  07-NOV-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  LERCH, JOSEPH B.
;      REGISTRATION NUMBER:  26,936
;      REFERENCE/DOCKET NUMBER:  0347/16898 US3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212)-527-7744
;      TELEFAX:  (212)-753-6237
;      TELEX:  236687
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  122 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  N-terminal
;    IMMEDIATE SOURCE:
;      CLONE:  V region of heavy chain
US-08-335-573-7

  Query Match             85.6%;  Score 77;  DB 1;  Length 122;
  Best Local Similarity   88.2%;  Pred. No. 3e-05;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              || |||||||| |||||
Db         49 EIDPDSSTINYTPSLKD 65


RESULT 40
US-09-840-459-52
; Sequence 52, Application US/09840459
; Patent No. 6696550
; GENERAL INFORMATION:
;  APPLICANT: LaRosa, Gregory J.
;  APPLICANT:  Horvath, Christopher
;  APPLICANT:  Newman, Walter
;  APPLICANT:  Jones, S. Tarran
;  APPLICANT:  O'Brien, Siobhan H.
;  APPLICANT:  O'Keefe, Theresa
;  TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
;  TITLE OF INVENTION:  METHODS OF USE THEREFOR
;  FILE REFERENCE: 1855.1052-012
;  CURRENT APPLICATION NUMBER: US/09/840,459
;  CURRENT FILING DATE:  2001-02-02
;  PRIOR APPLICATION NUMBER: PCT/US01/03537
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 09/497,625
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: 09/359,193
;  PRIOR FILING DATE: 1999-07-22
;  PRIOR APPLICATION NUMBER: 09/121,781
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 52
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-840-459-52

  Query Match             80.0%;  Score 72;  DB 2;  Length 98;
  Best Local Similarity   82.4%;  Pred. No. 0.00016;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:| |||||| |||||
Db         50 EINPGSSTINYTPSLKD 66


RESULT 41
```

```
US-09-497-625A-52
; Sequence 52, Application US/09497625A
; Patent No. 6727349
; GENERAL INFORMATION:
;  APPLICANT: LaRosa, Gregory J.
;  APPLICANT:  Horvath, Christopher
;  APPLICANT:  Newman, Walter
;  APPLICANT:  Jones, S. Tarran
;  APPLICANT:  O'Brien, Siobhan H.
;  APPLICANT:  O'Keefe, Theresa
;  TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
;  TITLE OF INVENTION:  METHODS OF USE THEREFOR
;  FILE REFERENCE: 1855.1052-004
;  CURRENT APPLICATION NUMBER: US/09/497,625A
;  CURRENT FILING DATE:  2000-02-03
;  PRIOR APPLICATION NUMBER: 09/359,193
;  PRIOR FILING DATE: 1999-07-22
;  PRIOR APPLICATION NUMBER: 09/121,781
;  PRIOR FILING DATE: 1998-07-23
;  NUMBER OF SEQ ID NOS: 106
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 52
;   LENGTH: 98
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-497-625A-52

  Query Match             80.0%;  Score 72;  DB 2;  Length 98;
  Best Local Similarity   82.4%;  Pred. No. 0.00016;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:| |||||| |||||
Db         50 EINPGSSTINYTPSLKD 66


RESULT 42
US-07-958-140-4
; Sequence 4, Application US/07958140
; Patent No. 5489525
;  GENERAL INFORMATION:
;    APPLICANT:  Pastan, Ira H.
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES TO PROSTATE CELLS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend
;      STREET:  One Market Plaza, Steuart Street Tower
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/958,140
;      FILING DATE:  19921008
;      CLASSIFICATION:  436
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parmelee, Steven W.
;      REGISTRATION NUMBER:  31,990
;      REFERENCE/DOCKET NUMBER:  15280-77
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 467-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  124 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-07-958-140-4

  Query Match             77.8%;  Score 70;  DB 1;  Length 124;
  Best Local Similarity   82.4%;  Pred. No. 0.00045;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||| | |||||
Db         50 EINPDSSTIIYTPSLKD 66


RESULT 43
PCT-US93-09166-4
; Sequence 4, Application PC/TUS9309166
;  GENERAL INFORMATION:
;    APPLICANT:  Pastan, Ira H.
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODIES TO PROSTATE CELLS
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend
;      STREET:  One Market Plaza, Steuart Street Tower
;      CITY:  San Francisco
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94105-1492
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/09166
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parmelee, Steven W.
;      REGISTRATION NUMBER:  31,990
;      REFERENCE/DOCKET NUMBER:  15280-77
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 467-9600
;      TELEFAX:  (415) 543-5043
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  124 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
PCT-US93-09166-4

  Query Match             77.8%;  Score 70;  DB 4;  Length 124;
  Best Local Similarity   82.4%;  Pred. No. 0.00045;
  Matches   14;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:|||||| | |||||
Db         50 EINPDSSTIIYTPSLKD 66


RESULT 44
US-09-136-315-2
; Sequence 2, Application US/09136315B
; Patent No. 6228360
; GENERAL INFORMATION:
;  APPLICANT: CO, MAN SUNG
;  APPLICANT: VASQUEZ, MAXIMILLIANO
;  TITLE OF INVENTION: ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND
;  TITLE OF INVENTION: FACTOR MONOCLONAL ANTIBODY
;  FILE REFERENCE: 0010-0933-0
;  CURRENT APPLICATION NUMBER: US/09/136,315B
;  CURRENT FILING DATE: 1998-08-19
;  NUMBER OF SEQ ID NOS: 8
```

```
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 139
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-136-315-2

  Query Match             76.7%;  Score 69;  DB 2;  Length 139;
  Best Local Similarity   64.7%;  Pred. No. 0.00075;
  Matches   11;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |::||::|:|| |||||
Db         68 EVNPDNNTMNYTPSLKD 84


RESULT 45
US-09-136-315-6
; Sequence 6, Application US/09136315B
; Patent No. 6228360
; GENERAL INFORMATION:
;  APPLICANT: CO, MAN SUNG
;  APPLICANT: VASQUEZ, MAXIMILLIANO
;  TITLE OF INVENTION: ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND
;  TITLE OF INVENTION: FACTOR MONOCLONAL ANTIBODY
;  FILE REFERENCE: 0010-0933-0
;  CURRENT APPLICATION NUMBER: US/09/136,315B
;  CURRENT FILING DATE: 1998-08-19
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 139
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-136-315-6

  Query Match             76.7%;  Score 69;  DB 2;  Length 139;
  Best Local Similarity   64.7%;  Pred. No. 0.00075;
  Matches   11;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |::||::|:|| |||||
Db         68 EVNPDNNTMNYTPSLKD 84


RESULT 46
US-09-767-888-2
; Sequence 2, Application US/09767888
; Patent No. 6613328
; GENERAL INFORMATION:
;  APPLICANT: CO, MAN SUNG
;  APPLICANT:  VASQUEZ, MAXIMILLIANO
;  TITLE OF INVENTION: ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND
;  TITLE OF INVENTION:  FACTOR MONOCLONAL ANTIBODY
;  FILE REFERENCE: 0010-0933-0
;  CURRENT APPLICATION NUMBER: US/09/767,888
;  CURRENT FILING DATE:  2001-01-24
;  PRIOR APPLICATION NUMBER: US/09/136,315
;  PRIOR FILING DATE: 1998-08-19
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 139
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-767-888-2

  Query Match             76.7%;  Score 69;  DB 2;  Length 139;
  Best Local Similarity   64.7%;  Pred. No. 0.00075;
  Matches   11;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |::||::|:|| |||||
Db         68 EVNPDNNTMNYTPSLKD 84


RESULT 47
US-09-767-888-6
; Sequence 6, Application US/09767888
; Patent No. 6613328
; GENERAL INFORMATION:
;  APPLICANT: CO, MAN SUNG
;  APPLICANT:  VASQUEZ, MAXIMILLIANO
;  TITLE OF INVENTION: ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND
;  TITLE OF INVENTION:  FACTOR MONOCLONAL ANTIBODY
;  FILE REFERENCE: 0010-0933-0
;  CURRENT APPLICATION NUMBER: US/09/767,888
;  CURRENT FILING DATE:  2001-01-24
;  PRIOR APPLICATION NUMBER: US/09/136,315
;  PRIOR FILING DATE: 1998-08-19
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 139
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-767-888-6

  Query Match             76.7%;  Score 69;  DB 2;  Length 139;
  Best Local Similarity   64.7%;  Pred. No. 0.00075;
  Matches   11;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |::||::|:|| |||||
Db         68 EVNPDNNTMNYTPSLKD 84


RESULT 48
US-08-480-434-34
; Sequence 34, Application US/08480434
; Patent No. 5811248
;  GENERAL INFORMATION:
;    APPLICANT:  Charles C. Ditlow, et al.
;    TITLE OF INVENTION:  ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
;    TITLE OF INVENTION:  ANTIBODIES THERETO, AND USES THEREOF
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,434
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Albert P. Halluin
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-053
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-3660
;      TELEFAX:  (415) 854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  19 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
US-08-480-434-34

  Query Match             75.6%;  Score 68;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 0.00011;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    2;  Gaps    1;

Qy          1 EIHP--DSSTINYAPSLKD 17
              ||:|  ||||||| |||||
Db          1 EINPKADSSTINYTPSLKD 19


RESULT 49
US-08-053-451B-34
; Sequence 34, Application US/08053451B
; Patent No. 5955584
;  GENERAL INFORMATION:
;    APPLICANT:  Chen, Francis W.
;    APPLICANT:  Ditlow, Charles C.
;    APPLICANT:  Calenoff, Emanuel
;    TITLE OF INVENTION:  ATHEROSCLEROTIC PLAQUE SPECIFIC
;    TITLE OF INVENTION:  ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
;    NUMBER OF SEQUENCES:  176
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/053,451B
;      FILING DATE:  26-APR-1993
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-033-999
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
US-08-053-451B-34

  Query Match             75.6%;  Score 68;  DB 1;  Length 19;
  Best Local Similarity   78.9%;  Pred. No. 0.00011;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    2;  Gaps    1;

Qy          1 EIHP--DSSTINYAPSLKD 17
              ||:|  ||||||| |||||
Db          1 EINPKADSSTINYTPSLKD 19


RESULT 50
US-08-480-434-30
; Sequence 30, Application US/08480434
; Patent No. 5811248
;  GENERAL INFORMATION:
;    APPLICANT:  Charles C. Ditlow, et al.
;    TITLE OF INVENTION:  ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
;    TITLE OF INVENTION:  ANTIBODIES THERETO, AND USES THEREOF
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/480,434
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Albert P. Halluin
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-053
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 854-3660
;      TELEFAX:  (415) 854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
US-08-480-434-30

  Query Match             75.6%;  Score 68;  DB 1;  Length 120;
  Best Local Similarity   78.9%;  Pred. No. 0.00092;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    2;  Gaps    1;

Qy          1 EIHP--DSSTINYAPSLKD 17
              ||:|  ||||||| |||||
Db         50 EINPKADSSTINYTPSLKD 68


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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:42:16 ; Search time 119.233 Seconds
(without alignments)
59.573 Million cell updates/sec

Title: US-10-755-382-24
Perfect score: 90
Sequence: 1 EIHPDSSTINYAPSLKD 17

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Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	90	100.0	119	3	US-09-253-794-2	Sequence 2, Appli
6	90	100.0	119	3	US-09-253-794-8	Sequence 8, Appli
7	90	100.0	119	3	US-09-253-794-9	Sequence 9, Appli
8	90	100.0	119	3	US-09-253-794-10	Sequence 10, Appl
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31	90	100.0	119	5	US-10-755-382-9	Sequence 9, Appli
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58	90	100.0	468	4	US-10-377-109-2	Sequence 2, Appli
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62	82	91.1	33	3	US-09-956-206A-28	Sequence 28, Appl
63	82	91.1	33	5	US-10-965-616-28	Sequence 28, Appl
64	79	87.8	17	3	US-09-995-529-28	Sequence 28, Appl
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68	79	87.8	17	5	US-10-842-011-31	Sequence 31, Appl
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70	79	87.8	98	4	US-10-766-773-47	Sequence 47, Appl
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81	79	87.8	142	6	US-11-013-537-35	Sequence 35, Appl
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83	79	87.8	215	4	US-10-683-815-5	Sequence 5, Appli
84	79	87.8	251	4	US-10-239-656-65	Sequence 65, Appl
85	79	87.8	252	4	US-10-239-656-55	Sequence 55, Appl
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87	79	87.8	258	4	US-10-239-656-71	Sequence 71, Appl
88	79	87.8	468	6	US-11-013-537-34	Sequence 34, Appl
89	79	87.8	499	4	US-10-239-656-73	Sequence 73, Appl
90	79	87.8	503	4	US-10-239-656-75	Sequence 75, Appl
91	79	87.8	505	4	US-10-239-656-79	Sequence 79, Appl
92	78	86.7	17	3	US-09-995-529-162	Sequence 162, App
93	78	86.7	17	3	US-09-995-529-162	Sequence 162, App
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95	76	84.4	17	3	US-09-995-529-51	Sequence 51, Appl
96	75	83.3	17	3	US-09-995-529-53	Sequence 53, Appl
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110	72	80.0	98	4	US-10-766-610-52	Sequence 52, Appl
111	72	80.0	98	4	US-10-733-563-52	Sequence 52, Appl
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113	71	78.9	17	3	US-09-995-529-154	Sequence 154, App
114	69	76.7	17	3	US-09-995-529-156	Sequence 156, App
115	69	76.7	17	3	US-09-995-529-156	Sequence 156, App
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122	69	76.7	140	5	US-10-491-653-16	Sequence 16, Appl
123	69	76.7	237	5	US-10-491-653-150	Sequence 150, App
124	68	75.6	17	3	US-09-995-529-155	Sequence 155, App
125	68	75.6	17	3	US-09-995-529-155	Sequence 155, App
126	62	68.9	17	3	US-09-995-529-49	Sequence 49, Appl
127	62	68.9	17	3	US-09-995-529-49	Sequence 49, Appl
128	59	65.6	126	5	US-10-828-559-95	Sequence 95, Appl
129	46	51.1	172	4	US-10-767-701-32789	Sequence 32789, A
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131	45	50.0	211	4	US-10-425-114-41309	Sequence 41309, A
132	45	50.0	566	6	US-11-097-143-12021	Sequence 12021, A
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134	44.5	49.4	250	6	US-11-017-030-22	Sequence 22, Appl
135	44	48.9	114	5	US-10-492-668-113	Sequence 113, App
136	44	48.9	114	5	US-10-492-668-116	Sequence 116, App
137	44	48.9	119	6	US-11-112-701-6	Sequence 6, Appli
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140	44	48.9	245	4	US-10-293-418-1902	Sequence 1902, Ap
141	44	48.9	252	4	US-10-479-670-167	Sequence 167, App
142	43	47.8	120	5	US-10-729-441-74	Sequence 74, Appl
143	43	47.8	120	5	US-10-897-406-74	Sequence 74, Appl
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145	43	47.8	382	4	US-10-282-122A-73650	Sequence 73650, A
146	43	47.8	397	4	US-10-424-599-241267	Sequence 241267,
147	43	47.8	535	4	US-10-425-115-267843	Sequence 267843,
148	43	47.8	580	4	US-10-425-114-53312	Sequence 53312, A
149	43	47.8	1102	5	US-10-450-763-59717	Sequence 59717, A
150	43	47.8	1456	5	US-10-450-763-59716	Sequence 59716, A
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154	42	46.7	47	3	US-09-986-480-200	Sequence 200, App
155	42	46.7	47	5	US-10-863-332-200	Sequence 200, App
156	42	46.7	103	4	US-10-630-406-2	Sequence 2, Appli
157	42	46.7	103	6	US-11-073-453-2	Sequence 2, Appli
158	42	46.7	169	4	US-10-424-599-196980	Sequence 196980,
159	42	46.7	180	5	US-10-504-582-109	Sequence 109, App
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163	42	46.7	265	5	US-10-450-763-32202	Sequence 32202, A
164	42	46.7	323	4	US-10-424-599-197424	Sequence 197424,
165	42	46.7	366	4	US-10-282-122A-51114	Sequence 51114, A
166	42	46.7	376	4	US-10-437-963-141658	Sequence 141658,
167	42	46.7	460	4	US-10-630-406-5	Sequence 5, Appli
168	42	46.7	460	6	US-11-073-453-5	Sequence 5, Appli
169	42	46.7	488	5	US-10-732-923-19741	Sequence 19741, A
170	42	46.7	521	4	US-10-094-749-2483	Sequence 2483, Ap
171	42	46.7	582	3	US-09-738-626-5406	Sequence 5406, Ap
172	42	46.7	1436	5	US-10-732-923-18422	Sequence 18422, A
173	42	46.7	1463	4	US-10-437-963-163410	Sequence 163410,
174	42	46.7	1855	4	US-10-334-143-21	Sequence 21, Appl
175	42	46.7	1871	4	US-10-144-194A-114	Sequence 114, App
176	42	46.7	1871	5	US-10-491-566-114	Sequence 114, App
177	42	46.7	1871	5	US-10-732-923-18421	Sequence 18421, A
178	42	46.7	1884	4	US-10-408-765A-283	Sequence 283, App
179	42	46.7	1884	5	US-10-732-923-18420	Sequence 18420, A
180	42	46.7	1884	5	US-10-756-149-5448	Sequence 5448, Ap
181	42	46.7	1906	4	US-10-144-194A-88	Sequence 88, Appl
182	42	46.7	1906	5	US-10-491-566-88	Sequence 88, Appl
183	41.5	46.1	117	5	US-10-727-155-18	Sequence 18, Appl
184	41.5	46.1	254	3	US-09-880-748-844	Sequence 844, App
185	41.5	46.1	254	4	US-10-293-418-844	Sequence 844, App
186	41.5	46.1	1116	4	US-10-332-284A-6	Sequence 6, Appli
187	41.5	46.1	1616	4	US-10-332-284A-8	Sequence 8, Appli
188	41	45.6	17	4	US-10-656-769-66	Sequence 66, Appl
189	41	45.6	17	5	US-10-996-316-122	Sequence 122, App
190	41	45.6	55	4	US-10-424-599-217574	Sequence 217574,
191	41	45.6	77	3	US-09-833-245-471	Sequence 471, App
192	41	45.6	88	4	US-10-803-622-172	Sequence 172, App
193	41	45.6	88	4	US-10-803-653-172	Sequence 172, App
194	41	45.6	96	3	US-09-905-243-15	Sequence 15, Appl
195	41	45.6	96	6	US-11-099-331-15	Sequence 15, Appl
196	41	45.6	97	4	US-10-425-115-256552	Sequence 256552,
197	41	45.6	116	3	US-09-726-258-50	Sequence 50, Appl
198	41	45.6	137	4	US-10-656-769-16	Sequence 16, Appl
199	41	45.6	172	4	US-10-425-115-214459	Sequence 214459,
200	41	45.6	173	4	US-10-437-963-132928	Sequence 132928,
201	41	45.6	214	4	US-10-424-599-218837	Sequence 218837,
202	41	45.6	222	4	US-10-424-599-197313	Sequence 197313,
203	41	45.6	226	4	US-10-425-114-43951	Sequence 43951, A
204	41	45.6	249	3	US-09-880-748-1957	Sequence 1957, Ap
205	41	45.6	249	4	US-10-293-418-1957	Sequence 1957, Ap
206	41	45.6	252	6	US-11-090-847-118	Sequence 118, App
207	41	45.6	277	5	US-10-450-763-34565	Sequence 34565, A
208	41	45.6	320	4	US-10-289-762-1208	Sequence 1208, Ap
209	41	45.6	400	6	US-11-097-143-27657	Sequence 27657, A
210	41	45.6	413	4	US-10-097-340-141	Sequence 141, App
211	41	45.6	413	5	US-10-723-860-736	Sequence 736, App
212	41	45.6	413	5	US-10-631-467-585	Sequence 585, App
213	41	45.6	413	6	US-11-050-926-141	Sequence 141, App
214	41	45.6	419	4	US-10-282-122A-55281	Sequence 55281, A
215	41	45.6	452	5	US-10-921-707-12	Sequence 12, Appl
216	41	45.6	463	4	US-10-656-769-34	Sequence 34, Appl
217	41	45.6	464	4	US-10-289-762-649	Sequence 649, App
218	41	45.6	464	4	US-10-282-122A-54743	Sequence 54743, A
219	41	45.6	464	4	US-10-656-769-36	Sequence 36, Appl
220	41	45.6	464	5	US-10-503-135-135	Sequence 135, App
221	41	45.6	467	4	US-10-656-769-32	Sequence 32, Appl
222	41	45.6	476	3	US-09-758-173-4	Sequence 4, Appli
223	41	45.6	476	3	US-09-948-429B-4	Sequence 4, Appli
224	41	45.6	476	4	US-10-124-905-4	Sequence 4, Appli
225	41	45.6	476	4	US-10-124-807-4	Sequence 4, Appli
226	41	45.6	476	4	US-10-291-532-4	Sequence 4, Appli
227	41	45.6	476	5	US-10-986-780-4	Sequence 4, Appli
228	41	45.6	483	4	US-10-369-493-16610	Sequence 16610, A
229	41	45.6	488	5	US-10-732-923-19776	Sequence 19776, A
230	41	45.6	499	4	US-10-331-061-11	Sequence 11, Appl
231	41	45.6	663	4	US-10-437-963-149153	Sequence 149153,
232	41	45.6	763	4	US-10-267-502-245	Sequence 245, App
233	41	45.6	763	6	US-11-097-143-20712	Sequence 20712, A
234	41	45.6	1207	4	US-10-437-963-111041	Sequence 111041,
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236	40.5	45.0	619	4	US-10-282-122A-65898	Sequence 65898, A
237	40.5	45.0	619	4	US-10-275-026A-28	Sequence 28, Appl
238	40	44.4	16	5	US-10-735-916A-10	Sequence 10, Appl
239	40	44.4	60	4	US-10-424-599-154519	Sequence 154519,
240	40	44.4	98	4	US-10-424-599-164690	Sequence 164690,
241	40	44.4	114	6	US-11-009-443-28	Sequence 28, Appl
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243	40	44.4	117	4	US-10-632-706-69	Sequence 69, Appl
244	40	44.4	117	5	US-10-735-916A-69	Sequence 69, Appl
245	40	44.4	117	5	US-10-735-916A-75	Sequence 75, Appl
246	40	44.4	117	5	US-10-735-916A-79	Sequence 79, Appl

247	40	44.4	117	5	US-10-735-916A-83	Sequence 83, Appl
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250	40	44.4	128	5	US-10-452-593-112	Sequence 112, App
251	40	44.4	135	5	US-10-735-916A-77	Sequence 77, Appl
252	40	44.4	135	5	US-10-735-916A-81	Sequence 81, Appl
253	40	44.4	135	5	US-10-735-916A-85	Sequence 85, Appl
254	40	44.4	148	4	US-10-424-599-276142	Sequence 276142,
255	40	44.4	190	4	US-10-425-115-196257	Sequence 196257,
256	40	44.4	245	3	US-09-880-748-1826	Sequence 1826, Ap
257	40	44.4	245	4	US-10-293-418-1826	Sequence 1826, Ap
258	40	44.4	250	3	US-09-880-748-1990	Sequence 1990, Ap
259	40	44.4	250	4	US-10-293-418-1990	Sequence 1990, Ap
260	40	44.4	264	4	US-10-080-170-289	Sequence 289, App
261	40	44.4	264	4	US-10-080-170-289	Sequence 289, App
262	40	44.4	264	4	US-10-468-356-289	Sequence 289, App
263	40	44.4	352	5	US-10-635-398-72	Sequence 72, Appl
264	40	44.4	361	5	US-10-739-930-6187	Sequence 6187, Ap
265	40	44.4	384	4	US-10-157-031-263	Sequence 263, App
266	40	44.4	384	4	US-10-021-660-77	Sequence 77, Appl
267	40	44.4	384	4	US-10-303-664A-21	Sequence 21, Appl
268	40	44.4	384	4	US-10-211-462-26	Sequence 26, Appl
269	40	44.4	384	4	US-10-322-281-12	Sequence 12, Appl
270	40	44.4	384	5	US-10-631-467-746	Sequence 746, App
271	40	44.4	386	4	US-10-173-999-119	Sequence 119, App
272	40	44.4	386	5	US-10-635-398-74	Sequence 74, Appl
273	40	44.4	386	5	US-10-635-398-76	Sequence 76, Appl
274	40	44.4	391	4	US-10-437-963-166359	Sequence 166359,
275	40	44.4	394	4	US-10-322-281-14	Sequence 14, Appl
276	40	44.4	425	6	US-11-097-143-19680	Sequence 19680, A
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280	40	44.4	807	4	US-10-675-226A-2	Sequence 2, Appli
281	40	44.4	1038	6	US-11-097-143-42540	Sequence 42540, A
282	40	44.4	1710	4	US-10-032-585-7238	Sequence 7238, Ap
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284	39.5	43.9	138	4	US-10-424-599-187030	Sequence 187030,
285	39.5	43.9	146	4	US-10-437-963-186172	Sequence 186172,
286	39.5	43.9	166	4	US-10-425-115-193303	Sequence 193303,
287	39.5	43.9	245	3	US-09-880-748-1864	Sequence 1864, Ap
288	39.5	43.9	245	4	US-10-293-418-1864	Sequence 1864, Ap
289	39.5	43.9	245	5	US-10-935-290-118	Sequence 118, App
290	39.5	43.9	313	4	US-10-369-493-2195	Sequence 2195, Ap
291	39.5	43.9	619	4	US-10-282-122A-65077	Sequence 65077, A
292	39.5	43.9	684	4	US-10-282-122A-47915	Sequence 47915, A
293	39.5	43.9	1116	4	US-10-332-284A-2	Sequence 2, Appli
294	39.5	43.9	1616	4	US-10-332-284A-4	Sequence 4, Appli
295	39	43.3	17	4	US-10-436-782-7	Sequence 7, Appli
296	39	43.3	17	4	US-10-844-424-114	Sequence 114, App
297	39	43.3	17	5	US-10-901-736-21	Sequence 21, Appl
298	39	43.3	17	6	US-11-004-795A-7	Sequence 7, Appli
299	39	43.3	17	6	US-11-004-794A-7	Sequence 7, Appli
300	39	43.3	38	6	US-11-013-537-42	Sequence 42, Appl
301	39	43.3	57	4	US-10-425-115-220951	Sequence 220951,
302	39	43.3	60	4	US-10-424-599-213663	Sequence 213663,
303	39	43.3	63	4	US-10-425-115-356987	Sequence 356987,
304	39	43.3	80	4	US-10-767-701-58402	Sequence 58402, A
305	39	43.3	100	3	US-09-905-243-50	Sequence 50, Appl
306	39	43.3	100	6	US-11-099-331-50	Sequence 50, Appl
307	39	43.3	116	4	US-10-767-701-35298	Sequence 35298, A
308	39	43.3	118	4	US-10-436-782-5	Sequence 5, Appli
309	39	43.3	118	6	US-11-004-795A-5	Sequence 5, Appli
310	39	43.3	118	6	US-11-004-794A-5	Sequence 5, Appli
311	39	43.3	124	4	US-10-251-085B-104	Sequence 104, App
312	39	43.3	124	4	US-10-251-085B-105	Sequence 105, App
313	39	43.3	124	4	US-10-737-252-104	Sequence 104, App
314	39	43.3	124	4	US-10-737-252-105	Sequence 105, App
315	39	43.3	124	4	US-10-844-424-18	Sequence 18, Appl
316	39	43.3	129	5	US-10-450-763-32415	Sequence 32415, A
317	39	43.3	130	5	US-10-450-763-54079	Sequence 54079, A
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319	39	43.3	133	4	US-10-466-242-3	Sequence 3, Appli
320	39	43.3	154	4	US-10-437-963-153066	Sequence 153066,
321	39	43.3	185	4	US-10-191-879-21	Sequence 21, Appl
322	39	43.3	204	4	US-10-191-879-6	Sequence 6, Appli
323	39	43.3	231	4	US-10-425-115-337515	Sequence 337515,
324	39	43.3	238	6	US-11-090-847-81	Sequence 81, Appl
325	39	43.3	241	4	US-10-480-172-12	Sequence 12, Appl
326	39	43.3	246	3	US-09-880-748-1847	Sequence 1847, Ap
327	39	43.3	246	4	US-10-293-418-1847	Sequence 1847, Ap
328	39	43.3	249	4	US-10-424-599-192190	Sequence 192190,
329	39	43.3	249	6	US-11-017-030-9	Sequence 9, Appli
330	39	43.3	250	6	US-11-090-847-121	Sequence 121, App
331	39	43.3	256	4	US-10-480-172-14	Sequence 14, Appl
332	39	43.3	260	6	US-11-090-847-112	Sequence 112, App
333	39	43.3	294	4	US-10-282-122A-61110	Sequence 61110, A
334	39	43.3	307	4	US-10-015-115-26	Sequence 26, Appl
335	39	43.3	319	4	US-10-015-115-22	Sequence 22, Appl
336	39	43.3	319	4	US-10-015-115-24	Sequence 24, Appl
337	39	43.3	334	4	US-10-282-122A-58232	Sequence 58232, A
338	39	43.3	334	5	US-10-795-159-626	Sequence 626, App
339	39	43.3	336	4	US-10-015-115-28	Sequence 28, Appl
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341	39	43.3	336	4	US-10-369-493-13731	Sequence 13731, A
342	39	43.3	336	4	US-10-282-122A-66798	Sequence 66798, A
343	39	43.3	336	4	US-10-332-947-53	Sequence 53, Appl
344	39	43.3	336	4	US-10-471-449-9	Sequence 9, Appli
345	39	43.3	336	4	US-10-480-172-8	Sequence 8, Appli
346	39	43.3	342	4	US-10-282-122A-50879	Sequence 50879, A
347	39	43.3	351	4	US-10-332-947-52	Sequence 52, Appl
348	39	43.3	353	4	US-10-032-585-7553	Sequence 7553, Ap
349	39	43.3	353	4	US-10-425-115-337516	Sequence 337516,
350	39	43.3	359	3	US-09-984-292-15	Sequence 15, Appl
351	39	43.3	359	3	US-09-984-292-23	Sequence 23, Appl
352	39	43.3	359	3	US-09-984-292-37	Sequence 37, Appl
353	39	43.3	359	3	US-09-989-497-15	Sequence 15, Appl
354	39	43.3	359	3	US-09-989-497-23	Sequence 23, Appl
355	39	43.3	359	3	US-09-989-497-37	Sequence 37, Appl
356	39	43.3	359	5	US-10-732-923-8002	Sequence 8002, Ap
357	39	43.3	359	5	US-10-952-773-15	Sequence 15, Appl
358	39	43.3	359	5	US-10-952-773-23	Sequence 23, Appl
359	39	43.3	359	5	US-10-952-773-37	Sequence 37, Appl
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361	39	43.3	367	5	US-10-631-467-1568	Sequence 1568, Ap
362	39	43.3	373	4	US-10-437-963-125070	Sequence 125070,
363	39	43.3	392	5	US-10-915-029-12	Sequence 12, Appl
364	39	43.3	393	4	US-10-424-599-263130	Sequence 263130,
365	39	43.3	482	4	US-10-425-115-337517	Sequence 337517,
366	39	43.3	496	3	US-09-808-483-14	Sequence 14, Appl
367	39	43.3	526	6	US-11-097-143-2760	Sequence 2760, Ap
368	39	43.3	538	4	US-10-425-114-53251	Sequence 53251, A
369	39	43.3	541	3	US-09-815-242-10746	Sequence 10746, A
370	39	43.3	552	5	US-10-741-849-7080	Sequence 7080, Ap
371	39	43.3	556	4	US-10-282-122A-49267	Sequence 49267, A
372	39	43.3	563	5	US-10-972-024-268	Sequence 268, App
373	39	43.3	568	4	US-10-424-599-152116	Sequence 152116,
374	39	43.3	573	4	US-10-437-963-170165	Sequence 170165,
375	39	43.3	579	4	US-10-437-963-131172	Sequence 131172,
376	39	43.3	600	4	US-10-424-599-196691	Sequence 196691,
377	39	43.3	626	3	US-09-712-363-151	Sequence 151, App
378	39	43.3	626	4	US-10-282-122A-62868	Sequence 62868, A
379	39	43.3	626	4	US-10-282-122A-64329	Sequence 64329, A
380	39	43.3	649	4	US-10-437-963-140038	Sequence 140038,
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383	39	43.3	728	4	US-10-036-492-5	Sequence 5, Appli
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385	39	43.3	804	5	US-10-450-763-59382	Sequence 59382, A
386	39	43.3	807	5	US-10-450-763-59024	Sequence 59024, A
387	39	43.3	1073	5	US-10-450-763-58958	Sequence 58958, A
388	39	43.3	1098	4	US-10-276-774-2074	Sequence 2074, Ap
389	39	43.3	1098	4	US-10-296-115-1235	Sequence 1235, Ap
390	39	43.3	1363	4	US-10-032-585-7800	Sequence 7800, Ap
391	39	43.3	1812	3	US-09-775-938A-38	Sequence 38, Appl
392	39	43.3	8601	5	US-10-496-377-7	Sequence 7, Appli

393	38.5	42.8	16	4	US-10-440-522-22	Sequence 22, Appl
394	38.5	42.8	16	4	US-10-396-578-69	Sequence 69, Appl
395	38.5	42.8	16	4	US-10-741-481-18	Sequence 18, Appl
396	38.5	42.8	16	6	US-11-074-803-69	Sequence 69, Appl
397	38.5	42.8	98	4	US-10-194-975-34	Sequence 34, Appl
398	38.5	42.8	98	4	US-10-308-817-77	Sequence 77, Appl
399	38.5	42.8	98	4	US-10-032-037B-98	Sequence 98, Appl
400	38.5	42.8	98	4	US-10-032-037B-99	Sequence 99, Appl
401	38.5	42.8	98	4	US-10-029-988B-98	Sequence 98, Appl
402	38.5	42.8	98	4	US-10-029-988B-99	Sequence 99, Appl
403	38.5	42.8	98	4	US-10-032-423A-98	Sequence 98, Appl
404	38.5	42.8	98	4	US-10-032-423A-99	Sequence 99, Appl
405	38.5	42.8	98	4	US-10-453-698-77	Sequence 77, Appl
406	38.5	42.8	98	4	US-10-029-926B-98	Sequence 98, Appl
407	38.5	42.8	98	4	US-10-029-926B-99	Sequence 99, Appl
408	38.5	42.8	98	4	US-10-038-591-34	Sequence 34, Appl
409	38.5	42.8	98	4	US-10-379-392-42	Sequence 42, Appl
410	38.5	42.8	98	4	US-10-775-444A-34	Sequence 34, Appl
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412	38.5	42.8	119	4	US-10-078-958-3	Sequence 3, Appli
413	38.5	42.8	119	4	US-10-779-461-142	Sequence 142, App
414	38.5	42.8	119	4	US-10-713-248-3	Sequence 3, Appli
415	38.5	42.8	119	4	US-10-713-248-7	Sequence 7, Appli
416	38.5	42.8	121	4	US-10-779-461-146	Sequence 146, App
417	38.5	42.8	121	4	US-10-779-461-150	Sequence 150, App
418	38.5	42.8	123	4	US-10-440-522-5	Sequence 5, Appli
419	38.5	42.8	128	4	US-10-741-481-2	Sequence 2, Appli
420	38.5	42.8	137	3	US-09-802-077-7	Sequence 7, Appli
421	38.5	42.8	137	3	US-09-802-096-7	Sequence 7, Appli
422	38.5	42.8	137	3	US-09-925-179-7	Sequence 7, Appli
423	38.5	42.8	137	5	US-10-968-237-7	Sequence 7, Appli
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427	38.5	42.8	248	4	US-10-779-461-31	Sequence 31, Appl
428	38.5	42.8	248	4	US-10-779-461-50	Sequence 50, Appl
429	38.5	42.8	248	4	US-10-779-461-53	Sequence 53, Appl
430	38.5	42.8	248	4	US-10-779-461-57	Sequence 57, Appl
431	38.5	42.8	248	4	US-10-779-461-58	Sequence 58, Appl
432	38.5	42.8	249	4	US-10-779-461-42	Sequence 42, Appl
433	38.5	42.8	249	4	US-10-779-461-54	Sequence 54, Appl
434	38.5	42.8	250	4	US-10-779-461-6	Sequence 6, Appli
435	38.5	42.8	250	4	US-10-779-461-22	Sequence 22, Appl
436	38.5	42.8	250	4	US-10-779-461-29	Sequence 29, Appl
437	38.5	42.8	250	4	US-10-779-461-52	Sequence 52, Appl
438	38.5	42.8	250	4	US-10-779-461-60	Sequence 60, Appl
439	38.5	42.8	251	4	US-10-779-461-25	Sequence 25, Appl
440	38.5	42.8	251	4	US-10-779-461-30	Sequence 30, Appl
441	38.5	42.8	251	4	US-10-779-461-36	Sequence 36, Appl
442	38.5	42.8	251	4	US-10-779-461-37	Sequence 37, Appl
443	38.5	42.8	251	4	US-10-779-461-48	Sequence 48, Appl
444	38.5	42.8	251	4	US-10-779-461-49	Sequence 49, Appl
445	38.5	42.8	251	4	US-10-779-461-51	Sequence 51, Appl
446	38.5	42.8	251	4	US-10-779-461-56	Sequence 56, Appl
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449	38.5	42.8	418	4	US-10-437-963-187650	Sequence 187650,
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451	38.5	42.8	453	4	US-10-425-115-271699	Sequence 271699,
452	38.5	42.8	455	4	US-10-425-114-63015	Sequence 63015, A
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483	38	42.2	242	5	US-10-732-923-651	Sequence 651, App
484	38	42.2	250	4	US-10-779-461-11	Sequence 11, Appl
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487	38	42.2	281	4	US-10-112-788-11	Sequence 11, Appl
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514	38	42.2	467	5	US-10-938-353-94	Sequence 94, Appl
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534	38	42.2	574	4	US-10-050-898-176	Sequence 176, App
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562	37.5	41.7	97	4	US-10-029-988B-87	Sequence 87, Appl
563	37.5	41.7	97	4	US-10-032-423A-87	Sequence 87, Appl
564	37.5	41.7	97	4	US-10-453-698-83	Sequence 83, Appl
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589	37.5	41.7	249	3	US-09-880-748-1321	Sequence 1321, Ap
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591	37.5	41.7	249	4	US-10-293-418-1321	Sequence 1321, Ap
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593	37.5	41.7	250	4	US-10-293-418-1413	Sequence 1413, Ap
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595	37.5	41.7	253	4	US-10-293-418-1333	Sequence 1333, Ap
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606	37.5	41.7	1022	4	US-10-301-822-163	Sequence 163, App
607	37.5	41.7	1022	4	US-10-648-593-244	Sequence 244, App
608	37.5	41.7	1022	5	US-10-753-267-52	Sequence 52, Appl
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647	37	41.1	98	4	US-10-029-926B-111	Sequence 111, App
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662	37	41.1	113	4	US-10-424-599-219386	Sequence 219386,
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725	37	41.1	350	4	US-10-369-493-2851	Sequence 2851, Ap
726	37	41.1	353	4	US-10-295-403-90	Sequence 90, Appl
727	37	41.1	353	4	US-10-412-699B-676	Sequence 676, App
728	37	41.1	359	4	US-10-424-599-264723	Sequence 264723,
729	37	41.1	366	4	US-10-437-963-181853	Sequence 181853,
730	37	41.1	372	4	US-10-320-797-3128	Sequence 3128, Ap
731	37	41.1	375	5	US-10-732-923-10359	Sequence 10359, A
732	37	41.1	379	4	US-10-437-963-194423	Sequence 194423,
733	37	41.1	379	5	US-10-732-923-2895	Sequence 2895, Ap
734	37	41.1	381	5	US-10-732-923-10325	Sequence 10325, A
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736	37	41.1	401	4	US-10-282-122A-45897	Sequence 45897, A
737	37	41.1	415	6	US-11-097-143-25320	Sequence 25320, A
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741	37	41.1	438	4	US-10-425-114-51149	Sequence 51149, A
742	37	41.1	440	4	US-10-437-963-172320	Sequence 172320,
743	37	41.1	443	4	US-10-425-115-221920	Sequence 221920,
744	37	41.1	454	4	US-10-156-761-14253	Sequence 14253, A
745	37	41.1	457	5	US-10-732-923-3057	Sequence 3057, Ap
746	37	41.1	458	5	US-10-732-923-3056	Sequence 3056, Ap
747	37	41.1	460	4	US-10-442-017-19	Sequence 19, Appl
748	37	41.1	460	4	US-10-442-017-20	Sequence 20, Appl
749	37	41.1	471	5	US-10-732-923-3060	Sequence 3060, Ap
750	37	41.1	472	5	US-10-732-923-3058	Sequence 3058, Ap
751	37	41.1	487	5	US-10-732-923-3059	Sequence 3059, Ap
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753	37	41.1	510	5	US-10-287-436A-624	Sequence 624, App
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755	37	41.1	530	4	US-10-425-114-52278	Sequence 52278, A
756	37	41.1	543	3	US-09-738-626-4285	Sequence 4285, Ap
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758	37	41.1	543	4	US-10-627-476-212	Sequence 212, App
759	37	41.1	543	6	US-11-073-550-6	Sequence 6, Appli
760	37	41.1	543	6	US-11-073-560-6	Sequence 6, Appli
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773	37	41.1	659	4	US-10-282-122A-60970	Sequence 60970, A
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884	37	41.1	839	4	US-10-238-196-54	Sequence 54, Appl
885	37	41.1	839	4	US-10-245-013-54	Sequence 54, Appl
886	37	41.1	839	4	US-10-211-858-36	Sequence 36, Appl
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895	37	41.1	1242	4	US-10-437-963-133094	Sequence 133094,
896	37	41.1	1427	4	US-10-282-122A-49525	Sequence 49525, A
897	37	41.1	1504	6	US-11-097-143-7866	Sequence 7866, Ap
898	37	41.1	1518	3	US-09-801-368-152	Sequence 152, App
899	37	41.1	1518	4	US-10-369-493-22243	Sequence 22243, A
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901	37	41.1	1620	5	US-10-745-237-200	Sequence 200, App
902	37	41.1	1774	4	US-10-437-963-106033	Sequence 106033,
903	37	41.1	1817	4	US-10-425-115-316186	Sequence 316186,
904	37	41.1	2103	4	US-10-437-963-123022	Sequence 123022,
905	37	41.1	2766	3	US-09-964-956-62	Sequence 62, Appl
906	37	41.1	2766	5	US-10-514-150-6	Sequence 6, Appli
907	37	41.1	5317	4	US-10-668-767-59	Sequence 59, Appl
908	36.5	40.6	94	4	US-10-767-701-37126	Sequence 37126, A
909	36.5	40.6	122	6	US-11-003-819-57	Sequence 57, Appl
910	36.5	40.6	132	3	US-09-773-876-7	Sequence 7, Appli
911	36.5	40.6	132	5	US-10-984-482-15	Sequence 15, Appl
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913	36.5	40.6	229	4	US-10-108-260A-3645	Sequence 3645, Ap
914	36.5	40.6	247	4	US-10-779-461-12	Sequence 12, Appl
915	36.5	40.6	247	4	US-10-779-461-39	Sequence 39, Appl
916	36.5	40.6	255	3	US-09-880-748-1642	Sequence 1642, Ap
917	36.5	40.6	255	4	US-10-293-418-1642	Sequence 1642, Ap
918	36.5	40.6	312	4	US-10-282-122A-73332	Sequence 73332, A
919	36.5	40.6	312	4	US-10-282-122A-75560	Sequence 75560, A
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922	36.5	40.6	423	4	US-10-369-493-10426	Sequence 10426, A
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924	36.5	40.6	674	4	US-10-437-963-204525	Sequence 204525,
925	36.5	40.6	867	4	US-10-389-532-2	Sequence 2, Appli
926	36.5	40.6	1002	6	US-11-135-597-189	Sequence 189, App
927	36.5	40.6	1029	4	US-10-437-963-114622	Sequence 114622,
928	36.5	40.6	1330	4	US-10-108-260A-3237	Sequence 3237, Ap
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931	36	40.0	17	4	US-10-727-737-28	Sequence 28, Appl
932	36	40.0	17	4	US-10-727-737-41	Sequence 41, Appl
933	36	40.0	17	4	US-10-844-424-70	Sequence 70, Appl
934	36	40.0	17	4	US-10-844-424-78	Sequence 78, Appl
935	36	40.0	17	5	US-10-769-308-33	Sequence 33, Appl
936	36	40.0	17	5	US-10-726-332-79	Sequence 79, Appl
937	36	40.0	17	5	US-10-726-332-97	Sequence 97, Appl
938	36	40.0	17	5	US-10-769-074-33	Sequence 33, Appl
939	36	40.0	17	5	US-10-949-135-22	Sequence 22, Appl
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944	36	40.0	62	3	US-09-983-802-231	Sequence 231, App
945	36	40.0	62	3	US-09-984-490-231	Sequence 231, App
946	36	40.0	64	4	US-10-424-599-175831	Sequence 175831,
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954	36	40.0	83	5	US-10-487-561-94	Sequence 94, Appl
955	36	40.0	87	4	US-10-425-115-320803	Sequence 320803,
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957	36	40.0	96	5	US-10-700-632-61	Sequence 61, Appl
958	36	40.0	97	4	US-10-194-975-49	Sequence 49, Appl
959	36	40.0	97	4	US-10-032-037B-86	Sequence 86, Appl
960	36	40.0	97	4	US-10-029-988B-86	Sequence 86, Appl
961	36	40.0	97	4	US-10-032-423A-86	Sequence 86, Appl
962	36	40.0	97	4	US-10-029-926B-86	Sequence 86, Appl
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964	36	40.0	98	5	US-10-884-830-665	Sequence 665, App
965	36	40.0	100	4	US-10-425-115-277772	Sequence 277772,
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968	36	40.0	108	4	US-10-425-115-196458	Sequence 196458,
969	36	40.0	113	4	US-10-231-417-163	Sequence 163, App
970	36	40.0	114	4	US-10-425-115-265176	Sequence 265176,
971	36	40.0	114	5	US-10-492-668-123	Sequence 123, App
972	36	40.0	116	5	US-10-492-668-126	Sequence 126, App
973	36	40.0	118	4	US-10-435-614-13	Sequence 13, Appl
974	36	40.0	119	4	US-10-412-703A-9	Sequence 9, Appli
975	36	40.0	119	4	US-10-412-703A-10	Sequence 10, Appl
976	36	40.0	119	4	US-10-412-703A-15	Sequence 15, Appl

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979	36	40.0	121	3	US-09-795-798-5	Sequence 5, Appli
980	36	40.0	121	4	US-10-727-737-5	Sequence 5, Appli
981	36	40.0	121	5	US-10-877-532-6	Sequence 6, Appli
982	36	40.0	123	6	US-11-003-819-61	Sequence 61, Appl
983	36	40.0	124	4	US-10-335-977-5605	Sequence 5605, Ap
984	36	40.0	124	4	US-10-844-424-123	Sequence 123, App
985	36	40.0	126	4	US-10-292-088-42	Sequence 42, Appl
986	36	40.0	126	4	US-10-767-701-33913	Sequence 33913, A
987	36	40.0	126	5	US-10-473-977-71	Sequence 71, Appl
988	36	40.0	126	5	US-10-949-135-18	Sequence 18, Appl
989	36	40.0	126	6	US-11-001-980-5	Sequence 5, Appli
990	36	40.0	127	4	US-10-425-115-299153	Sequence 299153,
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992	36	40.0	130	5	US-10-683-451-25	Sequence 25, Appl
993	36	40.0	136	4	US-10-437-963-204313	Sequence 204313,
994	36	40.0	137	4	US-10-425-115-323531	Sequence 323531,
995	36	40.0	139	4	US-10-767-701-51883	Sequence 51883, A
996	36	40.0	140	4	US-10-424-599-190986	Sequence 190986,
997	36	40.0	140	4	US-10-424-599-283151	Sequence 283151,
998	36	40.0	141	4	US-10-425-115-265814	Sequence 265814,
999	36	40.0	142	3	US-09-564-329A-13	Sequence 13, Appl
1000	36	40.0	142	3	US-09-855-153-13	Sequence 13, Appl

ALIGNMENTS

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RESULT 1
US-09-253-794-24
; Sequence 24, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 17 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-253-794-24

  Query Match            100.0%;  Score 90;  DB 3;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db          1 EIHPDSSTINYAPSLKD 17


RESULT 2
US-10-680-734-24
; Sequence 24, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 24
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-680-734-24

  Query Match            100.0%;  Score 90;  DB 4;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db          1 EIHPDSSTINYAPSLKD 17


RESULT 3
US-10-755-382-24
; Sequence 24, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
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;              APPLICATION NUMBER: US/09/253,794
;              FILING DATE: 22-Feb-1999
;              APPLICATION NUMBER: US 08/318,157
;              FILING DATE: 05-OCT-1994
;         ATTORNEY/AGENT INFORMATION:
;              NAME: SAXE, Bernhard D.
;              REGISTRATION NUMBER: 28,665
;              REFERENCE/DOCKET NUMBER: 18733/464
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (202)672-5300
;              TELEFAX: (202)672-5399
;              TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 24:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 17 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: <Unknown>
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-755-382-24

  Query Match           100.0%;  Score 90;  DB 5;  Length 17;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-07;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db          1 EIHPDSSTINYAPSLKD 17


RESULT 4
US-10-270-073-3
; Sequence 3, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14VH deduced amino acid sequence
US-10-270-073-3

  Query Match           100.0%;  Score 90;  DB 4;  Length 118;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 5
US-09-253-794-2
; Sequence 2, Application US/09253794
; Patent No. US20020018750A1
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-253-794-2

  Query Match           100.0%;  Score 90;  DB 3;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 6
US-09-253-794-8
; Sequence 8, Application US/09253794
; Patent No. US20020018750A1
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
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;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-253-794-8

  Query Match             100.0%;  Score 90;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 7
US-09-253-794-9
; Sequence 9, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-253-794-9

  Query Match             100.0%;  Score 90;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 8
US-09-253-794-10
; Sequence 10, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 10:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-253-794-10

  Query Match             100.0%;  Score 90;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66
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RESULT 9
US-09-253-794-11
; Sequence 11, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-253-794-11

  Query Match             100.0%;  Score 90;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 10
US-09-253-794-12
; Sequence 12, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-253-794-12

  Query Match             100.0%;  Score 90;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 11
US-09-253-794-13
; Sequence 13, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
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;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-253-794-13

  Query Match             100.0%;  Score 90;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 12
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

  Query Match             100.0%;  Score 90;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 13
US-09-253-794-15
; Sequence 15, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-253-794-15

  Query Match             100.0%;  Score 90;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 14
US-09-253-794-17
; Sequence 17, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
```

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;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-253-794-17

  Query Match             100.0%;  Score 90;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 15
US-09-253-794-57
; Sequence 57, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 57:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-253-794-57

  Query Match             100.0%;  Score 90;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 16
US-09-253-794-58
; Sequence 58, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 58:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-253-794-58
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  Query Match           100.0%;  Score 90;  DB 3;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 17
US-10-680-734-2
; Sequence 2, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-680-734-2

  Query Match           100.0%;  Score 90;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 18
US-10-680-734-8
; Sequence 8, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-8

  Query Match           100.0%;  Score 90;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 19
US-10-680-734-9
; Sequence 9, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-9

  Query Match           100.0%;  Score 90;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 20
US-10-680-734-10
; Sequence 10, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-10

  Query Match           100.0%;  Score 90;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 21
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US-10-680-734-11
; Sequence 11, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 11
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-11

  Query Match            100.0%;  Score 90;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 22
US-10-680-734-12
; Sequence 12, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-12

  Query Match            100.0%;  Score 90;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 23
US-10-680-734-13
; Sequence 13, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-13

  Query Match            100.0%;  Score 90;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 24
US-10-680-734-14
; Sequence 14, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-14

  Query Match            100.0%;  Score 90;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 25
US-10-680-734-15
; Sequence 15, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
```

```
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-15

  Query Match             100.0%;  Score 90;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 26
US-10-680-734-17
; Sequence 17, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-17

  Query Match             100.0%;  Score 90;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 27
US-10-680-734-26
; Sequence 26, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 26
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-26

  Query Match             100.0%;  Score 90;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 28
US-10-680-734-27
; Sequence 27, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 27
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-27

  Query Match             100.0%;  Score 90;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 29
US-10-755-382-2
; Sequence 2, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;
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;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/755,382
;            FILING DATE: 13-Jan-2004
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-755-382-2

  Query Match             100.0%;  Score 90;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 30
US-10-755-382-8
; Sequence 8, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/755,382
;            FILING DATE: 13-Jan-2004
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-755-382-8

  Query Match             100.0%;  Score 90;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 31
US-10-755-382-9
; Sequence 9, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/755,382
;            FILING DATE: 13-Jan-2004
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-755-382-9

  Query Match             100.0%;  Score 90;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 32
US-10-755-382-10
; Sequence 10, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-755-382-10

  Query Match            100.0%;  Score 90;  DB 5;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 33
US-10-755-382-11
; Sequence 11, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-755-382-11

  Query Match            100.0%;  Score 90;  DB 5;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 34
US-10-755-382-12
; Sequence 12, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;
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;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-755-382-12

  Query Match             100.0%;  Score 90;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 35
US-10-755-382-13
; Sequence 13, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-755-382-13

  Query Match             100.0%;  Score 90;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 36
US-10-755-382-14
; Sequence 14, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-755-382-14

  Query Match             100.0%;  Score 90;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
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              ||||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 37
US-10-755-382-15
; Sequence 15, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-755-382-15

  Query Match             100.0%;  Score 90;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 38
US-10-755-382-17
; Sequence 17, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-755-382-17

  Query Match             100.0%;  Score 90;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 39
US-10-755-382-57
; Sequence 57, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
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;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 57:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-755-382-57

  Query Match            100.0%;  Score 90;  DB 5;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 40
US-10-755-382-58
; Sequence 58, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 58:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-755-382-58

  Query Match            100.0%;  Score 90;  DB 5;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         50 EIHPDSSTINYAPSLKD 66


RESULT 41
US-10-006-771A-4
; Sequence 4, Application US/10006771A
; Publication No. US20020165360A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen
;  FILE REFERENCE: 002
;  CURRENT APPLICATION NUMBER: US/10/006,771A
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: 60/250,090
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 138
;   TYPE: PRT
;   ORGANISM: Homo sapiens and Mus sp.
US-10-006-771A-4

  Query Match            100.0%;  Score 90;  DB 4;  Length 138;
  Best Local Similarity  100.0%;  Pred. No. 2.2e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         69 EIHPDSSTINYAPSLKD 85


RESULT 42
US-10-270-073-6
; Sequence 6, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14-0 amino acid sequence
US-10-270-073-6
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  Query Match             100.0%;  Score 90;  DB 4;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 43
US-10-270-073-8
; Sequence 8, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 257
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14-1G amino acid sequence
US-10-270-073-8

  Query Match             100.0%;  Score 90;  DB 4;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 44
US-10-270-071-18
; Sequence 18, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of hMN14VK
US-10-270-071-18

  Query Match             100.0%;  Score 90;  DB 4;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 45
US-10-270-073-2
; Sequence 2, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14scFv-L5 amino acid sequence
US-10-270-073-2

  Query Match             100.0%;  Score 90;  DB 4;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 46
US-10-328-190-6
; Sequence 6, Application US/10328190
; Publication No. US20030162709A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID M.
;  TITLE OF INVENTION: METHODS OF GENERATING MULTISPECIFIC, MULTIVALENT AGENTS
;  TITLE OF INVENTION:  FROM VH AND VL DOMAINS
;  FILE REFERENCE: 042418/0115
;  CURRENT APPLICATION NUMBER: US/10/328,190
;  CURRENT FILING DATE:  2003-04-03
;  PRIOR APPLICATION NUMBER: 60/342,103
;  PRIOR FILING DATE: 2001-12-26
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
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;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: hMN14-scFv-L5
;   OTHER INFORMATION: protein sequence
US-10-328-190-6

  Query Match             100.0%;  Score 90;  DB 4;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 4.6e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 47
US-10-270-071-22
; Sequence 22, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
;   LENGTH: 267
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of polypeptide 2 of BS1
US-10-270-071-22

  Query Match             100.0%;  Score 90;  DB 4;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 48
US-10-270-071-26
; Sequence 26, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
;   LENGTH: 267
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of polypeptide 2 of BS1.5
US-10-270-071-26

  Query Match             100.0%;  Score 90;  DB 4;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 49
US-10-270-071-30
; Sequence 30, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
;   LENGTH: 267
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of polypeptide 2 of BS2
US-10-270-071-30

  Query Match             100.0%;  Score 90;  DB 4;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-06;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89


RESULT 50
US-10-270-071-36
; Sequence 36, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
;   LENGTH: 267
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence for polypetide 1 of BS1.5H (h679XhMN14 bispecific
;   OTHER INFORMATION: diabody)
US-10-270-071-36
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Query Match 100.0%; Score 90; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 4.7e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 EIHPDSSTINYAPSLKD 17
              |||||||||||||||||
Db         73 EIHPDSSTINYAPSLKD 89
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Search completed: March 23, 2006, 02:52:33
Job time : 129.376 secs

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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:44:01 ; Search time 14.4384 Seconds
(without alignments)
33.701 Million cell updates/sec

Title: US-10-755-382-24
Perfect score: 90
Sequence: 1 EIHPDSSTINYAPSLKD 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	83	92.2	119	6	US-10-982-357-41	Sequence 41, Appl
2	83	92.2	119	6	US-10-982-357-47	Sequence 47, Appl
3	79	87.8	17	6	US-10-982-357-16	Sequence 16, Appl
4	79	87.8	17	6	US-10-982-357-31	Sequence 31, Appl
5	79	87.8	119	6	US-10-982-357-5	Sequence 5, Appli
6	79	87.8	119	6	US-10-982-357-38	Sequence 38, Appl
7	79	87.8	119	6	US-10-982-357-45	Sequence 45, Appl
8	79	87.8	137	6	US-10-982-357-27	Sequence 27, Appl
9	68	75.6	17	7	US-11-105-708-21	Sequence 21, Appl
10	46	51.1	521	6	US-10-858-730-287	Sequence 287, App
11	44	48.9	119	7	US-11-112-481C-9	Sequence 9, Appli
12	44	48.9	245	7	US-11-054-515-1902	Sequence 1902, Ap
13	43	47.8	120	6	US-10-932-334-74	Sequence 74, Appl
14	43	47.8	389	6	US-10-517-939-136	Sequence 136, App
15	42	46.7	124	6	US-10-771-257-19	Sequence 19, Appl
16	42	46.7	124	7	US-11-127-677-19	Sequence 19, Appl
17	42	46.7	394	7	US-11-096-568A-8620	Sequence 8620, Ap
18	42	46.7	398	7	US-11-096-568A-8619	Sequence 8619, Ap
19	41.5	46.1	254	7	US-11-054-515-844	Sequence 844, App
20	41	45.6	138	7	US-11-089-872-3	Sequence 3, Appli
21	41	45.6	211	7	US-11-096-568A-3877	Sequence 3877, Ap
22	41	45.6	214	7	US-11-096-568A-3876	Sequence 3876, Ap
23	41	45.6	249	7	US-11-054-515-1957	Sequence 1957, Ap
24	41	45.6	476	7	US-11-139-499-4	Sequence 4, Appli
25	40	44.4	16	7	US-11-012-353-10	Sequence 10, Appl
26	40	44.4	117	7	US-11-012-353-69	Sequence 69, Appl
27	40	44.4	117	7	US-11-012-353-75	Sequence 75, Appl
28	40	44.4	117	7	US-11-012-353-79	Sequence 79, Appl
29	40	44.4	117	7	US-11-012-353-83	Sequence 83, Appl
30	40	44.4	127	7	US-11-012-353-52	Sequence 52, Appl
31	40	44.4	135	7	US-11-012-353-77	Sequence 77, Appl
32	40	44.4	135	7	US-11-012-353-81	Sequence 81, Appl
33	40	44.4	135	7	US-11-012-353-85	Sequence 85, Appl
34	40	44.4	245	7	US-11-054-515-1826	Sequence 1826, Ap
35	40	44.4	250	7	US-11-054-515-1990	Sequence 1990, Ap
36	40	44.4	290	7	US-11-098-686-10788	Sequence 10788, A
37	40	44.4	384	6	US-10-501-035-209	Sequence 209, App
38	40	44.4	387	6	US-10-510-386-212	Sequence 212, App
39	39.5	43.9	245	7	US-11-054-515-1864	Sequence 1864, Ap
40	39.5	43.9	668	6	US-10-467-657-5042	Sequence 5042, Ap
41	39	43.3	17	7	US-11-157-494-7	Sequence 7, Appli
42	39	43.3	17	7	US-11-157-494-8	Sequence 8, Appli
43	39	43.3	117	7	US-11-157-494-27	Sequence 27, Appl
44	39	43.3	117	7	US-11-157-494-28	Sequence 28, Appl
45	39	43.3	130	6	US-10-993-543-56	Sequence 56, Appl
46	39	43.3	205	7	US-11-096-568A-28652	Sequence 28652, A
47	39	43.3	223	7	US-11-096-568A-28651	Sequence 28651, A
48	39	43.3	246	7	US-11-054-515-1847	Sequence 1847, Ap
49	39	43.3	253	6	US-10-453-372-288	Sequence 288, App
50	39	43.3	271	7	US-11-195-739-3	Sequence 3, Appli
51	39	43.3	307	6	US-10-453-372-298	Sequence 298, App
52	39	43.3	309	6	US-10-453-372-302	Sequence 302, App
53	39	43.3	309	6	US-10-453-372-306	Sequence 306, App
54	39	43.3	315	6	US-10-453-372-290	Sequence 290, App
55	39	43.3	319	6	US-10-453-372-292	Sequence 292, App
56	39	43.3	319	6	US-10-453-372-296	Sequence 296, App
57	39	43.3	319	6	US-10-453-372-300	Sequence 300, App
58	39	43.3	320	6	US-10-453-372-312	Sequence 312, App
59	39	43.3	325	6	US-10-453-372-286	Sequence 286, App
60	39	43.3	325	6	US-10-453-372-294	Sequence 294, App
61	39	43.3	336	6	US-10-453-372-282	Sequence 282, App
62	39	43.3	336	6	US-10-453-372-304	Sequence 304, App
63	39	43.3	336	6	US-10-453-372-308	Sequence 308, App
64	39	43.3	336	6	US-10-453-372-310	Sequence 310, App
65	39	43.3	336	6	US-10-453-372-314	Sequence 314, App
66	39	43.3	336	6	US-10-453-372-316	Sequence 316, App
67	39	43.3	336	6	US-10-453-372-318	Sequence 318, App
68	39	43.3	344	6	US-10-453-372-284	Sequence 284, App
69	39	43.3	363	7	US-11-096-568A-28650	Sequence 28650, A
70	39	43.3	600	7	US-11-087-099-5756	Sequence 5756, Ap
71	39	43.3	716	7	US-11-239-325-11	Sequence 11, Appl
72	39	43.3	728	7	US-11-239-325-5	Sequence 5, Appli
73	39	43.3	859	7	US-11-053-100-52	Sequence 52, Appl
74	39	43.3	1309	7	US-11-053-100-53	Sequence 53, Appl
75	38.5	42.8	21	7	US-11-149-943-39	Sequence 39, Appl
76	38.5	42.8	98	7	US-11-144-248-34	Sequence 34, Appl
77	38.5	42.8	98	7	US-11-054-669-34	Sequence 34, Appl
78	38.5	42.8	98	7	US-11-144-222-34	Sequence 34, Appl
79	38.5	42.8	98	7	US-11-004-590-39	Sequence 39, Appl
80	38.5	42.8	98	7	US-11-182-343-34	Sequence 34, Appl
81	38.5	42.8	118	6	US-10-834-397-25	Sequence 25, Appl
82	38.5	42.8	430	7	US-11-096-568A-24054	Sequence 24054, A
83	38.5	42.8	452	7	US-11-096-568A-24053	Sequence 24053, A
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85	38	42.2	119	7	US-11-112-481C-11	Sequence 11, Appl
86	38	42.2	124	7	US-11-049-536-210	Sequence 210, App
87	38	42.2	248	7	US-11-096-568A-15984	Sequence 15984, A
88	38	42.2	297	6	US-10-793-626-2634	Sequence 2634, Ap
89	38	42.2	478	7	US-11-139-499-8	Sequence 8, Appli
90	38	42.2	574	6	US-10-493-909-45	Sequence 45, Appl
91	38	42.2	724	7	US-11-087-099-10669	Sequence 10669, A
92	38	42.2	808	7	US-11-087-099-7073	Sequence 7073, Ap
93	38	42.2	863	6	US-10-793-626-2010	Sequence 2010, Ap
94	38	42.2	1431	7	US-11-128-059-2	Sequence 2, Appli
95	37.5	41.7	21	7	US-11-149-943-44	Sequence 44, Appl
96	37.5	41.7	97	7	US-11-054-669-40	Sequence 40, Appl
97	37.5	41.7	97	7	US-11-004-590-44	Sequence 44, Appl
98	37.5	41.7	97	7	US-11-157-494-41	Sequence 41, Appl

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101	37.5	41.7	249	7	US-11-054-515-957	Sequence 957, App
102	37.5	41.7	249	7	US-11-054-515-1321	Sequence 1321, Ap
103	37.5	41.7	250	7	US-11-054-515-1413	Sequence 1413, Ap
104	37.5	41.7	253	7	US-11-054-515-1333	Sequence 1333, Ap
105	37.5	41.7	254	7	US-11-054-515-1659	Sequence 1659, Ap
106	37.5	41.7	302	7	US-11-087-099-2921	Sequence 2921, Ap
107	37.5	41.7	404	7	US-11-031-206-56	Sequence 56, Appl
108	37.5	41.7	431	6	US-10-525-674-26	Sequence 26, Appl
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110	37.5	41.7	1022	7	US-11-186-284-163	Sequence 163, App
111	37.5	41.7	1022	7	US-11-072-175-244	Sequence 244, App
112	37	41.1	17	6	US-10-665-658-41	Sequence 41, Appl
113	37	41.1	17	6	US-10-665-658-45	Sequence 45, Appl
114	37	41.1	17	6	US-10-665-658-48	Sequence 48, Appl
115	37	41.1	17	7	US-11-009-939-14	Sequence 14, Appl
116	37	41.1	22	7	US-11-149-943-30	Sequence 30, Appl
117	37	41.1	22	7	US-11-149-943-50	Sequence 50, Appl
118	37	41.1	98	7	US-11-054-669-28	Sequence 28, Appl
119	37	41.1	98	7	US-11-084-554-39	Sequence 39, Appl
120	37	41.1	98	7	US-11-004-590-30	Sequence 30, Appl
121	37	41.1	98	7	US-11-004-590-50	Sequence 50, Appl
122	37	41.1	98	7	US-11-136-250-39	Sequence 39, Appl
123	37	41.1	118	7	US-11-009-939-12	Sequence 12, Appl
124	37	41.1	119	7	US-11-049-536-474	Sequence 474, App
125	37	41.1	123	6	US-10-771-257-59	Sequence 59, Appl
126	37	41.1	123	7	US-11-127-677-57	Sequence 57, Appl
127	37	41.1	129	7	US-11-064-174-143	Sequence 143, App
128	37	41.1	219	7	US-11-087-099-1596	Sequence 1596, Ap
129	37	41.1	243	7	US-11-054-515-2102	Sequence 2102, Ap
130	37	41.1	248	7	US-11-054-515-2088	Sequence 2088, Ap
131	37	41.1	253	7	US-11-054-515-1418	Sequence 1418, Ap
132	37	41.1	253	7	US-11-054-515-1672	Sequence 1672, Ap
133	37	41.1	271	7	US-11-195-739-4	Sequence 4, Appli
134	37	41.1	348	7	US-11-174-816-11	Sequence 11, Appl
135	37	41.1	543	6	US-10-858-730-221	Sequence 221, App
136	37	41.1	645	7	US-11-087-099-2510	Sequence 2510, Ap
137	37	41.1	653	7	US-11-087-099-8946	Sequence 8946, Ap
138	37	41.1	1518	7	US-11-087-099-1886	Sequence 1886, Ap
139	37	41.1	2204	7	US-11-052-554A-174	Sequence 174, App
140	37	41.1	2766	6	US-10-877-346-62	Sequence 62, Appl
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142	36.5	40.6	625	7	US-11-055-822-522	Sequence 522, App
143	36	40.0	17	6	US-10-665-658-11	Sequence 11, Appl
144	36	40.0	17	6	US-10-665-658-32	Sequence 32, Appl
145	36	40.0	17	6	US-10-665-658-34	Sequence 34, Appl
146	36	40.0	17	6	US-10-665-658-47	Sequence 47, Appl
147	36	40.0	97	7	US-11-054-669-49	Sequence 49, Appl
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149	36	40.0	119	7	US-11-049-536-498	Sequence 498, App
150	36	40.0	119	7	US-11-049-536-662	Sequence 662, App
151	36	40.0	121	6	US-10-665-658-5	Sequence 5, Appli
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153	36	40.0	121	7	US-11-149-031-2	Sequence 2, Appli
154	36	40.0	126	7	US-11-049-536-322	Sequence 322, App
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161	36	40.0	217	6	US-10-467-657-552	Sequence 552, App
162	36	40.0	217	6	US-10-467-657-986	Sequence 986, App
163	36	40.0	217	6	US-10-467-657-2356	Sequence 2356, Ap
164	36	40.0	217	6	US-10-467-657-2380	Sequence 2380, Ap
165	36	40.0	217	6	US-10-467-657-3800	Sequence 3800, Ap
166	36	40.0	217	6	US-10-467-657-3930	Sequence 3930, Ap
167	36	40.0	217	6	US-10-467-657-4018	Sequence 4018, Ap
168	36	40.0	217	6	US-10-467-657-4240	Sequence 4240, Ap
169	36	40.0	217	6	US-10-467-657-4438	Sequence 4438, Ap
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172	36	40.0	217	6	US-10-467-657-6518	Sequence 6518, Ap
173	36	40.0	217	6	US-10-467-657-8044	Sequence 8044, Ap
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179	36	40.0	277	6	US-10-996-007B-14	Sequence 14, Appl
180	36	40.0	277	6	US-10-996-007B-16	Sequence 16, Appl
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183	36	40.0	437	7	US-11-096-568A-30320	Sequence 30320, A
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185	36	40.0	533	7	US-11-098-686-10529	Sequence 10529, A
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189	36	40.0	898	7	US-11-124-367A-330	Sequence 330, App
190	36	40.0	898	7	US-11-124-367A-333	Sequence 333, App
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193	35.5	39.4	216	7	US-11-087-099-3889	Sequence 3889, Ap
194	35.5	39.4	216	7	US-11-087-099-4047	Sequence 4047, Ap
195	35.5	39.4	216	7	US-11-087-099-8051	Sequence 8051, Ap
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199	35	38.9	16	7	US-11-102-424-24	Sequence 24, Appl
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203	35	38.9	21	7	US-11-149-943-47	Sequence 47, Appl
204	35	38.9	22	7	US-11-149-943-37	Sequence 37, Appl
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208	35	38.9	97	7	US-11-054-669-51	Sequence 51, Appl
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213	35	38.9	97	7	US-11-144-222-36	Sequence 36, Appl
214	35	38.9	97	7	US-11-144-222-44	Sequence 44, Appl
215	35	38.9	97	7	US-11-004-590-46	Sequence 46, Appl
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217	35	38.9	97	7	US-11-136-250-54	Sequence 54, Appl
218	35	38.9	97	7	US-11-182-343-36	Sequence 36, Appl
219	35	38.9	97	7	US-11-182-343-44	Sequence 44, Appl
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221	35	38.9	98	5	US-09-978-360A-681	Sequence 681, App
222	35	38.9	98	7	US-11-054-669-33	Sequence 33, Appl
223	35	38.9	98	7	US-11-084-554-47	Sequence 47, Appl
224	35	38.9	98	7	US-11-004-590-37	Sequence 37, Appl
225	35	38.9	98	7	US-11-136-250-47	Sequence 47, Appl
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227	35	38.9	99	7	US-11-084-554-55	Sequence 55, Appl
228	35	38.9	99	7	US-11-004-590-47	Sequence 47, Appl
229	35	38.9	99	7	US-11-136-250-55	Sequence 55, Appl
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231	35	38.9	113	7	US-11-144-222-20	Sequence 20, Appl
232	35	38.9	113	7	US-11-182-343-20	Sequence 20, Appl
233	35	38.9	116	7	US-11-102-424-5	Sequence 5, Appli
234	35	38.9	116	7	US-11-102-424-6	Sequence 6, Appli
235	35	38.9	116	7	US-11-102-424-9	Sequence 9, Appli
236	35	38.9	116	7	US-11-102-424-10	Sequence 10, Appl
237	35	38.9	116	7	US-11-102-424-12	Sequence 12, Appl
238	35	38.9	116	7	US-11-112-481C-7	Sequence 7, Appli
239	35	38.9	118	7	US-11-157-494-26	Sequence 26, Appl
240	35	38.9	119	6	US-10-834-397-39	Sequence 39, Appl
241	35	38.9	119	6	US-10-834-397-65	Sequence 65, Appl
242	35	38.9	119	7	US-11-105-268-21	Sequence 21, Appl
243	35	38.9	158	7	US-11-096-568A-20737	Sequence 20737, A
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247	35	38.9	249	7	US-11-054-515-1312	Sequence 1312, Ap
248	35	38.9	249	7	US-11-054-515-1720	Sequence 1720, Ap
249	35	38.9	250	7	US-11-054-515-1645	Sequence 1645, Ap
250	35	38.9	250	7	US-11-054-515-1952	Sequence 1952, Ap
251	35	38.9	251	7	US-11-054-515-1316	Sequence 1316, Ap
252	35	38.9	254	7	US-11-096-568A-20736	Sequence 20736, A
253	35	38.9	255	7	US-11-054-515-841	Sequence 841, App
254	35	38.9	255	7	US-11-054-515-1597	Sequence 1597, Ap
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258	35	38.9	292	7	US-11-096-568A-27788	Sequence 27788, A
259	35	38.9	295	7	US-11-096-568A-32901	Sequence 32901, A
260	35	38.9	309	7	US-11-096-568A-24859	Sequence 24859, A
261	35	38.9	318	7	US-11-096-568A-11049	Sequence 11049, A
262	35	38.9	334	7	US-11-156-084-317	Sequence 317, App
263	35	38.9	334	7	US-11-087-099-10792	Sequence 10792, A
264	35	38.9	334	7	US-11-096-568A-11048	Sequence 11048, A
265	35	38.9	351	7	US-11-096-568A-27787	Sequence 27787, A
266	35	38.9	355	7	US-11-096-568A-11047	Sequence 11047, A
267	35	38.9	360	7	US-11-096-568A-32900	Sequence 32900, A
268	35	38.9	362	7	US-11-096-568A-10485	Sequence 10485, A
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270	35	38.9	375	7	US-11-096-568A-10484	Sequence 10484, A
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272	35	38.9	446	7	US-11-087-099-6592	Sequence 6592, Ap
273	35	38.9	450	6	US-10-131-826A-378	Sequence 378, App
274	35	38.9	450	6	US-10-973-115B-378	Sequence 378, App
275	35	38.9	451	7	US-11-098-686-10437	Sequence 10437, A
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277	35	38.9	560	7	US-11-024-959-423	Sequence 423, App
278	35	38.9	562	7	US-11-024-959-422	Sequence 422, App
279	35	38.9	681	7	US-11-087-099-7134	Sequence 7134, Ap
280	35	38.9	701	7	US-11-087-099-8731	Sequence 8731, Ap
281	35	38.9	959	6	US-10-453-372-1074	Sequence 1074, Ap
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283	35	38.9	1025	6	US-10-453-372-1068	Sequence 1068, Ap
284	35	38.9	1025	6	US-10-453-372-1070	Sequence 1070, Ap
285	35	38.9	1063	6	US-10-453-372-1066	Sequence 1066, Ap
286	35	38.9	1068	6	US-10-453-372-1084	Sequence 1084, Ap
287	35	38.9	1068	6	US-10-453-372-1090	Sequence 1090, Ap
288	35	38.9	1077	6	US-10-453-372-1086	Sequence 1086, Ap
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292	35	38.9	3361	6	US-10-453-372-1082	Sequence 1082, Ap
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297	34.5	38.3	176	7	US-11-055-822-726	Sequence 726, App
298	34.5	38.3	349	7	US-11-055-822-196	Sequence 196, App
299	34.5	38.3	377	6	US-10-481-935A-230	Sequence 230, App
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306	34	37.8	17	7	US-11-051-453-76	Sequence 76, Appl
307	34	37.8	22	7	US-11-149-943-49	Sequence 49, Appl
308	34	37.8	46	6	US-10-467-657-6132	Sequence 6132, Ap
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310	34	37.8	98	7	US-11-084-554-56	Sequence 56, Appl
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312	34	37.8	98	7	US-11-061-848-24	Sequence 24, Appl
313	34	37.8	98	7	US-11-004-590-49	Sequence 49, Appl
314	34	37.8	98	7	US-11-136-250-56	Sequence 56, Appl
315	34	37.8	98	7	US-11-157-494-42	Sequence 42, Appl
316	34	37.8	116	6	US-10-925-366A-215	Sequence 215, App
317	34	37.8	118	7	US-11-112-240-26	Sequence 26, Appl
318	34	37.8	118	7	US-11-112-304A-26	Sequence 26, Appl
319	34	37.8	119	6	US-10-834-397-26	Sequence 26, Appl
320	34	37.8	119	7	US-11-049-536-570	Sequence 570, App
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323	34	37.8	120	7	US-11-149-943-57	Sequence 57, Appl
324	34	37.8	121	6	US-10-507-662-25	Sequence 25, Appl
325	34	37.8	121	6	US-10-507-662-26	Sequence 26, Appl
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327	34	37.8	131	6	US-10-993-543-48	Sequence 48, Appl
328	34	37.8	142	6	US-10-467-657-4408	Sequence 4408, Ap
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330	34	37.8	222	7	US-11-150-533-28	Sequence 28, Appl
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333	34	37.8	247	7	US-11-054-515-1455	Sequence 1455, Ap
334	34	37.8	247	7	US-11-054-515-2103	Sequence 2103, Ap
335	34	37.8	248	7	US-11-054-515-1995	Sequence 1995, Ap
336	34	37.8	249	7	US-11-054-515-1618	Sequence 1618, Ap
337	34	37.8	249	7	US-11-054-515-1891	Sequence 1891, Ap
338	34	37.8	249	7	US-11-054-515-1970	Sequence 1970, Ap
339	34	37.8	251	7	US-11-054-515-922	Sequence 922, App
340	34	37.8	251	7	US-11-054-515-1320	Sequence 1320, Ap
341	34	37.8	252	7	US-11-054-515-1537	Sequence 1537, Ap
342	34	37.8	256	7	US-11-054-515-8	Sequence 8, Appli
343	34	37.8	256	7	US-11-054-515-1253	Sequence 1253, Ap
344	34	37.8	256	7	US-11-054-515-1279	Sequence 1279, Ap
345	34	37.8	260	7	US-11-054-515-1039	Sequence 1039, Ap
346	34	37.8	288	7	US-11-087-099-2783	Sequence 2783, Ap
347	34	37.8	298	7	US-11-096-568A-6017	Sequence 6017, Ap
348	34	37.8	313	7	US-11-010-795-20	Sequence 20, Appl
349	34	37.8	331	6	US-10-467-657-1324	Sequence 1324, Ap
350	34	37.8	348	6	US-10-793-626-2866	Sequence 2866, Ap
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352	34	37.8	360	7	US-11-098-686-10783	Sequence 10783, A
353	34	37.8	363	7	US-11-098-686-10410	Sequence 10410, A
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355	34	37.8	390	7	US-11-096-568A-16376	Sequence 16376, A
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357	34	37.8	410	6	US-10-793-626-3258	Sequence 3258, Ap
358	34	37.8	410	6	US-10-467-657-3024	Sequence 3024, Ap
359	34	37.8	428	7	US-11-087-099-6406	Sequence 6406, Ap
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361	34	37.8	437	6	US-10-525-710-32	Sequence 32, Appl
362	34	37.8	449	7	US-11-150-533-27	Sequence 27, Appl
363	34	37.8	455	7	US-11-059-867-17	Sequence 17, Appl
364	34	37.8	458	7	US-11-087-099-1800	Sequence 1800, Ap
365	34	37.8	474	7	US-11-000-463-284	Sequence 284, App
366	34	37.8	477	6	US-10-793-626-3250	Sequence 3250, Ap
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368	34	37.8	497	7	US-11-087-099-3119	Sequence 3119, Ap
369	34	37.8	526	7	US-11-098-686-10516	Sequence 10516, A
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373	34	37.8	662	6	US-10-995-561-943	Sequence 943, App
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375	34	37.8	689	7	US-11-150-533-30	Sequence 30, Appl
376	34	37.8	702	6	US-10-995-561-942	Sequence 942, App
377	34	37.8	754	6	US-10-995-561-941	Sequence 941, App
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385	33.5	37.2	118	7	US-11-072-512-2712	Sequence 2712, Ap
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387	33.5	37.2	123	6	US-10-982-440-55	Sequence 55, Appl
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396	33.5	37.2	857	7	US-11-090-617-686	Sequence 686, App
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404	33	36.7	17	6	US-10-982-440-111	Sequence 111, App
405	33	36.7	22	7	US-11-149-943-16	Sequence 16, Appl
406	33	36.7	35	7	US-11-096-725-26	Sequence 26, Appl
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413	33	36.7	98	7	US-11-144-222-30	Sequence 30, Appl
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415	33	36.7	98	7	US-11-136-250-27	Sequence 27, Appl
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419	33	36.7	112	7	US-11-182-343-12	Sequence 12, Appl
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423	33	36.7	122	6	US-10-982-440-11	Sequence 11, Appl
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431	33	36.7	133	6	US-10-993-543-124	Sequence 124, App
432	33	36.7	137	7	US-11-087-099-5514	Sequence 5514, Ap
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479	33	36.7	248	7	US-11-054-515-2094	Sequence 2094, Ap
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484	33	36.7	250	7	US-11-096-568A-1424	Sequence 1424, Ap
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520	33	36.7	473	7	US-11-144-222-50	Sequence 50, Appl
521	33	36.7	473	7	US-11-182-343-50	Sequence 50, Appl
522	33	36.7	473	7	US-11-087-099-7361	Sequence 7361, Ap
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524	33	36.7	494	7	US-11-087-099-4874	Sequence 4874, Ap
525	33	36.7	513	7	US-11-087-099-7631	Sequence 7631, Ap
526	33	36.7	513	7	US-11-087-099-11726	Sequence 11726, A
527	33	36.7	542	7	US-11-087-099-6916	Sequence 6916, Ap
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543	33	36.7	653	6	US-10-917-905-2	Sequence 2, Appli
544	33	36.7	653	6	US-10-973-115B-438	Sequence 438, App
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549	33	36.7	722	6	US-10-981-267-6	Sequence 6, Appli
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551	33	36.7	739	7	US-11-009-063-31	Sequence 31, Appl
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553	33	36.7	760	7	US-11-087-099-1634	Sequence 1634, Ap
554	33	36.7	773	7	US-11-124-367A-505	Sequence 505, App
555	33	36.7	773	7	US-11-124-367A-506	Sequence 506, App
556	33	36.7	777	7	US-11-087-099-5818	Sequence 5818, Ap
557	33	36.7	912	7	US-11-042-988-12	Sequence 12, Appl
558	33	36.7	1077	7	US-11-054-281-110	Sequence 110, App
559	33	36.7	1135	7	US-11-087-099-2568	Sequence 2568, Ap
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561	33	36.7	1360	7	US-11-183-294-26	Sequence 26, Appl
562	33	36.7	1645	7	US-11-043-806-364	Sequence 364, App
563	33	36.7	1813	6	US-10-495-083-10	Sequence 10, Appl
564	33	36.7	1827	7	US-11-057-058-62	Sequence 62, Appl
565	33	36.7	2074	7	US-11-043-806-365	Sequence 365, App
566	33	36.7	2224	7	US-11-043-806-392	Sequence 392, App
567	33	36.7	2224	7	US-11-043-806-393	Sequence 393, App
568	33	36.7	2647	6	US-10-821-234-1303	Sequence 1303, Ap
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573	32.5	36.1	98	7	US-11-136-250-10	Sequence 10, Appl
574	32.5	36.1	98	7	US-11-096-568A-12341	Sequence 12341, A
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576	32.5	36.1	134	7	US-11-096-568A-20906	Sequence 20906, A
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582	32.5	36.1	233	6	US-10-923-327-18	Sequence 18, Appl
583	32.5	36.1	248	6	US-10-923-327-15	Sequence 15, Appl
584	32.5	36.1	249	7	US-11-054-515-946	Sequence 946, App
585	32.5	36.1	250	7	US-11-054-515-993	Sequence 993, App
586	32.5	36.1	253	7	US-11-054-515-954	Sequence 954, App
587	32.5	36.1	346	6	US-10-525-710-46	Sequence 46, Appl
588	32.5	36.1	410	7	US-11-051-720-1292	Sequence 1292, Ap
589	32.5	36.1	416	7	US-11-051-720-1291	Sequence 1291, Ap
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591	32.5	36.1	451	6	US-10-923-327-9	Sequence 9, Appli
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594	32.5	36.1	603	7	US-11-096-568A-28303	Sequence 28303, A
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596	32.5	36.1	701	7	US-11-096-568A-28302	Sequence 28302, A
597	32.5	36.1	751	7	US-11-051-720-1760	Sequence 1760, Ap
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605	32.5	36.1	871	7	US-11-051-720-1697	Sequence 1697, Ap
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612	32	35.6	43	7	US-11-096-568A-9880	Sequence 9880, Ap
613	32	35.6	73	7	US-11-051-481-27	Sequence 27, Appl
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641	32	35.6	119	7	US-11-049-536-506	Sequence 506, App
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645	32	35.6	120	7	US-11-049-536-518	Sequence 518, App
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655	32	35.6	148	7	US-11-075-400-16	Sequence 16, Appl
656	32	35.6	148	7	US-11-075-047A-89	Sequence 89, Appl
657	32	35.6	179	6	US-10-793-626-1092	Sequence 1092, Ap
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679	32	35.6	280	7	US-11-055-822-444	Sequence 444, App
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684	32	35.6	308	7	US-11-096-568A-20208	Sequence 20208, A
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695	32	35.6	381	7	US-11-194-246-340	Sequence 340, App
696	32	35.6	382	6	US-10-467-657-7540	Sequence 7540, Ap
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713	32	35.6	428	7	US-11-087-099-8857	Sequence 8857, Ap
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715	32	35.6	429	7	US-11-096-568A-1791	Sequence 1791, Ap
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717	32	35.6	434	7	US-11-156-084-229	Sequence 229, App
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722	32	35.6	462	6	US-10-821-234-1548	Sequence 1548, Ap
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735	32	35.6	503	6	US-10-934-944-152	Sequence 152, App
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738	32	35.6	503	7	US-11-116-881A-159	Sequence 159, App
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740	32	35.6	503	7	US-11-116-881A-201	Sequence 201, App
741	32	35.6	503	7	US-11-116-881A-209	Sequence 209, App
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743	32	35.6	504	7	US-11-116-881A-205	Sequence 205, App
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773	32	35.6	808	6	US-10-995-561-574	Sequence 574, App
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776	32	35.6	837	7	US-11-054-281-38	Sequence 38, Appl
777	32	35.6	842	7	US-11-038-284-38	Sequence 38, Appl
778	32	35.6	847	7	US-11-038-284-42	Sequence 42, Appl
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781	32	35.6	865	6	US-10-453-372-606	Sequence 606, App
782	32	35.6	865	6	US-10-453-372-614	Sequence 614, App
783	32	35.6	865	6	US-10-453-372-616	Sequence 616, App
784	32	35.6	865	7	US-11-080-991-110	Sequence 110, App
785	32	35.6	865	7	US-11-054-281-132	Sequence 132, App
786	32	35.6	869	7	US-11-072-512-2532	Sequence 2532, Ap
787	32	35.6	871	7	US-11-072-175-237	Sequence 237, App
788	32	35.6	873	7	US-11-038-284-35	Sequence 35, Appl
789	32	35.6	889	7	US-11-038-284-15	Sequence 15, Appl
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795	32	35.6	1131	7	US-11-072-512-2866	Sequence 2866, Ap
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797	32	35.6	1174	7	US-11-096-568A-30807	Sequence 30807, A
798	32	35.6	1181	7	US-11-096-568A-27847	Sequence 27847, A
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805	32	35.6	1340	7	US-11-070-575-6	Sequence 6, Appli
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808	32	35.6	1476	6	US-10-647-956A-4	Sequence 4, Appli
809	32	35.6	1484	6	US-10-517-939-74	Sequence 74, Appl
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812	32	35.6	2410	7	US-11-175-689-8	Sequence 8, Appli
813	32	35.6	2479	7	US-11-087-099-2391	Sequence 2391, Ap
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815	32	35.6	2768	6	US-10-510-101-72	Sequence 72, Appl
816	32	35.6	3507	7	US-11-075-185-7	Sequence 7, Appli
817	32	35.6	3655	7	US-11-075-185-5	Sequence 5, Appli
818	32	35.6	3689	7	US-11-075-185-4	Sequence 4, Appli
819	32	35.6	4384	6	US-10-821-234-1120	Sequence 1120, Ap
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821	32	35.6	16990	7	US-11-175-689-7	Sequence 7, Appli
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823	31.5	35.0	16	7	US-11-102-424-26	Sequence 26, Appl
824	31.5	35.0	116	7	US-11-102-424-7	Sequence 7, Appli
825	31.5	35.0	116	7	US-11-102-424-14	Sequence 14, Appl
826	31.5	35.0	175	5	US-09-995-493-172	Sequence 172, App
827	31.5	35.0	203	6	US-10-467-657-3482	Sequence 3482, Ap
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833	31.5	35.0	4128	6	US-10-770-726-77	Sequence 77, Appl
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836	31	34.4	17	6	US-10-507-662-52	Sequence 52, Appl
837	31	34.4	17	6	US-10-665-658-36	Sequence 36, Appl
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839	31	34.4	22	7	US-11-149-943-1	Sequence 1, Appli
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841	31	34.4	26	7	US-11-129-741-2799	Sequence 2799, Ap
842	31	34.4	41	6	US-10-467-657-7196	Sequence 7196, Ap
843	31	34.4	43	6	US-10-467-657-2066	Sequence 2066, Ap
844	31	34.4	98	6	US-10-932-334-57	Sequence 57, Appl
845	31	34.4	98	7	US-11-054-669-1	Sequence 1, Appli
846	31	34.4	98	7	US-11-084-554-16	Sequence 16, Appl
847	31	34.4	98	7	US-11-004-590-1	Sequence 1, Appli
848	31	34.4	98	7	US-11-136-250-16	Sequence 16, Appl
849	31	34.4	113	7	US-11-049-536-106	Sequence 106, App
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851	31	34.4	115	7	US-11-127-903-25	Sequence 25, Appl
852	31	34.4	116	7	US-11-097-812-19	Sequence 19, Appl
853	31	34.4	116	7	US-11-102-424-15	Sequence 15, Appl
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855	31	34.4	117	7	US-11-049-536-178	Sequence 178, App
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857	31	34.4	117	7	US-11-049-536-226	Sequence 226, App
858	31	34.4	118	7	US-11-049-536-514	Sequence 514, App
859	31	34.4	118	7	US-11-049-536-626	Sequence 626, App
860	31	34.4	118	7	US-11-049-536-654	Sequence 654, App
861	31	34.4	119	6	US-10-477-950-2	Sequence 2, Appli
862	31	34.4	119	6	US-10-925-366A-210	Sequence 210, App
863	31	34.4	119	7	US-11-054-669-124	Sequence 124, App
864	31	34.4	119	7	US-11-049-536-370	Sequence 370, App
865	31	34.4	120	6	US-10-507-662-61	Sequence 61, Appl
866	31	34.4	120	6	US-10-834-397-36	Sequence 36, Appl
867	31	34.4	120	6	US-10-834-397-59	Sequence 59, Appl
868	31	34.4	120	6	US-10-946-836A-14	Sequence 14, Appl
869	31	34.4	120	6	US-10-946-836A-19	Sequence 19, Appl
870	31	34.4	120	6	US-10-988-207-14	Sequence 14, Appl
871	31	34.4	120	6	US-10-988-207-19	Sequence 19, Appl
872	31	34.4	120	6	US-10-988-207-26	Sequence 26, Appl
873	31	34.4	121	7	US-11-049-536-426	Sequence 426, App
874	31	34.4	122	6	US-10-771-257-57	Sequence 57, Appl
875	31	34.4	122	7	US-11-127-677-55	Sequence 55, Appl
876	31	34.4	123	6	US-10-932-334-87	Sequence 87, Appl
877	31	34.4	123	7	US-11-049-536-406	Sequence 406, App
878	31	34.4	124	6	US-10-932-334-7	Sequence 7, Appli
879	31	34.4	124	6	US-10-932-334-70	Sequence 70, Appl
880	31	34.4	124	7	US-11-040-159-8	Sequence 8, Appli
881	31	34.4	125	7	US-11-049-536-466	Sequence 466, App
882	31	34.4	126	7	US-11-049-536-342	Sequence 342, App
883	31	34.4	128	7	US-11-049-536-578	Sequence 578, App
884	31	34.4	128	7	US-11-096-568A-8920	Sequence 8920, Ap
885	31	34.4	132	7	US-11-049-536-4	Sequence 4, Appli
886	31	34.4	135	6	US-10-993-543-60	Sequence 60, Appl
887	31	34.4	135	6	US-10-993-543-64	Sequence 64, Appl
888	31	34.4	135	7	US-11-096-568A-17745	Sequence 17745, A
889	31	34.4	139	7	US-11-096-568A-8919	Sequence 8919, Ap
890	31	34.4	139	7	US-11-096-568A-8921	Sequence 8921, Ap
891	31	34.4	141	7	US-11-096-568A-12434	Sequence 12434, A
892	31	34.4	143	6	US-10-932-334-52	Sequence 52, Appl
893	31	34.4	143	7	US-11-087-099-12156	Sequence 12156, A
894	31	34.4	145	6	US-10-481-935A-11	Sequence 11, Appl
895	31	34.4	145	6	US-10-481-935A-14	Sequence 14, Appl
896	31	34.4	145	6	US-10-481-935A-17	Sequence 17, Appl
897	31	34.4	150	7	US-11-096-568A-4894	Sequence 4894, Ap
898	31	34.4	151	7	US-11-096-568A-19648	Sequence 19648, A
899	31	34.4	157	7	US-11-049-536-110	Sequence 110, App
900	31	34.4	158	7	US-11-096-568A-20699	Sequence 20699, A
901	31	34.4	158	7	US-11-096-568A-25008	Sequence 25008, A
902	31	34.4	165	7	US-11-096-568A-8918	Sequence 8918, Ap
903	31	34.4	167	7	US-11-072-512-2412	Sequence 2412, Ap
904	31	34.4	171	7	US-11-087-099-9916	Sequence 9916, Ap
905	31	34.4	180	7	US-11-096-568A-12433	Sequence 12433, A
906	31	34.4	181	7	US-11-096-568A-17743	Sequence 17743, A
907	31	34.4	183	7	US-11-096-568A-20698	Sequence 20698, A
908	31	34.4	188	7	US-11-098-686-10628	Sequence 10628, A
909	31	34.4	216	7	US-11-087-099-7174	Sequence 7174, Ap
910	31	34.4	219	6	US-10-821-234-1482	Sequence 1482, Ap
911	31	34.4	223	7	US-11-018-868-140	Sequence 140, App
912	31	34.4	234	6	US-10-491-468-22	Sequence 22, Appl
913	31	34.4	237	7	US-11-096-568A-21993	Sequence 21993, A
914	31	34.4	238	7	US-11-054-515-1907	Sequence 1907, Ap
915	31	34.4	241	7	US-11-054-515-2008	Sequence 2008, Ap
916	31	34.4	241	7	US-11-054-515-2032	Sequence 2032, Ap
917	31	34.4	242	7	US-11-054-515-2021	Sequence 2021, Ap
918	31	34.4	242	7	US-11-054-515-2046	Sequence 2046, Ap
919	31	34.4	242	7	US-11-054-515-2106	Sequence 2106, Ap
920	31	34.4	243	7	US-11-054-515-2009	Sequence 2009, Ap
921	31	34.4	243	7	US-11-054-515-2012	Sequence 2012, Ap
922	31	34.4	243	7	US-11-054-515-2014	Sequence 2014, Ap
923	31	34.4	243	7	US-11-054-515-2063	Sequence 2063, Ap
924	31	34.4	243	7	US-11-054-515-2107	Sequence 2107, Ap
925	31	34.4	243	7	US-11-054-515-2109	Sequence 2109, Ap
926	31	34.4	243	7	US-11-087-099-12434	Sequence 12434, A
927	31	34.4	244	6	US-10-477-507A-4	Sequence 4, Appli
928	31	34.4	244	7	US-11-054-515-1908	Sequence 1908, Ap
929	31	34.4	244	7	US-11-054-515-2011	Sequence 2011, Ap
930	31	34.4	244	7	US-11-054-515-2026	Sequence 2026, Ap
931	31	34.4	244	7	US-11-054-515-2037	Sequence 2037, Ap
932	31	34.4	245	7	US-11-054-515-1714	Sequence 1714, Ap
933	31	34.4	245	7	US-11-054-515-1946	Sequence 1946, Ap
934	31	34.4	245	7	US-11-054-515-2004	Sequence 2004, Ap
935	31	34.4	245	7	US-11-054-515-2042	Sequence 2042, Ap
936	31	34.4	245	7	US-11-054-515-2116	Sequence 2116, Ap
937	31	34.4	246	7	US-11-092-140-111	Sequence 111, App
938	31	34.4	247	7	US-11-054-515-1729	Sequence 1729, Ap
939	31	34.4	248	7	US-11-054-515-1721	Sequence 1721, Ap
940	31	34.4	248	7	US-11-076-164-9	Sequence 9, Appli
941	31	34.4	249	7	US-11-054-515-1635	Sequence 1635, Ap
942	31	34.4	250	7	US-11-054-515-1722	Sequence 1722, Ap
943	31	34.4	250	7	US-11-054-515-1723	Sequence 1723, Ap
944	31	34.4	251	7	US-11-054-515-871	Sequence 871, App
945	31	34.4	251	7	US-11-054-515-1336	Sequence 1336, Ap
946	31	34.4	251	7	US-11-054-515-1688	Sequence 1688, Ap
947	31	34.4	251	7	US-11-054-515-1806	Sequence 1806, Ap
948	31	34.4	252	7	US-11-096-568A-26846	Sequence 26846, A
949	31	34.4	253	7	US-11-054-515-1936	Sequence 1936, Ap
950	31	34.4	254	7	US-11-096-568A-25007	Sequence 25007, A
951	31	34.4	255	7	US-11-054-515-1407	Sequence 1407, Ap
952	31	34.4	255	7	US-11-054-515-1626	Sequence 1626, Ap
953	31	34.4	256	6	US-10-642-272A-4	Sequence 4, Appli
954	31	34.4	256	7	US-11-054-515-1640	Sequence 1640, Ap
955	31	34.4	261	7	US-11-096-568A-17990	Sequence 17990, A
956	31	34.4	265	7	US-11-091-643-8	Sequence 8, Appli
957	31	34.4	270	7	US-11-052-554A-315	Sequence 315, App
958	31	34.4	272	7	US-11-096-568A-21992	Sequence 21992, A
959	31	34.4	273	7	US-11-096-568A-16687	Sequence 16687, A
960	31	34.4	274	7	US-11-096-568A-17414	Sequence 17414, A
961	31	34.4	278	7	US-11-098-686-11408	Sequence 11408, A
962	31	34.4	278	7	US-11-096-568A-19647	Sequence 19647, A
963	31	34.4	281	6	US-10-491-468-2	Sequence 2, Appli
964	31	34.4	282	7	US-11-087-099-5672	Sequence 5672, Ap
965	31	34.4	283	7	US-11-205-109-5	Sequence 5, Appli
966	31	34.4	287	7	US-11-096-568A-19646	Sequence 19646, A
967	31	34.4	291	6	US-10-481-935A-36	Sequence 36, Appl
968	31	34.4	291	6	US-10-481-935A-39	Sequence 39, Appl
969	31	34.4	291	6	US-10-481-935A-46	Sequence 46, Appl
970	31	34.4	291	6	US-10-481-935A-49	Sequence 49, Appl
971	31	34.4	293	7	US-11-096-568A-25006	Sequence 25006, A
972	31	34.4	301	7	US-11-096-568A-12824	Sequence 12824, A
973	31	34.4	302	7	US-11-096-568A-12823	Sequence 12823, A
974	31	34.4	306	7	US-11-087-099-12178	Sequence 12178, A

975	31	34.4	309	7	US-11-124-368A-197	Sequence 197, App
976	31	34.4	310	7	US-11-096-568A-17880	Sequence 17880, A
977	31	34.4	316	7	US-11-130-821-9	Sequence 9, Appli
978	31	34.4	317	7	US-11-087-099-11988	Sequence 11988, A
979	31	34.4	318	7	US-11-096-568A-26067	Sequence 26067, A
980	31	34.4	319	7	US-11-087-099-2953	Sequence 2953, Ap
981	31	34.4	319	7	US-11-087-099-5248	Sequence 5248, Ap
982	31	34.4	319	7	US-11-087-099-9981	Sequence 9981, Ap
983	31	34.4	319	7	US-11-096-568A-26066	Sequence 26066, A
984	31	34.4	320	7	US-11-096-568A-17879	Sequence 17879, A
985	31	34.4	320	7	US-11-096-568A-21991	Sequence 21991, A
986	31	34.4	320	7	US-11-096-568A-27640	Sequence 27640, A
987	31	34.4	321	7	US-11-087-099-5956	Sequence 5956, Ap
988	31	34.4	324	7	US-11-096-568A-17413	Sequence 17413, A
989	31	34.4	325	7	US-11-087-099-11142	Sequence 11142, A
990	31	34.4	327	7	US-11-087-099-12170	Sequence 12170, A
991	31	34.4	327	7	US-11-096-568A-16686	Sequence 16686, A
992	31	34.4	329	7	US-11-087-099-11839	Sequence 11839, A
993	31	34.4	351	7	US-11-096-568A-26845	Sequence 26845, A
994	31	34.4	359	7	US-11-087-099-10369	Sequence 10369, A
995	31	34.4	363	7	US-11-096-568A-33271	Sequence 33271, A
996	31	34.4	368	7	US-11-087-099-8464	Sequence 8464, Ap
997	31	34.4	369	7	US-11-096-568A-12822	Sequence 12822, A
998	31	34.4	379	7	US-11-060-029-17	Sequence 17, Appl
999	31	34.4	384	6	US-10-517-939-358	Sequence 358, App
1000	31	34.4	389	7	US-11-096-568A-17878	Sequence 17878, A

ALIGNMENTS

RESULT 1
US-10-982-357-41
; Sequence 41, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/982,357
; CURRENT FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-982-357-41

Query Match 92.2%; Score 83; DB 6; Length 119;
Best Local Similarity 94.1%; Pred. No. 1.7e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:||||||||||||||
Db 50 EINPDSSTINYAPSLKD 66

RESULT 2
US-10-982-357-47
; Sequence 47, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/982,357
; CURRENT FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo saiens
US-10-982-357-47

Query Match 92.2%; Score 83; DB 6; Length 119;
Best Local Similarity 94.1%; Pred. No. 1.7e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:||||||||||||||
Db 50 EINPDSSTINYAPSLKD 66

RESULT 3
US-10-982-357-16
; Sequence 16, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/982,357
; CURRENT FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-982-357-16

Query Match 87.8%; Score 79; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.1e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:|||||||| |||||
Db 1 EINPDSSTINYTPSLKD 17

RESULT 4
US-10-982-357-31
; Sequence 31, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/982,357
; CURRENT FILING DATE: 2004-11-05
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mus Musculus
US-10-982-357-31

Query Match 87.8%; Score 79; DB 6; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.1e-07;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIHPDSSTINYAPSLKD 17
||:|||||||| |||||
Db 1 EINPDSSTINYTPSLKD 17

RESULT 5
US-10-982-357-5
; Sequence 5, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs
; TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES

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;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-5

  Query Match            87.8%;  Score 79;  DB 6;  Length 119;
  Best Local Similarity  88.2%;  Pred. No. 7.6e-06;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:||||||| |||||
Db         50 EINPDSSTINYTPSLKD 66


RESULT 6
US-10-982-357-38
; Sequence 38, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-38

  Query Match            87.8%;  Score 79;  DB 6;  Length 119;
  Best Local Similarity  88.2%;  Pred. No. 7.6e-06;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:||||||| |||||
Db         50 EINPDSSTINYTPSLKD 66


RESULT 7
US-10-982-357-45
; Sequence 45, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-45

  Query Match            87.8%;  Score 79;  DB 6;  Length 119;
  Best Local Similarity  88.2%;  Pred. No. 7.6e-06;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:||||||| |||||
Db         50 EINPDSSTINYTPSLKD 66


RESULT 8
US-10-982-357-27
; Sequence 27, Application US/10982357
; Publication No. US20060024296A1
; GENERAL INFORMATION:
;  APPLICANT: Protein Design Labs
;  TITLE OF INVENTION: THERAPEUTIC USE OF ANTI-CS1 ANTIBODIES
;  FILE REFERENCE: file
;  CURRENT APPLICATION NUMBER: US/10/982,357
;  CURRENT FILING DATE:  2004-11-05
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
;   LENGTH: 137
;   TYPE: PRT
;   ORGANISM: Mus Musculus
US-10-982-357-27

  Query Match            87.8%;  Score 79;  DB 6;  Length 137;
  Best Local Similarity  88.2%;  Pred. No. 9e-06;
  Matches   15;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:||||||| |||||
Db         68 EINPDSSTINYTPSLKD 84


RESULT 9
US-11-105-708-21
; Sequence 21, Application US/11105708
; Publication No. US20050281821A1
; GENERAL INFORMATION:
;  APPLICANT: Pernasetti, Flavia
;  APPLICANT:  Freimark, Bruce
;  APPLICANT:  Van Epps, Dennis
;  APPLICANT:  Brooks, Peter C
;  TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition
;  FILE REFERENCE: 30797-704.501
;  CURRENT APPLICATION NUMBER: US/11/105,708
;  CURRENT FILING DATE:  2005-04-13
;  PRIOR APPLICATION NUMBER: 09/478,977
;  PRIOR FILING DATE: 2000-01-06
;  PRIOR APPLICATION NUMBER: 60/152,496
;  PRIOR FILING DATE: 1999-09-02
;  PRIOR APPLICATION NUMBER: 60/143,534
;  PRIOR FILING DATE: 1999-09-02
;  PRIOR APPLICATION NUMBER: 60/114,878
;  PRIOR FILING DATE: 1999-01-06
;  PRIOR APPLICATION NUMBER: 60/114,877
;  PRIOR FILING DATE: 1999-01-06
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic peptide
US-11-105-708-21

  Query Match            75.6%;  Score 68;  DB 7;  Length 17;
  Best Local Similarity  76.5%;  Pred. No. 4.8e-05;
  Matches   13;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              ||:||||| || | |||
Db          1 EINPDSSTANYTPYLKD 17


RESULT 10
US-10-858-730-287
; Sequence 287, Application US/10858730
```

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; Publication No. US20050255568A1
; GENERAL INFORMATION:
;  APPLICANT: Bailey, Richard B.
;  APPLICANT:  Blomquist, Paul
;  APPLICANT:  Doten, Reed
;  APPLICANT:  Driggers, Edward M.
;  APPLICANT:  Madden, Kevin T.
;  APPLICANT:  O'Leary, Jessica
;  APPLICANT:  O'Toole, George
;  APPLICANT:  Trueheart, Joshua
;  APPLICANT:  Walbridge, Michael J.
;  APPLICANT:  Yorgey, Peter S.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
;  TITLE OF INVENTION:  PRODUCTION
;  FILE REFERENCE: 14184-030001
;  CURRENT APPLICATION NUMBER: US/10/858,730
;  CURRENT FILING DATE:  2004-06-01
;  PRIOR APPLICATION NUMBER: US 60/475,000
;  PRIOR FILING DATE: 2003-05-30
;  PRIOR APPLICATION NUMBER: US 60/551,860
;  PRIOR FILING DATE: 2004-03-10
;  NUMBER OF SEQ ID NOS: 364
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 287
;   LENGTH: 521
;   TYPE: PRT
;   ORGANISM: Micobacterium smegmatis
US-10-858-730-287

  Query Match             51.1%;  Score 46;  DB 6;  Length 521;
  Best Local Similarity   66.7%;  Pred. No. 8.5;
  Matches    8;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYA 12
              | ||| |::|||
Db        391 ENHPDVSSVNYA 402


RESULT 11
US-11-112-481C-9
; Sequence 9, Application US/11112481C
; Publication No. US20060039900A1
; GENERAL INFORMATION:
;  APPLICANT: Centocor, Inc.
;  APPLICANT:  O'Neil, Karyn
;  APPLICANT:  Sweet, Raymond
;  TITLE OF INVENTION: EPITOPE DIRECTED SELECTION OF ANTIBODIES TO MURINE TISSUE FACTOR
;  FILE REFERENCE: CEN5054
;  CURRENT APPLICATION NUMBER: US/11/112,481C
;  CURRENT FILING DATE:  2005-04-22
;  PRIOR APPLICATION NUMBER: 60/565674
;  PRIOR FILING DATE: 2004-04-26
;  PRIOR APPLICATION NUMBER: 60/565633
;  PRIOR FILING DATE: 2004-04-26
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: BINDING
;   LOCATION: (26)..(34)
;   OTHER INFORMATION: CDR1
;   FEATURE:
;   NAME/KEY: BINDING
;   LOCATION: (49)..(65)
;   OTHER INFORMATION: CDR2
;   FEATURE:
;   NAME/KEY: BINDING
;   LOCATION: (98)..(108)
;   OTHER INFORMATION: CDR3
US-11-112-481C-9

  Query Match             48.9%;  Score 44;  DB 7;  Length 119;
  Best Local Similarity   53.3%;  Pred. No. 3.3;
  Matches    8;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              | || |  ||:|| :
Db         50 IDPDDSDTNYSPSFQ 64


RESULT 12
US-11-054-515-1902
; Sequence 1902, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1902
;   LENGTH: 245
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1902

  Query Match             48.9%;  Score 44;  DB 7;  Length 245;
  Best Local Similarity   40.0%;  Pred. No. 7.5;
  Matches    6;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              :||:  ::|||   |
Db         51 VHPNDGSVNYAQKFK 65


RESULT 13
US-10-932-334-74
; Sequence 74, Application US/10932334
; Publication No. US20050249728A1
; GENERAL INFORMATION:
;  APPLICANT: ImmunoGen, Inc.
;  TITLE OF INVENTION: ANTI-IGF-I RECEPTOR ANTIBODY
;  FILE REFERENCE: A8689
;  CURRENT APPLICATION NUMBER: US/10/932,334
;  CURRENT FILING DATE:  2004-09-02
;  PRIOR APPLICATION NUMBER: US/10/729,441
;  PRIOR FILING DATE: 2003-12-08
;  PRIOR APPLICATION NUMBER: 10/170,390
;  PRIOR FILING DATE: 2002-06-14
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: PatentIn version 3.2
```

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; SEQ ID NO 74
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic antibody structure
US-10-932-334-74

  Query Match             47.8%;  Score 43;  DB 6;  Length 120;
  Best Local Similarity   50.0%;  Pred. No. 4.8;
  Matches    8;  Conservative    1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLK 16
              ||||:|   ||    |
Db         50 EIHPNSGNTNYNEKFK 65


RESULT 14
US-10-517-939-136
; Sequence 136, Application US/10517939
; Publication No. US20060003433A1
; GENERAL INFORMATION:
;  APPLICANT: Steer, Brian
;  APPLICANT:  Callen, Walter
;  APPLICANT:  Healey, Shaun
;  APPLICANT:  Hazlewood, Geoff
;  APPLICANT:  Wu, Di
;  APPLICANT:  Blum, David
;  APPLICANT:  Esteghlalian, Alireza
;  TITLE OF INVENTION: XYLANASES, NUCLEIC ACIDS ENCODING THEM
;  TITLE OF INVENTION:  AND METHODS FOR MAKING AND USING THEM
;  FILE REFERENCE: 564462007901
;  CURRENT APPLICATION NUMBER: US/10/517,939
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: PCT/US03/19153
;  PRIOR FILING DATE: 2003-06-16
;  PRIOR APPLICATION NUMBER: 60/389,299
;  PRIOR FILING DATE: 2002-06-14
;  NUMBER OF SEQ ID NOS: 380
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 136
;   LENGTH: 389
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Obtained from an environmental sample
;   FEATURE:
;   NAME/KEY: SIGNAL
;   LOCATION: (1)...(25)
US-10-517-939-136

  Query Match             47.8%;  Score 43;  DB 6;  Length 389;
  Best Local Similarity   42.9%;  Pred. No. 18;
  Matches    6;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPS 14
              |:||::   |: ||
Db         81 EVHPEADRYNFEPS 94


RESULT 15
US-10-771-257-19
; Sequence 19, Application US/10771257
; Publication No. US20050288864A1
; GENERAL INFORMATION:
;  APPLICANT: Medical Research Council
;  APPLICANT:  SISSA - Scuola Superiore Internazionale di Studi Avanzati
;  APPLICANT:  Cattaneo, Antonino
;  APPLICANT:  Maritan, Amos
;  APPLICANT:  Visintin, Michela
;  APPLICANT:  Rabbitts, Terrence H
;  APPLICANT:  Settanni, Giovanni
;  TITLE OF INVENTION: Intracellular antibodies
;  FILE REFERENCE: 18396/2272
;  CURRENT APPLICATION NUMBER: US/10/771,257
;  CURRENT FILING DATE:  2004-02-03
;  PRIOR APPLICATION NUMBER: PCT/GB02/03512
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: GB 0119004.0
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: GB 0121577.1
;  PRIOR FILING DATE: 2001-09-06
;  PRIOR APPLICATION NUMBER: GB 0200928.0
;  PRIOR FILING DATE: 2002-01-16
;  PRIOR APPLICATION NUMBER: GB 0203569.9
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: IT RM2001A000633
;  PRIOR FILING DATE: 2001-10-25
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 124
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-771-257-19

  Query Match             46.7%;  Score 42;  DB 6;  Length 124;
  Best Local Similarity   60.0%;  Pred. No. 7.2;
  Matches    9;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              || | ||  || |:|
Db         51 IHNDGSTTYYADSVK 65


RESULT 16
US-11-127-677-19
; Sequence 19, Application US/11127677
; Publication No. US20050272107A1
; GENERAL INFORMATION:
;  APPLICANT: Medical Research Council
;  APPLICANT:  Rabbitts, Terence H
;  APPLICANT:  Tanaka, Tomoyuki
;  TITLE OF INVENTION: Intracellular antibodies
;  FILE REFERENCE: 18396/2462
;  CURRENT APPLICATION NUMBER: US/11/127,677
;  CURRENT FILING DATE:  2005-05-12
;  PRIOR APPLICATION NUMBER: PCT/GB03/04942
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: GB 0226729.2
;  PRIOR FILING DATE: 2002-11-15
;  NUMBER OF SEQ ID NOS: 150
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 124
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Derived protein sequence of scFv
US-11-127-677-19

  Query Match             46.7%;  Score 42;  DB 7;  Length 124;
  Best Local Similarity   60.0%;  Pred. No. 7.2;
  Matches    9;  Conservative    1;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              || | ||  || |:|
Db         51 IHNDGSTTYYADSVK 65


RESULT 17
US-11-096-568A-8620
; Sequence 8620, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
```

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;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 8620
;   LENGTH: 394
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(394)
;   OTHER INFORMATION: Ceres Seq. ID no. 15169116
US-11-096-568A-8620

  Query Match             46.7%;  Score 42;  DB 7;  Length 394;
  Best Local Similarity   50.0%;  Pred. No. 27;
  Matches    7;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSL 15
              ||  |||: | |::
Db         30 IHKSSSTVGYRPNV 43


RESULT 18
US-11-096-568A-8619
; Sequence 8619, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 8619
;   LENGTH: 398
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(398)
;   OTHER INFORMATION: Ceres Seq. ID no. 15169115
US-11-096-568A-8619

  Query Match             46.7%;  Score 42;  DB 7;  Length 398;
  Best Local Similarity   50.0%;  Pred. No. 27;
  Matches    7;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSL 15
              ||  |||: | |::
Db         34 IHKSSSTVGYRPNV 47


RESULT 19
US-11-054-515-844
; Sequence 844, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 844
;   LENGTH: 254
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-844

  Query Match             46.1%;  Score 41.5;  DB 7;  Length 254;
  Best Local Similarity   66.7%;  Pred. No. 20;
  Matches   10;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          2 IHPDSSTINYAPSLK 16
              |:|  || || ||||
Db         53 IYPTGST-NYNPSLK 66


RESULT 20
US-11-089-872-3
; Sequence 3, Application US/11089872
; Publication No. US20050260212A1
; GENERAL INFORMATION:
;  APPLICANT: Zhang, Yongke
;  APPLICANT:  Ramakrishnan, Vanitha
;  APPLICANT:  Law, Debbie
;  TITLE OF INVENTION: ANTI-LFL2 ANTIBODIES FOR THE DIAGNOSIS, PROGNOSIS AND TREATMENT
;  TITLE OF INVENTION:  OF CANCER
;  FILE REFERENCE: 05882.0223.NPUS02
;  CURRENT APPLICATION NUMBER: US/11/089,872
;  CURRENT FILING DATE:  2005-03-25
;  PRIOR APPLICATION NUMBER: 60/557,440
;  PRIOR FILING DATE: 2004-03-26
;  PRIOR APPLICATION NUMBER: 60/638,708
;  PRIOR FILING DATE: 2004-12-22
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 138
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-089-872-3

  Query Match             45.6%;  Score 41;  DB 7;  Length 138;
  Best Local Similarity   52.9%;  Pred. No. 12;
  Matches    9;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 EIHPDSSTINYAPSLKD 17
              || | | | ||    ||
Db         69 EILPGSDTTNYNEKFKD 85


RESULT 21
US-11-096-568A-3877
; Sequence 3877, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
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;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 3877
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(211)
;   OTHER INFORMATION: Ceres Seq. ID no. 15221298
US-11-096-568A-3877

  Query Match             45.6%;  Score 41;  DB 7;  Length 211;
  Best Local Similarity   63.6%;  Pred. No. 19;
  Matches    7;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 HPDSSTINYAP 13
              |||  :|| ||
Db         15 HPDKGSINRAP 25


RESULT 22
US-11-096-568A-3876
; Sequence 3876, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 3876
;   LENGTH: 214
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(214)
;   OTHER INFORMATION: Ceres Seq. ID no. 15221297
US-11-096-568A-3876

  Query Match             45.6%;  Score 41;  DB 7;  Length 214;
  Best Local Similarity   63.6%;  Pred. No. 19;
  Matches    7;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 HPDSSTINYAP 13
              |||  :|| ||
Db         18 HPDKGSINRAP 28


RESULT 23
US-11-054-515-1957
; Sequence 1957, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1957
;   LENGTH: 249
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1957

  Query Match             45.6%;  Score 41;  DB 7;  Length 249;
  Best Local Similarity   46.7%;  Pred. No. 23;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              |:|| |:  | || :
Db         51 IYPDDSSTTYRPSFQ 65


RESULT 24
US-11-139-499-4
; Sequence 4, Application US/11139499
; Publication No. US20050260205A1
; GENERAL INFORMATION:
;  APPLICANT: ANDERSON, DARRELL R.
;  APPLICANT:  HANNA, NABIL
;  APPLICANT:  BRAMS, PETER
;  APPLICANT:  HEARD, CHERYL
;  TITLE OF INVENTION: INDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN
;  TITLE OF INVENTION:  CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
;  TITLE OF INVENTION:  CO-STIMULATORY ANTIGENS
;  FILE REFERENCE: 37003-275681
;  CURRENT APPLICATION NUMBER: US/11/139,499
;  CURRENT FILING DATE:  2005-05-31
;  PRIOR APPLICATION NUMBER: US/09/576,424
;  PRIOR FILING DATE: 2000-05-22
;  PRIOR APPLICATION NUMBER: PCT/US97/19906
;  PRIOR FILING DATE: 1997-10-29
;  PRIOR APPLICATION NUMBER: 08/746,361
;  PRIOR FILING DATE: 1996-11-08
;  PRIOR APPLICATION NUMBER: 08/487,550
;  PRIOR FILING DATE: 1995-06-07
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 476
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-139-499-4

  Query Match             45.6%;  Score 41;  DB 7;  Length 476;
  Best Local Similarity   53.3%;  Pred. No. 49;
  Matches    8;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              |: : :| || ||||
Db         71 IYGNGATTNYNPSLK 85


RESULT 25
US-11-012-353-10
; Sequence 10, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
;  APPLICANT: GOETSCH, LILIANE
```

```
;  APPLICANT:  CORVAIA, NATHALIE
;  APPLICANT:  DUFLOS, ALAIN
;  APPLICANT:  HAEUW, JEAN-FRANCOIS
;  APPLICANT:  LEGER, OLIVIER
;  APPLICANT:  BECK, ALAIN
;  TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
;  TITLE OF INVENTION:  RECEPTORS ANTIBODIES AND USES THEREOF
;  FILE REFERENCE: 017753-198
;  CURRENT APPLICATION NUMBER: US/11/012,353
;  CURRENT FILING DATE:  2004-12-16
;  PRIOR APPLICATION NUMBER: 10/735,916
;  PRIOR FILING DATE: 2003-12-16
;  PRIOR APPLICATION NUMBER: FR 0308538
;  PRIOR FILING DATE: 2003-07-11
;  PRIOR APPLICATION NUMBER: PCT/FR03/00178
;  PRIOR FILING DATE: 2003-01-20
;  PRIOR APPLICATION NUMBER: FR 0205753
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: FR 0200653
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: FR 0200654
;  PRIOR FILING DATE: 2002-01-18
;  NUMBER OF SEQ ID NOS: 162
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 10
;   LENGTH: 16
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-012-353-10

  Query Match             44.4%;  Score 40;  DB 7;  Length 16;
  Best Local Similarity   80.0%;  Pred. No. 1.4;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TINYAPSLKD 17
              | || |||||
Db          7 TNNYKPSLKD 16


RESULT 26
US-11-012-353-69
; Sequence 69, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
;  APPLICANT: GOETSCH, LILIANE
;  APPLICANT:  CORVAIA, NATHALIE
;  APPLICANT:  DUFLOS, ALAIN
;  APPLICANT:  HAEUW, JEAN-FRANCOIS
;  APPLICANT:  LEGER, OLIVIER
;  APPLICANT:  BECK, ALAIN
;  TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
;  TITLE OF INVENTION:  RECEPTORS ANTIBODIES AND USES THEREOF
;  FILE REFERENCE: 017753-198
;  CURRENT APPLICATION NUMBER: US/11/012,353
;  CURRENT FILING DATE:  2004-12-16
;  PRIOR APPLICATION NUMBER: 10/735,916
;  PRIOR FILING DATE: 2003-12-16
;  PRIOR APPLICATION NUMBER: FR 0308538
;  PRIOR FILING DATE: 2003-07-11
;  PRIOR APPLICATION NUMBER: PCT/FR03/00178
;  PRIOR FILING DATE: 2003-01-20
;  PRIOR APPLICATION NUMBER: FR 0205753
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: FR 0200653
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: FR 0200654
;  PRIOR FILING DATE: 2002-01-18
;  NUMBER OF SEQ ID NOS: 162
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 69
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-012-353-69

  Query Match             44.4%;  Score 40;  DB 7;  Length 117;
  Best Local Similarity   80.0%;  Pred. No. 14;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TINYAPSLKD 17
              | || |||||
Db         57 TNNYKPSLKD 66


RESULT 27
US-11-012-353-75
; Sequence 75, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
;  APPLICANT: GOETSCH, LILIANE
;  APPLICANT:  CORVAIA, NATHALIE
;  APPLICANT:  DUFLOS, ALAIN
;  APPLICANT:  HAEUW, JEAN-FRANCOIS
;  APPLICANT:  LEGER, OLIVIER
;  APPLICANT:  BECK, ALAIN
;  TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
;  TITLE OF INVENTION:  RECEPTORS ANTIBODIES AND USES THEREOF
;  FILE REFERENCE: 017753-198
;  CURRENT APPLICATION NUMBER: US/11/012,353
;  CURRENT FILING DATE:  2004-12-16
;  PRIOR APPLICATION NUMBER: 10/735,916
;  PRIOR FILING DATE: 2003-12-16
;  PRIOR APPLICATION NUMBER: FR 0308538
;  PRIOR FILING DATE: 2003-07-11
;  PRIOR APPLICATION NUMBER: PCT/FR03/00178
;  PRIOR FILING DATE: 2003-01-20
;  PRIOR APPLICATION NUMBER: FR 0205753
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: FR 0200653
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: FR 0200654
;  PRIOR FILING DATE: 2002-01-18
;  NUMBER OF SEQ ID NOS: 162
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 75
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-012-353-75

  Query Match             44.4%;  Score 40;  DB 7;  Length 117;
  Best Local Similarity   80.0%;  Pred. No. 14;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TINYAPSLKD 17
              | || |||||
Db         57 TNNYKPSLKD 66


RESULT 28
US-11-012-353-79
; Sequence 79, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
;  APPLICANT: GOETSCH, LILIANE
;  APPLICANT:  CORVAIA, NATHALIE
;  APPLICANT:  DUFLOS, ALAIN
;  APPLICANT:  HAEUW, JEAN-FRANCOIS
;  APPLICANT:  LEGER, OLIVIER
;  APPLICANT:  BECK, ALAIN
;  TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
;  TITLE OF INVENTION:  RECEPTORS ANTIBODIES AND USES THEREOF
;  FILE REFERENCE: 017753-198
;  CURRENT APPLICATION NUMBER: US/11/012,353
;  CURRENT FILING DATE:  2004-12-16
;  PRIOR APPLICATION NUMBER: 10/735,916
```

```
;  PRIOR FILING DATE: 2003-12-16
;  PRIOR APPLICATION NUMBER: FR 0308538
;  PRIOR FILING DATE: 2003-07-11
;  PRIOR APPLICATION NUMBER: PCT/FR03/00178
;  PRIOR FILING DATE: 2003-01-20
;  PRIOR APPLICATION NUMBER: FR 0205753
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: FR 0200653
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: FR 0200654
;  PRIOR FILING DATE: 2002-01-18
;  NUMBER OF SEQ ID NOS: 162
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 79
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-012-353-79

  Query Match             44.4%;  Score 40;  DB 7;  Length 117;
  Best Local Similarity   80.0%;  Pred. No. 14;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TINYAPSLKD 17
              | || |||||
Db         57 TNNYKPSLKD 66


RESULT 29
US-11-012-353-83
; Sequence 83, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
;  APPLICANT: GOETSCH, LILIANE
;  APPLICANT:  CORVAIA, NATHALIE
;  APPLICANT:  DUFLOS, ALAIN
;  APPLICANT:  HAEUW, JEAN-FRANCOIS
;  APPLICANT:  LEGER, OLIVIER
;  APPLICANT:  BECK, ALAIN
;  TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
;  TITLE OF INVENTION:  RECEPTORS ANTIBODIES AND USES THEREOF
;  FILE REFERENCE: 017753-198
;  CURRENT APPLICATION NUMBER: US/11/012,353
;  CURRENT FILING DATE:  2004-12-16
;  PRIOR APPLICATION NUMBER: 10/735,916
;  PRIOR FILING DATE: 2003-12-16
;  PRIOR APPLICATION NUMBER: FR 0308538
;  PRIOR FILING DATE: 2003-07-11
;  PRIOR APPLICATION NUMBER: PCT/FR03/00178
;  PRIOR FILING DATE: 2003-01-20
;  PRIOR APPLICATION NUMBER: FR 0205753
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: FR 0200653
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: FR 0200654
;  PRIOR FILING DATE: 2002-01-18
;  NUMBER OF SEQ ID NOS: 162
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 83
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-012-353-83

  Query Match             44.4%;  Score 40;  DB 7;  Length 117;
  Best Local Similarity   80.0%;  Pred. No. 14;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TINYAPSLKD 17
              | || |||||
Db         57 TNNYKPSLKD 66


RESULT 30
US-11-012-353-52
; Sequence 52, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
;  APPLICANT: GOETSCH, LILIANE
;  APPLICANT:  CORVAIA, NATHALIE
;  APPLICANT:  DUFLOS, ALAIN
;  APPLICANT:  HAEUW, JEAN-FRANCOIS
;  APPLICANT:  LEGER, OLIVIER
;  APPLICANT:  BECK, ALAIN
;  TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
;  TITLE OF INVENTION:  RECEPTORS ANTIBODIES AND USES THEREOF
;  FILE REFERENCE: 017753-198
;  CURRENT APPLICATION NUMBER: US/11/012,353
;  CURRENT FILING DATE:  2004-12-16
;  PRIOR APPLICATION NUMBER: 10/735,916
;  PRIOR FILING DATE: 2003-12-16
;  PRIOR APPLICATION NUMBER: FR 0308538
;  PRIOR FILING DATE: 2003-07-11
;  PRIOR APPLICATION NUMBER: PCT/FR03/00178
;  PRIOR FILING DATE: 2003-01-20
;  PRIOR APPLICATION NUMBER: FR 0205753
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: FR 0200653
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: FR 0200654
;  PRIOR FILING DATE: 2002-01-18
;  NUMBER OF SEQ ID NOS: 162
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 52
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-012-353-52

  Query Match             44.4%;  Score 40;  DB 7;  Length 127;
  Best Local Similarity   80.0%;  Pred. No. 15;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TINYAPSLKD 17
              | || |||||
Db         67 TNNYKPSLKD 76


RESULT 31
US-11-012-353-77
; Sequence 77, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
;  APPLICANT: GOETSCH, LILIANE
;  APPLICANT:  CORVAIA, NATHALIE
;  APPLICANT:  DUFLOS, ALAIN
;  APPLICANT:  HAEUW, JEAN-FRANCOIS
;  APPLICANT:  LEGER, OLIVIER
;  APPLICANT:  BECK, ALAIN
;  TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
;  TITLE OF INVENTION:  RECEPTORS ANTIBODIES AND USES THEREOF
;  FILE REFERENCE: 017753-198
;  CURRENT APPLICATION NUMBER: US/11/012,353
;  CURRENT FILING DATE:  2004-12-16
;  PRIOR APPLICATION NUMBER: 10/735,916
;  PRIOR FILING DATE: 2003-12-16
;  PRIOR APPLICATION NUMBER: FR 0308538
;  PRIOR FILING DATE: 2003-07-11
;  PRIOR APPLICATION NUMBER: PCT/FR03/00178
;  PRIOR FILING DATE: 2003-01-20
;  PRIOR APPLICATION NUMBER: FR 0205753
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: FR 0200653
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: FR 0200654
;  PRIOR FILING DATE: 2002-01-18
```

```
;  NUMBER OF SEQ ID NOS: 162
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 77
;   LENGTH: 135
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-012-353-77

  Query Match             44.4%;  Score 40;  DB 7;  Length 135;
  Best Local Similarity   80.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TINYAPSLKD 17
              | || |||||
Db         75 TNNYKPSLKD 84


RESULT 32
US-11-012-353-81
; Sequence 81, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
;  APPLICANT: GOETSCH, LILIANE
;  APPLICANT:  CORVAIA, NATHALIE
;  APPLICANT:  DUFLOS, ALAIN
;  APPLICANT:  HAEUW, JEAN-FRANCOIS
;  APPLICANT:  LEGER, OLIVIER
;  APPLICANT:  BECK, ALAIN
;  TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
;  TITLE OF INVENTION:  RECEPTORS ANTIBODIES AND USES THEREOF
;  FILE REFERENCE: 017753-198
;  CURRENT APPLICATION NUMBER: US/11/012,353
;  CURRENT FILING DATE:  2004-12-16
;  PRIOR APPLICATION NUMBER: 10/735,916
;  PRIOR FILING DATE: 2003-12-16
;  PRIOR APPLICATION NUMBER: FR 0308538
;  PRIOR FILING DATE: 2003-07-11
;  PRIOR APPLICATION NUMBER: PCT/FR03/00178
;  PRIOR FILING DATE: 2003-01-20
;  PRIOR APPLICATION NUMBER: FR 0205753
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: FR 0200653
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: FR 0200654
;  PRIOR FILING DATE: 2002-01-18
;  NUMBER OF SEQ ID NOS: 162
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 81
;   LENGTH: 135
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-012-353-81

  Query Match             44.4%;  Score 40;  DB 7;  Length 135;
  Best Local Similarity   80.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TINYAPSLKD 17
              | || |||||
Db         75 TNNYKPSLKD 84


RESULT 33
US-11-012-353-85
; Sequence 85, Application US/11012353
; Publication No. US20050249730A1
; GENERAL INFORMATION:
;  APPLICANT: GOETSCH, LILIANE
;  APPLICANT:  CORVAIA, NATHALIE
;  APPLICANT:  DUFLOS, ALAIN
;  APPLICANT:  HAEUW, JEAN-FRANCOIS
;  APPLICANT:  LEGER, OLIVIER
;  APPLICANT:  BECK, ALAIN
;  TITLE OF INVENTION: NOVEL ANTI-IGF-IR AND/OR ANTI-INSULIN/IGF-I HYBRID
;  TITLE OF INVENTION:  RECEPTORS ANTIBODIES AND USES THEREOF
;  FILE REFERENCE: 017753-198
;  CURRENT APPLICATION NUMBER: US/11/012,353
;  CURRENT FILING DATE:  2004-12-16
;  PRIOR APPLICATION NUMBER: 10/735,916
;  PRIOR FILING DATE: 2003-12-16
;  PRIOR APPLICATION NUMBER: FR 0308538
;  PRIOR FILING DATE: 2003-07-11
;  PRIOR APPLICATION NUMBER: PCT/FR03/00178
;  PRIOR FILING DATE: 2003-01-20
;  PRIOR APPLICATION NUMBER: FR 0205753
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: FR 0200653
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: FR 0200654
;  PRIOR FILING DATE: 2002-01-18
;  NUMBER OF SEQ ID NOS: 162
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 85
;   LENGTH: 135
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-012-353-85

  Query Match             44.4%;  Score 40;  DB 7;  Length 135;
  Best Local Similarity   80.0%;  Pred. No. 17;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 TINYAPSLKD 17
              | || |||||
Db         75 TNNYKPSLKD 84


RESULT 34
US-11-054-515-1826
; Sequence 1826, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1826
;   LENGTH: 245
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1826

  Query Match             44.4%;  Score 40;  DB 7;  Length 245;
```

```
  Best Local Similarity   60.0%;  Pred. No. 33;
  Matches    9;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              |   ||||:|| |:|
Db         51 IDSSSSTIHYADSVK 65


RESULT 35
US-11-054-515-1990
; Sequence 1990, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1990
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1990

  Query Match             44.4%;  Score 40;  DB 7;  Length 250;
  Best Local Similarity   72.7%;  Pred. No. 34;
  Matches    8;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 SSTINYAPSLK 16
              | :||| ||||
Db         55 SGSINYNPSLK 65


RESULT 36
US-11-098-686-10788
; Sequence 10788, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
;  APPLICANT: Kapur, Vivek and Gebhart, Connie J.
;  TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
;  TITLE OF INVENTION:  FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
;  FILE REFERENCE: 09531-128001
;  CURRENT APPLICATION NUMBER: US/11/098,686
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: PCT/US03/31318
;  PRIOR FILING DATE: 2003-10-01
;  PRIOR APPLICATION NUMBER: US 60/416,395
;  PRIOR FILING DATE: 2002-10-04
;  NUMBER OF SEQ ID NOS: 11433
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10788
;   LENGTH: 290
;   TYPE: PRT
;   ORGANISM: Lawsonia intracellularis
US-11-098-686-10788

  Query Match             44.4%;  Score 40;  DB 7;  Length 290;
  Best Local Similarity   42.9%;  Pred. No. 40;
  Matches    6;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 PDSSTINYAPSLKD 17
              |||  :|  ||:::
Db        177 PDSPVVNMLPSIRE 190


RESULT 37
US-10-501-035-209
; Sequence 209, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
;  TITLE OF INVENTION:  ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINASES
;  TITLE OF INVENTION:  AND/OR PROTEIN TYROSINE KINASE PATHWAYS
;  FILE REFERENCE: D0185 PCT
;  CURRENT APPLICATION NUMBER: US/10/501,035
;  CURRENT FILING DATE:  2004-07-09
;  PRIOR APPLICATION NUMBER: US 60/350,061
;  PRIOR FILING DATE: 2002-01-18
;  NUMBER OF SEQ ID NOS: 795
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 209
;   LENGTH: 384
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-501-035-209

  Query Match             44.4%;  Score 40;  DB 6;  Length 384;
  Best Local Similarity   50.0%;  Pred. No. 55;
  Matches    7;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSL 15
              :|| || ::||  |
Db         79 LHPGSSALHYAVEL 92


RESULT 38
US-10-510-386-212
; Sequence 212, Application US/10510386
; Publication No. US20050244922A1
; GENERAL INFORMATION:
;  APPLICANT: Andersen, Jens Tonne
;  APPLICANT:  Clausen, Ib Groth
;  APPLICANT:  Jorgensen, Steen Troels
;  APPLICANT:  Olsen, Peter Bjarke
;  APPLICANT:  Rasmussen, Michael Dolberg
;  TITLE OF INVENTION: Improved Bacillus Host Cell
;  FILE REFERENCE: 10294.204-US
;  CURRENT APPLICATION NUMBER: US/10/510,386
;  CURRENT FILING DATE:  2004-10-04
;  NUMBER OF SEQ ID NOS: 248
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 212
;   LENGTH: 387
;   TYPE: PRT
;   ORGANISM: Bacillus licheniformis
US-10-510-386-212

  Query Match             44.4%;  Score 40;  DB 6;  Length 387;
  Best Local Similarity   50.0%;  Pred. No. 56;
  Matches    7;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 PDSSTINYAPSLKD 17
              ||   | |||: :|
```

```
Db        206 PDQKVILYAPTYRD 219


RESULT 39
US-11-054-515-1864
; Sequence 1864, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1864
;   LENGTH: 245
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1864

  Query Match             43.9%;  Score 39.5;  DB 7;  Length 245;
  Best Local Similarity   66.7%;  Pred. No. 40;
  Matches   10;  Conservative    0;  Mismatches    4;  Indels    1;  Gaps    1;

Qy          1 EIHPDSSTINYAPSL 15
              |||  | | || |||
Db         51 EIH-HSGTTNYNPSL 64


RESULT 40
US-10-467-657-5042
; Sequence 5042, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5042
;   LENGTH: 668
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5042

  Query Match             43.9%;  Score 39.5;  DB 6;  Length 668;
  Best Local Similarity   52.9%;  Pred. No. 1.3e+02;
  Matches    9;  Conservative    4;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 EIHPDSSTINYAPSLKD 17
              ::| |  || :||:|||
Db        396 KLHTDVYTI-HAPTLKD 411


RESULT 41
US-11-157-494-7
; Sequence 7, Application US/11157494
; Publication No. US20060029601A1
; GENERAL INFORMATION:
;  APPLICANT: Cardarelli, Josephine M.
;  APPLICANT:  Witte, Alison
;  APPLICANT:  Srinvasan, Mohan
;  TITLE OF INVENTION: INTERFERON ALPHA RECEPTOR 1 ANTIBODIES AND THEIR USES
;  FILE REFERENCE: 04280/1201494-US1
;  CURRENT APPLICATION NUMBER: US/11/157,494
;  CURRENT FILING DATE:  2005-06-20
;  PRIOR APPLICATION NUMBER: 60/581,747
;  PRIOR FILING DATE: 2004-06-21
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-157-494-7

  Query Match             43.3%;  Score 39;  DB 7;  Length 17;
  Best Local Similarity   46.7%;  Pred. No. 2.2;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              |:|  | | |:|| :
Db          2 IYPGDSDIRYSPSFQ 16


RESULT 42
US-11-157-494-8
; Sequence 8, Application US/11157494
; Publication No. US20060029601A1
; GENERAL INFORMATION:
;  APPLICANT: Cardarelli, Josephine M.
;  APPLICANT:  Witte, Alison
;  APPLICANT:  Srinvasan, Mohan
;  TITLE OF INVENTION: INTERFERON ALPHA RECEPTOR 1 ANTIBODIES AND THEIR USES
;  FILE REFERENCE: 04280/1201494-US1
;  CURRENT APPLICATION NUMBER: US/11/157,494
;  CURRENT FILING DATE:  2005-06-20
;  PRIOR APPLICATION NUMBER: 60/581,747
;  PRIOR FILING DATE: 2004-06-21
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 8
;   LENGTH: 17
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-157-494-8

  Query Match             43.3%;  Score 39;  DB 7;  Length 17;
  Best Local Similarity   46.7%;  Pred. No. 2.2;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              |:|  | | |:|| :
Db          2 IYPGDSDIRYSPSFQ 16


RESULT 43
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US-11-157-494-27
; Sequence 27, Application US/11157494
; Publication No. US20060029601A1
; GENERAL INFORMATION:
;  APPLICANT: Cardarelli, Josephine M.
;  APPLICANT:  Witte, Alison
;  APPLICANT:  Srinvasan, Mohan
;  TITLE OF INVENTION: INTERFERON ALPHA RECEPTOR 1 ANTIBODIES AND THEIR USES
;  FILE REFERENCE: 04280/1201494-US1
;  CURRENT APPLICATION NUMBER: US/11/157,494
;  CURRENT FILING DATE:  2005-06-20
;  PRIOR APPLICATION NUMBER: 60/581,747
;  PRIOR FILING DATE: 2004-06-21
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-157-494-27

  Query Match             43.3%;  Score 39;  DB 7;  Length 117;
  Best Local Similarity   46.7%;  Pred. No. 20;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              |:|  | | |:|| :
Db         51 IYPGDSDIRYSPSFQ 65


RESULT 44
US-11-157-494-28
; Sequence 28, Application US/11157494
; Publication No. US20060029601A1
; GENERAL INFORMATION:
;  APPLICANT: Cardarelli, Josephine M.
;  APPLICANT:  Witte, Alison
;  APPLICANT:  Srinvasan, Mohan
;  TITLE OF INVENTION: INTERFERON ALPHA RECEPTOR 1 ANTIBODIES AND THEIR USES
;  FILE REFERENCE: 04280/1201494-US1
;  CURRENT APPLICATION NUMBER: US/11/157,494
;  CURRENT FILING DATE:  2005-06-20
;  PRIOR APPLICATION NUMBER: 60/581,747
;  PRIOR FILING DATE: 2004-06-21
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
;   LENGTH: 117
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-157-494-28

  Query Match             43.3%;  Score 39;  DB 7;  Length 117;
  Best Local Similarity   46.7%;  Pred. No. 20;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              |:|  | | |:|| :
Db         51 IYPGDSDIRYSPSFQ 65


RESULT 45
US-10-993-543-56
; Sequence 56, Application US/10993543
; Publication No. US20060036076A1
; GENERAL INFORMATION:
;  APPLICANT: Dransfield, Daniel T.
;  APPLICANT:  Rookey, Kristin
;  APPLICANT:  Ladner, Robert C.
;  TITLE OF INVENTION: Metalloproteinase-Binding Proteins
;  FILE REFERENCE: 10280-088001
;  CURRENT APPLICATION NUMBER: US/10/993,543
;  CURRENT FILING DATE:  2004-11-19
;  PRIOR APPLICATION NUMBER: US 60/523,745
;  PRIOR FILING DATE: 2003-11-19
;  NUMBER OF SEQ ID NOS: 299
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56
;   LENGTH: 130
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-993-543-56

  Query Match             43.3%;  Score 39;  DB 6;  Length 130;
  Best Local Similarity   46.7%;  Pred. No. 23;
  Matches    7;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLK 16
              |:|   : ||| |:|
Db         51 IYPSGGSTNYADSVK 65


RESULT 46
US-11-096-568A-28652
; Sequence 28652, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28652
;   LENGTH: 205
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(205)
;   OTHER INFORMATION: Ceres Seq. ID no. 3031116
US-11-096-568A-28652

  Query Match             43.3%;  Score 39;  DB 7;  Length 205;
  Best Local Similarity   43.8%;  Pred. No. 39;
  Matches    7;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLKD 17
              |||  :| ||  :  |
Db        177 IHPSEATYNYMGNFLD 192


RESULT 47
US-11-096-568A-28651
; Sequence 28651, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28651
;   LENGTH: 223
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(223)
;   OTHER INFORMATION: Ceres Seq. ID no. 3031115
US-11-096-568A-28651

  Query Match             43.3%;  Score 39;  DB 7;  Length 223;
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  Best Local Similarity   43.8%;  Pred. No. 43;
  Matches    7;  Conservative    2;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          2 IHPDSSTINYAPSLKD 17
              |||  :| ||  :  |
Db        195 IHPSEATYNYMGNFLD 210


RESULT 48
US-11-054-515-1847
; Sequence 1847, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
;  FILE REFERENCE: PF523P3
;  CURRENT APPLICATION NUMBER: US/11/054,515
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: 60/543,296
;  PRIOR FILING DATE: 2004-02-11
;  PRIOR APPLICATION NUMBER: 60/580,347
;  PRIOR FILING DATE: 2004-06-18
;  PRIOR APPLICATION NUMBER: 10/293,418
;  PRIOR FILING DATE: 2002-11-14
;  PRIOR APPLICATION NUMBER: 60/331,469
;  PRIOR FILING DATE: 2001-11-16
;  PRIOR APPLICATION NUMBER: 60/340,817
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: 09/880,748
;  PRIOR FILING DATE: 2001-06-15
;  PRIOR APPLICATION NUMBER: 60/293,499
;  PRIOR FILING DATE: 2001-05-25
;  PRIOR APPLICATION NUMBER: 60/277,379
;  PRIOR FILING DATE: 2001-03-21
;  PRIOR APPLICATION NUMBER: 60/276,248
;  PRIOR FILING DATE: 2001-03-16
;  PRIOR APPLICATION NUMBER: 60/240,816
;  PRIOR FILING DATE: 2000-10-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1847
;   LENGTH: 246
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-515-1847

  Query Match             43.3%;  Score 39;  DB 7;  Length 246;
  Best Local Similarity   72.7%;  Pred. No. 48;
  Matches    8;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 SSTINYAPSLK 16
              | | || ||||
Db         55 SGTTNYNPSLK 65


RESULT 49
US-10-453-372-288
; Sequence 288, Application US/10453372
; Publication No. US20060003323A1
; GENERAL INFORMATION:
;  APPLICANT: Alsobrook, et al.
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
;  FILE REFERENCE: 21402-589 A
;  CURRENT APPLICATION NUMBER: US/10/453,372
;  CURRENT FILING DATE:  2003-06-03
;  PRIOR APPLICATION NUMBER: 09/789390
;  PRIOR FILING DATE: 2001-02-23
;  PRIOR APPLICATION NUMBER: 60/185967
;  PRIOR FILING DATE: 2000-03-01
;  PRIOR APPLICATION NUMBER: 09/823187
;  PRIOR FILING DATE: 2001-03-29
;  PRIOR APPLICATION NUMBER: 60/195792
;  PRIOR FILING DATE: 2000-03-10
;  PRIOR APPLICATION NUMBER: 09/839446
;  PRIOR FILING DATE: 2001-03-19
;  PRIOR APPLICATION NUMBER: 60/199476
;  PRIOR FILING DATE: 2000-03-25
;  PRIOR APPLICATION NUMBER: 09/863776
;  PRIOR FILING DATE: 2001-05-23
;  PRIOR APPLICATION NUMBER: 60/208263
;  PRIOR FILING DATE: 2000-05-31
;  PRIOR APPLICATION NUMBER: 09/939398
;  PRIOR FILING DATE: 2001-08-24
;  PRIOR APPLICATION NUMBER: 60/227800
;  PRIOR FILING DATE: 2000-08-25
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1609
;  SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 288
;   LENGTH: 253
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-453-372-288

  Query Match             43.3%;  Score 39;  DB 6;  Length 253;
  Best Local Similarity   44.4%;  Pred. No. 49;
  Matches    8;  Conservative    3;  Mismatches    3;  Indels    4;  Gaps    1;

Qy          4 PDSS----TINYAPSLKD 17
              |||      |:|| |:: |
Db        162 PDSRRVLVTVNYPPTITD 179


RESULT 50
US-11-195-739-3
; Sequence 3, Application US/11195739
; Publication No. US20060019324A1
; GENERAL INFORMATION:
;  APPLICANT: ALZARI, PEDRO
;  APPLICANT:  BOITEL, BIRGITTE
;  APPLICANT:  VILLARINO, ANDREA
;  APPLICANT:  FERNANDEZ, PABLO
;  APPLICANT:  COLE, STEWART
;  TITLE OF INVENTION: PKNB KINASE AND PSTP PHOSPHATASE AND METHODS OF IDENTIFYING
;  TITLE OF INVENTION:  INHIBITORY SUBSTANCES
;  FILE REFERENCE: 252853US
;  CURRENT APPLICATION NUMBER: US/11/195,739
;  CURRENT FILING DATE:  2005-08-03
;  PRIOR APPLICATION NUMBER: US/10/892,170
;  PRIOR FILING DATE: 2004-07-16
;  PRIOR APPLICATION NUMBER: US 60/487,943
;  PRIOR FILING DATE: 2003-07-18
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 271
;   TYPE: PRT
;   ORGANISM: Mycobacterium tuberculosis
US-11-195-739-3

  Query Match             43.3%;  Score 39;  DB 7;  Length 271;
  Best Local Similarity   53.8%;  Pred. No. 53;
  Matches    7;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 PDSSTINYAPSLK 16
              || ||: || ::|
Db         75 PDVSTLTYAEAVK 87


Search completed: March 23, 2006, 02:53:10
Job time : 17.4384 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:40:10 ; Search time 86.9863 Seconds
(without alignments)
50.511 Million cell updates/sec

Title: US-10-755-382-25
Perfect score: 64
Sequence: 1 LYFGFPWFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	64	100.0	10	2	AAR97318	Aar97318 Humanised
2	64	100.0	10	8	ADM95107	Adm95107 Murine MN
3	64	100.0	10	8	ADM98316	Adm98316 Humanised
4	64	100.0	118	6	ABR42755	Abr42755 Anti-CEA
5	64	100.0	119	2	AAR97336	Aar97336 Humanised
6	64	100.0	119	2	AAR97334	Aar97334 Murine NE
7	64	100.0	119	8	ADM95101	Adm95101 Humanised
8	64	100.0	119	8	ADM95095	Adm95095 Murine MN
9	64	100.0	119	8	ADM98324	Adm98324 Humanised
10	64	100.0	119	8	ADM98318	Adm98318 Murine MN
11	64	100.0	138	6	ABG76489	Abg76489 Heavy cha
12	64	100.0	256	6	ABR42757	Abr42757 Anti-CEA
13	64	100.0	257	6	ABR42758	Abr42758 Anti-CEA
14	64	100.0	261	6	ABR42289	Abr42289 Diabody 6
15	64	100.0	261	6	ABR42754	Abr42754 Anti-CEA
16	64	100.0	261	6	ABR83645	Abr83645 hMN14-scF
17	64	100.0	267	6	ABR42292	Abr42292 Bispecifi
18	64	100.0	267	6	ABR42299	Abr42299 Bispecifi
19	64	100.0	267	6	ABR42296	Abr42296 Bispecifi
20	64	100.0	267	6	ABR42294	Abr42294 Bispecifi
21	64	100.0	358	8	ADU26571	Adu26571 Chimeric
22	64	100.0	363	8	ADU26561	Adu26561 Chimeric
23	64	100.0	364	8	ADU26570	Adu26570 Chimeric
24	64	100.0	370	8	ADU26560	Adu26560 Chimeric
25	64	100.0	415	6	ABR83648	Abr83648 TS1 VH ch
26	64	100.0	443	6	ABG76488	Abg76488 Humanised
27	64	100.0	443	6	ABG74240	Abg74240 Chimaeric
28	64	100.0	468	7	ADE64201	Ade64201 MN14HCF p
29	64	100.0	468	7	ADF60815	Adf60815 hMN-14 he
30	64	100.0	669	9	ADY97271	Ady97271 Exemplary
31	48	75.0	253	2	AAR72599	Aar72599 Anti-dans
32	44	68.8	2210	3	AAB10040	Aab10040 LCMV L pr
33	43	67.2	116	2	AAW04592	Aaw04592 Anti-DNA
34	43	67.2	812	9	AEB39735	Aeb39735 L. pneumo
35	43	67.2	812	9	AEB36318	Aeb36318 L. pneumo
36	42	65.6	12	2	AAR83375	Aar83375 Kbm1-bind
37	42	65.6	117	5	ABP02212	Abp02212 Human ORF
38	42	65.6	119	2	AAW01585	Aaw01585 Lead bind
39	42	65.6	153	4	AAU10305	Aau10305 G-protein
40	42	65.6	246	6	ABP56821	Abp56821 Human glu
41	42	65.6	349	2	AAR48750	Aar48750 G-protein
42	42	65.6	349	2	AAW02722	Aaw02722 G-protein
43	42	65.6	369	4	AAB73388	Aab73388 Anti-VHSV
44	42	65.6	422	6	ABP56819	Abp56819 Rat gluco
45	42	65.6	423	2	AAW34512	Aaw34512 G protein
46	42	65.6	423	2	AAW32797	Aaw32797 Human der
47	42	65.6	423	2	AAW81460	Aaw81460 Human G-p
48	42	65.6	423	4	AAE03740	Aae03740 Mouse G-p
49	42	65.6	423	4	AAE03739	Aae03739 Human G-p
50	42	65.6	423	4	AAM51507	Aam51507 Mouse 5HT
51	42	65.6	423	5	AAE20598	Aae20598 Homo sapi
52	42	65.6	423	6	ABP82004	Abp82004 Human G p
53	42	65.6	423	6	ABP56820	Abp56820 Human glu
54	42	65.6	423	7	ADB99301	Adb99301 Human G-p
55	42	65.6	423	7	ADC77649	Adc77649 Human 177
56	42	65.6	423	8	ADO29447	Ado29447 Mouse GPC
57	42	65.6	423	8	ADO29446	Ado29446 Human GPC
58	42	65.6	519	8	ADN22876	Adn22876 Bacterial
59	42	65.6	661	7	ADF70500	Adf70500 Orphan re
60	41	64.1	67	4	AAG76239	Aag76239 Human col
61	41	64.1	118	8	ADI26480	Adi26480 H. pylori
62	41	64.1	140	2	AAR12234	Aar12234 Mouse MAb
63	41	64.1	141	2	AAR12356	Aar12356 Heavy cha
64	41	64.1	222	7	ADC00898	Adc00898 Enterohae
65	41	64.1	247	7	ADC01034	Adc01034 Enterohae
66	41	64.1	323	4	ABG30065	Abg30065 Novel hum
67	40	62.5	62	1	AAP92262	Aap92262 Sequence
68	40	62.5	71	4	AAO05036	Aao05036 Human pol
69	40	62.5	117	8	ADT74977	Adt74977 Heavy cha
70	40	62.5	117	8	ADT74983	Adt74983 Heavy cha
71	40	62.5	117	8	ADT74987	Adt74987 Heavy cha
72	40	62.5	118	5	AAE29269	Aae29269 S. aureus
73	40	62.5	118	5	AAE29265	Aae29265 S. aureus
74	40	62.5	281	5	ABP69038	Abp69038 Human pol
75	40	62.5	289	7	ADJ70353	Adj70353 Human hea
76	40	62.5	299	2	AAW61629	Aaw61629 Clone HMW
77	40	62.5	299	2	AAW78168	Aaw78168 Human sec
78	40	62.5	299	2	AAW78295	Aaw78295 Fragment
79	40	62.5	299	2	AAW80985	Aaw80985 B cell re
80	40	62.5	299	2	AAW80984	Aaw80984 Amino aci
81	40	62.5	299	3	AAY94443	Aay94443 Human rep
82	40	62.5	299	6	ABP56745	Abp56745 Human BAP
83	40	62.5	299	7	ADB85515	Adb85515 Human CG1
84	40	62.5	299	7	ABW01511	Abw01511 Human rec
85	40	62.5	299	7	ABW01525	Abw01525 Protein #
86	40	62.5	299	7	ADD69022	Add69022 Human B-c
87	40	62.5	299	7	ADE62956	Ade62956 Human Pro
88	40	62.5	299	8	ADK15383	Adk15383 Human BAP
89	40	62.5	299	8	ABM81338	Abm81338 Tumour-as
90	40	62.5	299	8	ADX97570	Adx97570 Pancreati
91	40	62.5	299	9	AEB98457	Aeb98457 Human B-c
92	40	62.5	299	9	AEB98442	Aeb98442 Human HMW
93	40	62.5	305	8	ADJ66531	Adj66531 B-cell re
94	40	62.5	309	4	ABB11913	Abb11913 Human B-c
95	40	62.5	309	5	ABP41873	Abp41873 Human ova
96	40	62.5	309	7	ADC32757	Adc32757 Human nov
97	40	62.5	309	8	ADX97593	Adx97593 Pancreati

98	40	62.5	442	3	AAG49900	Aag49900	Arabidops
99	40	62.5	442	3	AAG31862	Aag31862	Arabidops
100	40	62.5	442	5	ABB92870	Abb92870	Herbicida
101	40	62.5	442	5	ABB91843	Abb91843	Herbicida
102	40	62.5	445	4	AAG89873	Aag89873	C glutami
103	40	62.5	445	7	ADL65645	Adl65645	C. glutam
104	40	62.5	447	5	ABB93806	Abb93806	Herbicida
105	40	62.5	447	5	ABB91450	Abb91450	Herbicida
106	40	62.5	452	5	ABB91451	Abb91451	Herbicida
107	40	62.5	958	8	ADN25851	Adn25851	Bacterial
108	39.5	61.7	195	7	ABR84724	Abr84724	Vector pG
109	39.5	61.7	195	7	ABR84722	Abr84722	Vector pG
110	39	60.9	31	3	AAB51946	Aab51946	Human sec
111	39	60.9	94	4	AAM88218	Aam88218	Human imm
112	39	60.9	120	2	AAW04176	Aaw04176	Variant v
113	39	60.9	120	2	AAW16619	Aaw16619	Anti-huma
114	39	60.9	121	2	AAW00833	Aaw00833	Variable
115	39	60.9	187	6	ABU38091	Abu38091	Protein e
116	39	60.9	256	6	ABM72553	Abm72553	Staphyloc
117	39	60.9	285	4	ABG13938	Abg13938	Novel hum
118	39	60.9	287	8	ADS52148	Ads52148	Human sec
119	39	60.9	345	7	ADC24067	Adc24067	Protein s
120	39	60.9	345	8	ADH36168	Adh36168	Chemical
121	39	60.9	345	8	ADG93868	Adg93868	Nitrilase
122	39	60.9	345	8	ADI62466	Adi62466	Nitrilase
123	39	60.9	345	8	ADI64587	Adi64587	Nitrilase
124	39	60.9	363	4	AAG81604	Aag81604	S. epider
125	39	60.9	369	6	ABJ19161	Abj19161	Pathogen
126	39	60.9	370	5	ABP39548	Abp39548	Staphyloc
127	39	60.9	370	8	ADS05504	Ads05504	Staphyloc
128	39	60.9	419	7	ADI21556	Adi21556	Novel hum
129	39	60.9	479	9	ABM97256	Abm97256	M. xanthu
130	39	60.9	490	8	ADO26830	Ado26830	Human rec
131	39	60.9	559	5	ABP43486	Abp43486	Human sec
132	39	60.9	559	6	ADA54123	Ada54123	Human pro
133	39	60.9	559	7	ADI21066	Adi21066	Novel hum
134	39	60.9	1075	4	AAB30804	Aab30804	Amino aci
135	38.5	60.2	514	7	ABM89076	Abm89076	Rice abio
136	38.5	60.2	576	7	ABM88274	Abm88274	Rice abio
137	38.5	60.2	1204	7	ABM86823	Abm86823	Rice abio
138	38	59.4	15	9	ADW77816	Adw77816	Human can
139	38	59.4	58	4	AAE01775	Aae01775	Human gen
140	38	59.4	58	4	AAE01807	Aae01807	Human gen
141	38	59.4	58	5	ABG64190	Abg64190	Human alb
142	38	59.4	58	5	ABG64193	Abg64193	Human alb
143	38	59.4	58	8	ADL77455	Adl77455	Albumin f
144	38	59.4	58	8	ADL77458	Adl77458	Albumin f
145	38	59.4	104	4	AAU63177	Aau63177	Propionib
146	38	59.4	104	6	ABM59696	Abm59696	Propionib
147	38	59.4	227	4	AAM91983	Aam91983	Human dig
148	38	59.4	275	9	ABM95810	Abm95810	M. xanthu
149	38	59.4	318	6	ABU49698	Abu49698	Protein e
150	38	59.4	357	4	AAG82732	Aag82732	S. epider
151	38	59.4	357	9	ABM90704	Abm90704	M. xanthu
152	38	59.4	415	5	ABP40256	Abp40256	Staphyloc
153	38	59.4	415	8	ADS06705	Ads06705	Staphyloc
154	38	59.4	481	6	ADB09454	Adb09454	Alloiococ
155	38	59.4	520	7	ADM25497	Adm25497	Hyperther
156	38	59.4	528	6	ADB09456	Adb09456	Alloiococ
157	38	59.4	555	6	ADB09458	Adb09458	Alloiococ
158	38	59.4	557	6	ADB09460	Adb09460	Alloiococ
159	38	59.4	567	7	ABO78268	Abo78268	Pseudomon
160	38	59.4	750	8	ADN20442	Adn20442	Bacterial
161	38	59.4	936	8	ABM80670	Abm80670	Tumour-as
162	37.5	58.6	295	6	ABP57742	Abp57742	C. elegan
163	37	57.8	11	4	AAB86083	Aab86083	H. pylori
164	37	57.8	11	4	AAB86051	Aab86051	H. pylori
165	37	57.8	47	4	AAM16491	Aam16491	Peptide #
166	37	57.8	47	4	ABB35476	Abb35476	Peptide #
167	37	57.8	47	4	ABB30307	Abb30307	Peptide #
168	37	57.8	47	4	AAM68673	Aam68673	Human bon
169	37	57.8	47	4	AAM04216	Aam04216	Peptide #
170	37	57.8	47	5	ABG38254	Abg38254	Human pep
171	37	57.8	67	8	ADX76590	Adx76590	Plant ful
172	37	57.8	120	4	AAB86107	Aab86107	H. pylori
173	37	57.8	120	4	AAB86069	Aab86069	H. pylori
174	37	57.8	224	8	ADX72561	Adx72561	Plant ful
175	37	57.8	296	7	ADF04387	Adf04387	Bacterial
176	37	57.8	307	8	ADX71952	Adx71952	Plant ful
177	37	57.8	349	7	ABO70241	Abo70241	Pseudomon
178	37	57.8	357	9	AEB37414	Aeb37414	L. pneumo
179	37	57.8	367	7	ADE58275	Ade58275	Rat Prote
180	37	57.8	429	6	ABM67687	Abm67687	Photorhab
181	37	57.8	434	3	AAG49901	Aag49901	Arabidops
182	37	57.8	434	3	AAG31863	Aag31863	Arabidops
183	37	57.8	479	6	ABU40260	Abu40260	Protein e
184	37	57.8	483	7	ABO80521	Abo80521	Pseudomon
185	37	57.8	485	6	ABU48689	Abu48689	Protein e
186	37	57.8	520	6	ABU39238	Abu39238	Protein e
187	37	57.8	583	8	ADJ93707	Adj93707	AChE1 pro
188	37	57.8	585	8	ADJ93706	Adj93706	AChE1 pro
189	37	57.8	695	4	AAB76535	Aab76535	Corynebac
190	37	57.8	771	7	ADB79935	Adb79935	Human put
191	37	57.8	771	8	ADH09712	Adh09712	Human hos
192	37	57.8	795	8	ADU23197	Adu23197	Murine To
193	37	57.8	806	3	AAY88055	Aay88055	Murine To
194	37	57.8	806	8	ADU23194	Adu23194	Murine To
195	37	57.8	806	8	ADU23196	Adu23196	Murine To
196	37	57.8	806	8	ADU23195	Adu23195	Murine To
197	37	57.8	831	8	ADY24712	Ady24712	Plant ful
198	37	57.8	850	2	AAW62040	Aaw62040	Protein i
199	37	57.8	876	8	ADH09711	Adh09711	Human hos
200	37	57.8	985	5	ABP43746	Abp43746	2 PUMH2 p
201	37	57.8	987	7	ADD01184	Add01184	Human nuc
202	37	57.8	989	6	ABU23252	Abu23252	Protein e
203	37	57.8	1064	7	ADB65676	Adb65676	Human pro
204	37	57.8	1064	8	ADH09713	Adh09713	Human hos
205	37	57.8	1064	8	ADH09714	Adh09714	Human hos
206	37	57.8	1064	8	ADI24520	Adi24520	Human mod
207	37	57.8	1064	8	ADU60174	Adu60174	Housekeep
208	37	57.8	1064	9	ADX06467	Adx06467	Cyclin-de
209	37	57.8	2012	4	AAB76534	Aab76534	Corynebac
210	37	57.8	2993	4	AAG92485	Aag92485	C glutami
211	36.5	57.0	95	5	ABP33975	Abp33975	Human ORF
212	36.5	57.0	381	8	ADS21905	Ads21905	Bacterial
213	36.5	57.0	400	5	AAM51027	Aam51027	Soybean p
214	36.5	57.0	424	7	ADK41172	Adk41172	CaaX pren
215	36.5	57.0	424	8	ADM98461	Adm98461	Soybean c
216	36	56.2	15	9	ADW78220	Adw78220	Human met
217	36	56.2	43	3	AAB34617	Aab34617	Human sec
218	36	56.2	123	2	AAR45187	Aar45187	Heavy cha
219	36	56.2	135	4	ABB68451	Abb68451	Drosophil
220	36	56.2	139	7	ADF30320	Adf30320	Human can
221	36	56.2	141	9	ABM96289	Abm96289	M. xanthu
222	36	56.2	157	7	ADM25656	Adm25656	Hyperther
223	36	56.2	158	5	AAG66170	Aag66170	L. helvet
224	36	56.2	158	6	ABP98175	Abp98175	Amino aci
225	36	56.2	159	6	ABP98180	Abp98180	Amino aci
226	36	56.2	201	9	ABM94565	Abm94565	M. xanthu
227	36	56.2	212	2	AAW37815	Aaw37815	Human sec
228	36	56.2	214	6	ABU02149	Abu02149	S. pneumo
229	36	56.2	214	6	ABP81443	Abp81443	Streptoco
230	36	56.2	214	8	ADK46671	Adk46671	Streptoco
231	36	56.2	216	8	ADL27023	Adl27023	Human 587
232	36	56.2	253	9	AEB39554	Aeb39554	L. pneumo
233	36	56.2	253	9	AEB36131	Aeb36131	L. pneumo
234	36	56.2	256	4	ABG18699	Abg18699	Novel hum
235	36	56.2	275	7	ADF77694	Adf77694	Human mat
236	36	56.2	282	6	ABU26517	Abu26517	Protein e
237	36	56.2	285	8	ADX92220	Adx92220	Plant ful
238	36	56.2	287	9	AEB40074	Aeb40074	L. pneumo
239	36	56.2	287	9	AEB36682	Aeb36682	L. pneumo
240	36	56.2	295	2	AAW37943	Aaw37943	Amino aci
241	36	56.2	295	2	AAW82588	Aaw82588	Human ATG
242	36	56.2	295	2	AAW37814	Aaw37814	Murine se
243	36	56.2	295	2	AAW75102	Aaw75102	Human sec

244	36	56.2	295	2	AAW49082	Aaw49082 Homo sapi
245	36	56.2	295	2	AAY41748	Aay41748 Human PRO
246	36	56.2	295	2	AAY06923	Aay06923 Human sec
247	36	56.2	295	3	AAB44304	Aab44304 Human PRO
248	36	56.2	295	5	ABB84861	Abb84861 Human PRO
249	36	56.2	295	5	ABG31500	Abg31500 Murine se
250	36	56.2	295	5	ABG31499	Abg31499 Human sec
251	36	56.2	295	5	ABB95467	Abb95467 Human ang
252	36	56.2	295	6	ABO25250	Abo25250 Novel hum
253	36	56.2	295	6	ABU72256	Abu72256 Novel hum
254	36	56.2	295	6	ABU55908	Abu55908 Human pro
255	36	56.2	295	6	ABU84936	Abu84936 Human sec
256	36	56.2	295	6	AAE34062	Aae34062 SARP 2 pr
257	36	56.2	295	6	ABR47455	Abr47455 Breast ca
258	36	56.2	295	6	ABU61134	Abu61134 Human PRO
259	36	56.2	295	6	ABU80403	Abu80403 Human sec
260	36	56.2	295	6	ABO01978	Abo01978 Novel hum
261	36	56.2	295	6	ADA24954	Ada24954 Novel hum
262	36	56.2	295	6	ABO19705	Abo19705 Novel hum
263	36	56.2	295	6	ADA12615	Ada12615 Human sec
264	36	56.2	295	6	ABO19596	Abo19596 Novel hum
265	36	56.2	295	7	ADB73921	Adb73921 Human PRO
266	36	56.2	295	7	ADB76637	Adb76637 Human PRO
267	36	56.2	295	7	ADC44063	Adc44063 Human sec
268	36	56.2	295	7	ADC61823	Adc61823 Human sec
269	36	56.2	295	7	ADC63787	Adc63787 Human sec
270	36	56.2	295	7	ADC66887	Adc66887 Human sec
271	36	56.2	295	7	ADC69011	Adc69011 Human sec
272	36	56.2	295	7	ADC63071	Adc63071 Human sec
273	36	56.2	295	7	ADC68136	Adc68136 Human sec
274	36	56.2	295	7	ADC41456	Adc41456 Human sec
275	36	56.2	295	7	ADC67511	Adc67511 Human sec
276	36	56.2	295	7	ADC62447	Adc62447 Human sec
277	36	56.2	295	7	ADC42080	Adc42080 Human sec
278	36	56.2	295	7	ADD10379	Add10379 Human sec
279	36	56.2	295	7	ADD11339	Add11339 Human sec
280	36	56.2	295	7	ADD37132	Add37132 Human sec
281	36	56.2	295	7	ADE49449	Ade49449 Human sec
282	36	56.2	295	7	ADE35503	Ade35503 Human sec
283	36	56.2	295	7	ADE16617	Ade16617 Human sec
284	36	56.2	295	7	ADD73232	Add73232 Human sec
285	36	56.2	295	7	ADD72590	Add72590 Human sec
286	36	56.2	295	7	ADE17241	Ade17241 Human sec
287	36	56.2	295	7	ADF47255	Adf47255 Human sec
288	36	56.2	295	7	ADF77693	Adf77693 Human ful
289	36	56.2	295	7	ADG53012	Adg53012 Human sec
290	36	56.2	295	7	ADG60332	Adg60332 Human sec
291	36	56.2	295	7	ADI61092	Adi61092 Human sec
292	36	56.2	295	7	ADJ70064	Adj70064 Human hea
293	36	56.2	295	7	ADN40027	Adn40027 Cancer/an
294	36	56.2	295	8	ADE48749	Ade48749 Human sec
295	36	56.2	295	8	ADE41340	Ade41340 Human sec
296	36	56.2	295	8	ADE89850	Ade89850 Human sec
297	36	56.2	295	8	ADF61490	Adf61490 Human sec
298	36	56.2	295	8	ADF40182	Adf40182 Human sec
299	36	56.2	295	8	ADF45978	Adf45978 Human sec
300	36	56.2	295	8	ADF24374	Adf24374 Human sec
301	36	56.2	295	8	ADF40806	Adf40806 Human sec
302	36	56.2	295	8	ADF23750	Adf23750 Human sec
303	36	56.2	295	8	ADF33733	Adf33733 Human sec
304	36	56.2	295	8	ADF27200	Adf27200 Human sec
305	36	56.2	295	8	ADF27836	Adf27836 Human sec
306	36	56.2	295	8	ADF41430	Adf41430 Human sec
307	36	56.2	295	8	ADF33109	Adf33109 Human sec
308	36	56.2	295	8	ADF25475	Adf25475 Human sec
309	36	56.2	295	8	ADF26576	Adf26576 Human sec
310	36	56.2	295	8	ADF34365	Adf34365 Human sec
311	36	56.2	295	8	ADF46602	Adf46602 Human sec
312	36	56.2	295	8	ADG50588	Adg50588 Human sec
313	36	56.2	295	8	ADG49964	Adg49964 Human sec
314	36	56.2	295	8	ADG51836	Adg51836 Human sec
315	36	56.2	295	8	ADG49340	Adg49340 Human sec
316	36	56.2	295	8	ADG48716	Adg48716 Human sec
317	36	56.2	295	8	ADG51212	Adg51212 Human sec
318	36	56.2	295	8	ADH43523	Adh43523 Human PRO
319	36	56.2	295	8	ADG59156	Adg59156 Human sec
320	36	56.2	295	8	ADG62612	Adg62612 Human sec
321	36	56.2	295	8	ADH25637	Adh25637 Human neu
322	36	56.2	295	8	ADK82868	Adk82868 Human PRO
323	36	56.2	295	8	ADM17414	Adm17414 Human sec
324	36	56.2	295	8	ADL07248	Adl07248 Human sec
325	36	56.2	295	8	ADN05090	Adn05090 Antipsori
326	36	56.2	295	8	ADR46694	Adr46694 Cancer-as
327	36	56.2	295	8	ADU50370	Adu50370 PRO697, S
328	36	56.2	295	8	ADU86504	Adu86504 Human sec
329	36	56.2	295	8	ADU86507	Adu86507 Mouse sec
330	36	56.2	295	9	ADW49649	Adw49649 PRO697 pr
331	36	56.2	295	9	ADZ12379	Adz12379 Human sec
332	36	56.2	295	9	ADZ52310	Adz52310 Human sec
333	36	56.2	296	2	AAW75160	Aaw75160 Human sec
334	36	56.2	296	6	ABO02036	Abo02036 Novel hum
335	36	56.2	296	8	ADU06371	Adu06371 Novel bro
336	36	56.2	296	9	ADZ12437	Adz12437 Human sec
337	36	56.2	298	6	ABP56746	Abp56746 Mouse BAP
338	36	56.2	317	4	ABG19316	Abg19316 Novel hum
339	36	56.2	337	5	ABG69056	Abg69056 Amino aci
340	36	56.2	338	6	ABU16912	Abu16912 Protein e
341	36	56.2	347	8	ADN46886	Adn46886 Thermococ
342	36	56.2	348	6	ADA35556	Ada35556 Acinetoba
343	36	56.2	350	2	AAR20230	Aar20230 hUOG-1. 5
344	36	56.2	350	3	AAY53644	Aay53644 Protein e
345	36	56.2	350	6	ABR58529	Abr58529 Human gro
346	36	56.2	350	7	ADN38928	Adn38928 Cancer/an
347	36	56.2	359	6	ABU09147	Abu09147 Arthrobac
348	36	56.2	373	6	ABU29649	Abu29649 Protein e
349	36	56.2	373	7	ADC94892	Adc94892 E. faeciu
350	36	56.2	377	4	AAG75608	Aag75608 Human col
351	36	56.2	377	7	ABM74358	Abm74358 DNA clone
352	36	56.2	378	7	ABG75208	Abg75208 A sativa
353	36	56.2	378	9	AEA21699	Aea21699 A. sativa
354	36	56.2	385	7	ADE58277	Ade58277 Human Pro
355	36	56.2	404	6	ABU17049	Abu17049 Protein e
356	36	56.2	408	2	AAY74087	Aay74087 Human pro
357	36	56.2	410	6	ADA33573	Ada33573 Acinetoba
358	36	56.2	423	5	ABP66063	Abp66063 Bifidobac
359	36	56.2	424	2	AAW43038	Aaw43038 Amino aci
360	36	56.2	424	4	ABB56331	Abb56331 Non-endog
361	36	56.2	424	6	ABP81925	Abp81925 Human vas
362	36	56.2	424	6	AAO30985	Aao30985 Human vas
363	36	56.2	424	7	ADD47976	Add47976 Human Pro
364	36	56.2	424	7	ADE55192	Ade55192 Human Pro
365	36	56.2	424	8	ADM46107	Adm46107 Human AVP
366	36	56.2	424	8	ADO29191	Ado29191 Human GPC
367	36	56.2	425	8	ADT60623	Adt60623 Plant pol
368	36	56.2	435	2	AAY11026	Aay11026 H. pylori
369	36	56.2	437	8	ADY08436	Ady08436 Plant ful
370	36	56.2	453	5	ABB93808	Abb93808 Herbicida
371	36	56.2	477	5	ABB53673	Abb53673 Lactococc
372	36	56.2	477	8	ADS29296	Ads29296 Bacterial
373	36	56.2	567	6	ABU21519	Abu21519 Protein e
374	36	56.2	578	7	ADE08748	Ade08748 Novel pro
375	36	56.2	594	5	ABB92580	Abb92580 Herbicida
376	36	56.2	613	7	ABO74408	Abo74408 Pseudomon
377	36	56.2	630	7	ABO70956	Abo70956 Pseudomon
378	36	56.2	700	4	ABB59309	Abb59309 Drosophil
379	36	56.2	700	4	AAU38926	Aau38926 Drosophil
380	36	56.2	700	7	ADC35760	Adc35760 Drosophil
381	36	56.2	728	8	ADS28884	Ads28884 Bacterial
382	36	56.2	763	6	ABU33126	Abu33126 Protein e
383	36	56.2	794	9	AEB38662	Aeb38662 L. pneumo
384	36	56.2	794	9	AEB41896	Aeb41896 L. pneumo
385	36	56.2	800	3	AAB25537	Aab25537 Eucalyptu
386	36	56.2	819	8	ADN21313	Adn21313 Bacterial
387	36	56.2	878	8	ADJ66574	Adj66574 VAV-2 pro
388	36	56.2	1058	4	ABB62096	Abb62096 Drosophil
389	36	56.2	1082	6	ABU26260	Abu26260 Protein e

390	36	56.2	1211	6	ADA36680	Ada36680	Acinetoba
391	36	56.2	2694	9	AEB00342	Aeb00342	Plastid t
392	36	56.2	3116	9	AEB00338	Aeb00338	Plastid t
393	36	56.2	3530	9	AEB00359	Aeb00359	Plastid t
394	35.5	55.5	116	2	AAR79246	Aar79246	Heavy cha
395	35.5	55.5	120	2	AAR79889	Aar79889	Anti-EGFR
396	35	54.7	9	6	ABG71651	Abg71651	CDR3 of H
397	35	54.7	10	8	ADP84862	Adp84862	Complemen
398	35	54.7	10	8	ADT75012	Adt75012	Murine he
399	35	54.7	12	9	ADY93308	Ady93308	mAb CG10
400	35	54.7	20	2	AAY08711	Aay08711	Human mil
401	35	54.7	20	9	ADY58492	Ady58492	Peptide u
402	35	54.7	40	2	AAW19269	Aaw19269	Lactobaci
403	35	54.7	44	3	AAB38023	Aab38023	Fragment
404	35	54.7	68	4	AAB51248	Aab51248	Mouse ami
405	35	54.7	75	4	AAG92042	Aag92042	C glutami
406	35	54.7	84	4	AAB51246	Aab51246	Mouse ami
407	35	54.7	95	4	AAU49465	Aau49465	Propionib
408	35	54.7	95	6	ABM45984	Abm45984	Propionib
409	35	54.7	105	4	AAG62629	Aag62629	C vulgari
410	35	54.7	105	4	AAG62630	Aag62630	C vulgari
411	35	54.7	105	4	AAG62631	Aag62631	C sorokin
412	35	54.7	105	8	ADQ65097	Adq65097	Novel hum
413	35	54.7	112	4	AAU22165	Aau22165	Human car
414	35	54.7	112	7	ADE46133	Ade46133	Human car
415	35	54.7	112	8	ADJ07551	Adj07551	Human car
416	35	54.7	116	3	AAB10443	Aab10443	Murine mo
417	35	54.7	118	2	AAR22421	Aar22421	Antibody
418	35	54.7	118	2	AAR22420	Aar22420	Murine he
419	35	54.7	118	2	AAR54757	Aar54757	Mouse HMF
420	35	54.7	118	2	AAR54758	Aar54758	Humanised
421	35	54.7	119	8	ADP84915	Adp84915	Variable
422	35	54.7	119	8	ADP84918	Adp84918	Variable
423	35	54.7	119	8	ADP84921	Adp84921	Variable
424	35	54.7	119	8	ADP84925	Adp84925	Variable
425	35	54.7	119	8	ADP84930	Adp84930	Variable
426	35	54.7	119	8	ADP84908	Adp84908	Variable
427	35	54.7	119	8	ADP84909	Adp84909	Variable
428	35	54.7	119	8	ADP84917	Adp84917	Variable
429	35	54.7	119	8	ADP84934	Adp84934	Variable
430	35	54.7	119	8	ADP84910	Adp84910	Variable
431	35	54.7	119	8	ADP84911	Adp84911	Variable
432	35	54.7	119	8	ADP84912	Adp84912	Variable
433	35	54.7	119	8	ADP84931	Adp84931	Variable
434	35	54.7	119	8	ADP84906	Adp84906	Variable
435	35	54.7	119	8	ADP84924	Adp84924	Variable
436	35	54.7	119	8	ADP84922	Adp84922	Variable
437	35	54.7	119	8	ADP84937	Adp84937	Variable
438	35	54.7	119	8	ADP84935	Adp84935	Variable
439	35	54.7	119	8	ADP84920	Adp84920	Variable
440	35	54.7	119	8	ADP84927	Adp84927	Variable
441	35	54.7	119	8	ADP84907	Adp84907	Variable
442	35	54.7	119	8	ADP84914	Adp84914	Variable
443	35	54.7	119	8	ADP84919	Adp84919	Variable
444	35	54.7	119	8	ADP84923	Adp84923	Variable
445	35	54.7	119	8	ADP84913	Adp84913	Variable
446	35	54.7	119	8	ADP84928	Adp84928	Variable
447	35	54.7	119	8	ADP84929	Adp84929	Variable
448	35	54.7	119	8	ADP84933	Adp84933	Variable
449	35	54.7	119	8	ADP84936	Adp84936	Variable
450	35	54.7	119	8	ADP84916	Adp84916	Variable
451	35	54.7	119	8	ADP84926	Adp84926	Variable
452	35	54.7	119	8	ADP84932	Adp84932	Variable
453	35	54.7	119	8	ADR42621	Adr42621	Mouse ant
454	35	54.7	124	3	AAB38021	Aab38021	Fragment
455	35	54.7	127	9	ADY93376	Ady93376	VH domain
456	35	54.7	137	6	ABG71659	Abg71659	HMFG-1 he
457	35	54.7	141	9	AEB41708	Aeb41708	L. pneumo
458	35	54.7	150	4	AAU14622	Aau14622	Novel bon
459	35	54.7	154	6	ABM69939	Abm69939	Photorhab
460	35	54.7	157	3	AAG23969	Aag23969	Arabidops
461	35	54.7	158	9	AEB38448	Aeb38448	L. pneumo
462	35	54.7	173	3	AAG45492	Aag45492	Arabidops
463	35	54.7	175	4	AAU31048	Aau31048	Novel hum
464	35	54.7	177	3	AAG15765	Aag15765	Arabidops
465	35	54.7	187	8	ADX67299	Adx67299	Plant ful
466	35	54.7	216	5	ABP27809	Abp27809	Streptoco
467	35	54.7	220	4	AAG62632	Aag62632	Chlorella
468	35	54.7	220	6	ABU27816	Abu27816	Protein e
469	35	54.7	235	8	ADY12976	Ady12976	Plant ful
470	35	54.7	247	9	ADZ76001	Adz76001	huHMFG1 (
471	35	54.7	255	3	AAG43309	Aag43309	Arabidops
472	35	54.7	255	3	AAG23968	Aag23968	Arabidops
473	35	54.7	258	8	ADS22368	Ads22368	Bacterial
474	35	54.7	259	3	AAG43308	Aag43308	Arabidops
475	35	54.7	259	3	AAG23967	Aag23967	Arabidops
476	35	54.7	263	8	ADS25793	Ads25793	Bacterial
477	35	54.7	266	6	ABP79364	Abp79364	N. gonorr
478	35	54.7	272	2	AAW00557	Aaw00557	Nematode
479	35	54.7	272	2	AAW43913	Aaw43913	Mus muscu
480	35	54.7	277	6	ABU25916	Abu25916	Protein e
481	35	54.7	281	6	ABU37963	Abu37963	Protein e
482	35	54.7	285	6	ABU16637	Abu16637	Protein e
483	35	54.7	288	3	AAG43307	Aag43307	Arabidops
484	35	54.7	288	7	ADD30142	Add30142	Plant yie
485	35	54.7	288	8	ADI44291	Adi44291	Plant tra
486	35	54.7	290	2	AAW98335	Aaw98335	H. pylori
487	35	54.7	290	2	AAW71474	Aaw71474	Helicobac
488	35	54.7	290	4	AAB46294	Aab46294	H. pylori
489	35	54.7	290	4	AAB46352	Aab46352	H. pylori
490	35	54.7	290	6	ABU30818	Abu30818	Protein e
491	35	54.7	290	6	ADA33036	Ada33036	Acinetoba
492	35	54.7	294	4	AAB46293	Aab46293	Fusion co
493	35	54.7	296	3	AAB25314	Aab25314	Eucalyptu
494	35	54.7	303	6	ABU37361	Abu37361	Protein e
495	35	54.7	304	5	ABP29658	Abp29658	Streptoco
496	35	54.7	304	8	ADV88562	Adv88562	Streptoco
497	35	54.7	304	8	ADV79815	Adv79815	Streptoco
498	35	54.7	304	8	ADV81969	Adv81969	Streptoco
499	35	54.7	308	4	AAG71524	Aag71524	Human olf
500	35	54.7	308	4	ABB44525	Abb44525	Human GPC
501	35	54.7	308	4	AAU24742	Aau24742	Human olf
502	35	54.7	308	5	ABP95703	Abp95703	Human GPC
503	35	54.7	308	5	AAU95729	Aau95729	Human olf
504	35	54.7	308	5	AAU85362	Aau85362	G-coupled
505	35	54.7	308	7	ADC86333	Adc86333	Human GPC
506	35	54.7	308	7	ABW02126	Abw02126	Human GPC
507	35	54.7	309	2	AAY28246	Aay28246	Human sec
508	35	54.7	309	4	AAU39023	Aau39023	Human sec
509	35	54.7	309	5	ABB55732	Abb55732	Human pol
510	35	54.7	309	9	ADW09157	Adw09157	Human sec
511	35	54.7	316	5	ABP25572	Abp25572	Streptoco
512	35	54.7	316	6	ABR01671	Abr01671	Human G p
513	35	54.7	322	6	ABU02606	Abu02606	S. pneumo
514	35	54.7	331	4	AAB96558	Aab96558	Putative
515	35	54.7	336	7	ADC87473	Adc87473	Human GPC
516	35	54.7	336	9	ADY93404	Ady93404	Hybrid pr
517	35	54.7	341	6	ABU39449	Abu39449	Protein e
518	35	54.7	342	7	ADC96785	Adc96785	E. faeciu
519	35	54.7	368	5	ABB90024	Abb90024	Human pol
520	35	54.7	392	6	ABU45168	Abu45168	Protein e
521	35	54.7	397	6	ABU29814	Abu29814	Protein e
522	35	54.7	405	7	ADC97139	Adc97139	E. faeciu
523	35	54.7	409	7	ADJ71150	Adj71150	Human hea
524	35	54.7	416	3	AAB56817	Aab56817	Human pro
525	35	54.7	422	4	AAB79581	Aab79581	Corynebac
526	35	54.7	422	4	AAG90357	Aag90357	C glutami
527	35	54.7	426	4	AAG62628	Aag62628	Chlorella
528	35	54.7	428	6	ABU33541	Abu33541	Protein e
529	35	54.7	434	6	ABR41161	Abr41161	Human DIT
530	35	54.7	444	8	ADT05606	Adt05606	Haemophil
531	35	54.7	448	8	ADP84969	Adp84969	Chimeric
532	35	54.7	455	2	AAY41751	Aay41751	Human PRO
533	35	54.7	455	3	AAB44307	Aab44307	Human PRO
534	35	54.7	455	4	AAB74708	Aab74708	Human mem
535	35	54.7	455	4	AAU29030	Aau29030	Human PRO

536	35	54.7	455	4	AAB87527	Aab87527 Human PRO
537	35	54.7	455	5	ABG95852	Abg95852 Human sec
538	35	54.7	455	5	ABP61441	Abp61441 Human NF-
539	35	54.7	455	6	ABU58406	Abu58406 Human PRO
540	35	54.7	455	6	ABU87954	Abu87954 Novel hum
541	35	54.7	455	6	ABU84269	Abu84269 Human sec
542	35	54.7	455	6	ABR66143	Abr66143 Human sec
543	35	54.7	455	6	ABR65533	Abr65533 Human sec
544	35	54.7	455	6	ABU99473	Abu99473 Human sec
545	35	54.7	455	6	ABU82712	Abu82712 Human PRO
546	35	54.7	455	6	ABU89833	Abu89833 Novel hum
547	35	54.7	455	6	ABR68082	Abr68082 Human sec
548	35	54.7	455	6	ABU96135	Abu96135 Novel hum
549	35	54.7	455	6	ABU92566	Abu92566 Human sec
550	35	54.7	455	6	ABO08643	Abo08643 Human sec
551	35	54.7	455	6	ABO02695	Abo02695 Human sec
552	35	54.7	455	6	ABR74849	Abr74849 Human sec
553	35	54.7	455	6	ABR94611	Abr94611 Human sec
554	35	54.7	455	6	ABO25253	Abo25253 Novel hum
555	35	54.7	455	6	ABU85584	Abu85584 Human PRO
556	35	54.7	455	6	ABU98744	Abu98744 Novel hum
557	35	54.7	455	6	ABU97959	Abu97959 Novel hum
558	35	54.7	455	6	ABU91665	Abu91665 Novel hum
559	35	54.7	455	6	ABU72259	Abu72259 Novel hum
560	35	54.7	455	6	ABU89358	Abu89358 Human PRO
561	35	54.7	455	6	ABU86199	Abu86199 Human sec
562	35	54.7	455	6	ABU67412	Abu67412 Human sec
563	35	54.7	455	6	ABU80440	Abu80440 Human PRO
564	35	54.7	455	6	ABU90877	Abu90877 Novel hum
565	35	54.7	455	6	ABO33936	Abo33936 Human sec
566	35	54.7	455	6	ABR99358	Abr99358 Human sec
567	35	54.7	455	6	ABR98748	Abr98748 Human sec
568	35	54.7	455	6	ABO16271	Abo16271 Human sec
569	35	54.7	455	6	ABR92171	Abr92171 Human sec
570	35	54.7	455	6	ABO18812	Abo18812 Human sec
571	35	54.7	455	6	ABR78233	Abr78233 Human sec
572	35	54.7	455	6	ABU71953	Abu71953 Novel hum
573	35	54.7	455	6	ABU84969	Abu84969 Novel hum
574	35	54.7	455	6	ABO00108	Abo00108 Novel hum
575	35	54.7	455	6	ABO11440	Abo11440 Human sec
576	35	54.7	455	6	ABO02085	Abo02085 Human sec
577	35	54.7	455	6	ABU88659	Abu88659 Novel hum
578	35	54.7	455	6	ABU83354	Abu83354 Human sec
579	35	54.7	455	6	ABO06155	Abo06155 Novel hum
580	35	54.7	455	6	ABR59191	Abr59191 Human sec
581	35	54.7	455	6	ABO09253	Abo09253 Human sec
582	35	54.7	455	6	ABO19117	Abo19117 Novel hum
583	35	54.7	455	6	ABO11135	Abo11135 Human sec
584	35	54.7	455	6	ABR66753	Abr66753 Human sec
585	35	54.7	455	6	ABO15966	Abo15966 Human sec
586	35	54.7	455	6	ABO13672	Abo13672 Human sec
587	35	54.7	455	6	ABU84939	Abu84939 Human sec
588	35	54.7	455	6	ABU71507	Abu71507 Human sec
589	35	54.7	455	6	ABU65575	Abu65575 Human sec
590	35	54.7	455	6	ABO07423	Abo07423 Human PRO
591	35	54.7	455	6	ABO03610	Abo03610 Human sec
592	35	54.7	455	6	ABR67058	Abr67058 Human sec
593	35	54.7	455	6	ABO15661	Abo15661 Human sec
594	35	54.7	455	6	ABU55942	Abu55942 Human sec
595	35	54.7	455	6	ABU61137	Abu61137 Human PRO
596	35	54.7	455	6	ABU72288	Abu72288 Human PRO
597	35	54.7	455	6	ABU65270	Abu65270 Human PRO
598	35	54.7	455	6	ABU95215	Abu95215 Novel hum
599	35	54.7	455	6	ABU71118	Abu71118 Human PRO
600	35	54.7	455	6	ABO07728	Abo07728 Human PRO
601	35	54.7	455	6	ABR69969	Abr69969 Human sec
602	35	54.7	455	6	ABR69302	Abr69302 Human sec
603	35	54.7	455	6	ABO01443	Abo01443 Human PRO
604	35	54.7	455	6	ABU81245	Abu81245 Human PRO
605	35	54.7	455	6	ABR60042	Abr60042 Human sec
606	35	54.7	455	6	ABU90961	Abu90961 Human PRO
607	35	54.7	455	6	ABR67777	Abr67777 Human sec
608	35	54.7	455	6	ABR65165	Abr65165 Human sec
609	35	54.7	455	6	ABR68387	Abr68387 Human sec
610	35	54.7	455	6	ABR71799	Abr71799 Human sec
611	35	54.7	455	6	ABU85279	Abu85279 Human PRO
612	35	54.7	455	6	ABU88969	Abu88969 Human sec
613	35	54.7	455	6	ABU83049	Abu83049 Human sec
614	35	54.7	455	6	ABU94905	Abu94905 Novel hum
615	35	54.7	455	6	ABU90453	Abu90453 Novel hum
616	35	54.7	455	6	ABU83964	Abu83964 Human sec
617	35	54.7	455	6	ABU93615	Abu93615 Novel hum
618	35	54.7	455	6	ABR64860	Abr64860 Human sec
619	35	54.7	455	6	ABO27282	Abo27282 Human sec
620	35	54.7	455	6	ABR68692	Abr68692 Human sec
621	35	54.7	455	6	ABO06508	Abo06508 Human sec
622	35	54.7	455	6	ABR99053	Abr99053 Human sec
623	35	54.7	455	6	ABU56937	Abu56937 Human PRO
624	35	54.7	455	6	ABU85889	Abu85889 Novel hum
625	35	54.7	455	6	ABU82176	Abu82176 Novel hum
626	35	54.7	455	6	ABU87187	Abu87187 Human PRO
627	35	54.7	455	6	ABU83659	Abu83659 Human sec
628	35	54.7	455	6	ABO08033	Abo08033 Human PRO
629	35	54.7	455	6	ABU92477	Abu92477 Human sec
630	35	54.7	455	6	ABP81711	Abp81711 Human G p
631	35	54.7	455	6	ABU81744	Abu81744 Novel hum
632	35	54.7	455	6	ABU65908	Abu65908 Novel hum
633	35	54.7	455	6	ABU81147	Abu81147 Human sec
634	35	54.7	455	6	ABR59737	Abr59737 Human sec
635	35	54.7	455	6	ABU93925	Abu93925 Novel hum
636	35	54.7	455	6	ABU80406	Abu80406 Human sec
637	35	54.7	455	6	ABU99778	Abu99778 Novel hum
638	35	54.7	455	6	ABR66448	Abr66448 Human sec
639	35	54.7	455	6	ABR90866	Abr90866 Human sec
640	35	54.7	455	6	ABO53262	Abo53262 Novel hum
641	35	54.7	455	6	ABU94293	Abu94293 Human PRO
642	35	54.7	455	6	ABU79175	Abu79175 Human PRO
643	35	54.7	455	6	ABU86504	Abu86504 Human sec
644	35	54.7	455	6	ABU86809	Abu86809 Novel hum
645	35	54.7	455	6	ABU94598	Abu94598 Human PRO
646	35	54.7	455	6	ABO04525	Abo04525 Human PRO
647	35	54.7	455	6	ABR70274	Abr70274 Human sec
648	35	54.7	455	6	ABU98439	Abu98439 Human PRO
649	35	54.7	455	6	ABR65838	Abr65838 Human sec
650	35	54.7	455	6	ABR64555	Abr64555 Human sec
651	35	54.7	455	6	ABR41016	Abr41016 Human MAP
652	35	54.7	455	6	ABU79480	Abu79480 Human PRO
653	35	54.7	455	6	ABU92871	Abu92871 Human sec
654	35	54.7	455	6	ABU95830	Abu95830 Human PRO
655	35	54.7	455	6	ABU91050	Abu91050 Novel hum
656	35	54.7	455	6	ABU90143	Abu90143 Novel hum
657	35	54.7	455	6	ABO09558	Abo09558 Human sec
658	35	54.7	455	6	ABO10830	Abo10830 Human sec
659	35	54.7	455	6	ABR70884	Abr70884 Human sec
660	35	54.7	455	6	ABU98264	Abu98264 Novel hum
661	35	54.7	455	6	ABU87492	Abu87492 Human PRO
662	35	54.7	455	6	ABU91360	Abu91360 Human PRO
663	35	54.7	455	6	ABU89269	Abu89269 Novel hum
664	35	54.7	455	6	ABU84574	Abu84574 Human sec
665	35	54.7	455	6	ABR69664	Abr69664 Human sec
666	35	54.7	455	6	ABU80041	Abu80041 Human PRO
667	35	54.7	455	6	ABU82476	Abu82476 Novel hum
668	35	54.7	455	6	ABU93310	Abu93310 Human PRO
669	35	54.7	455	6	ABO09863	Abo09863 Human sec
670	35	54.7	455	6	ABO08948	Abo08948 Human sec
671	35	54.7	455	6	ABU96440	Abu96440 Human PRO
672	35	54.7	455	6	ABU10516	Abu10516 Human sec
673	35	54.7	455	6	ABU72110	Abu72110 Human PRO
674	35	54.7	455	6	ABU95525	Abu95525 Human PRO
675	35	54.7	455	6	ABU96734	Abu96734 Novel hum
676	35	54.7	455	6	ABR70579	Abr70579 Human sec
677	35	54.7	455	6	ABO04930	Abo04930 Novel hum
678	35	54.7	455	6	ABO08338	Abo08338 Human sec
679	35	54.7	455	6	ABO05545	Abo05545 Human sec
680	35	54.7	455	6	ABR73934	Abr73934 Human sec
681	35	54.7	455	6	ABR95526	Abr95526 Human sec

682	35	54.7	455	6	ABR80823	Abr80823 Human sec
683	35	54.7	455	6	ABR81128	Abr81128 Human sec
684	35	54.7	455	6	ABM00824	Abm00824 Human sec
685	35	54.7	455	6	ABR88426	Abr88426 Human sec
686	35	54.7	455	6	ABM77247	Abm77247 Human sec
687	35	54.7	455	6	ABO28731	Abo28731 Human sec
688	35	54.7	455	6	ABO31476	Abo31476 Human sec
689	35	54.7	455	6	ABM07893	Abm07893 Human sec
690	35	54.7	455	6	ABO40373	Abo40373 Human sec
691	35	54.7	455	6	ABO35798	Abo35798 Human PRO
692	35	54.7	455	6	ABO43937	Abo43937 Human PRO
693	35	54.7	455	6	ADA77766	Ada77766 Human sec
694	35	54.7	455	6	ABM24732	Abm24732 Human sec
695	35	54.7	455	6	ABO03000	Abo03000 Human sec
696	35	54.7	455	6	ABR90256	Abr90256 Human sec
697	35	54.7	455	6	ABM17170	Abm17170 Human sec
698	35	54.7	455	6	ABR94916	Abr94916 Human sec
699	35	54.7	455	6	ABR95221	Abr95221 Human sec
700	35	54.7	455	6	ADB17061	Adb17061 Human tra
701	35	54.7	455	6	ABO21459	Abo21459 Human sec
702	35	54.7	455	6	ABR97723	Abr97723 Human sec
703	35	54.7	455	6	ABR87511	Abr87511 Human sec
704	35	54.7	455	6	ABM77552	Abm77552 Human sec
705	35	54.7	455	6	ABM27782	Abm27782 Human sec
706	35	54.7	455	6	ABM06063	Abm06063 Human sec
707	35	54.7	455	6	ABM03569	Abm03569 Human sec
708	35	54.7	455	6	ABM35020	Abm35020 Human sec
709	35	54.7	455	6	ABM26257	Abm26257 Human sec
710	35	54.7	455	6	ABO48039	Abo48039 Human sec
711	35	54.7	455	6	ABR92781	Abr92781 Human sec
712	35	54.7	455	6	ABO24542	Abo24542 Human sec
713	35	54.7	455	6	ABM11553	Abm11553 Human sec
714	35	54.7	455	6	ABM02654	Abm02654 Human sec
715	35	54.7	455	6	ABM15950	Abm15950 Human sec
716	35	54.7	455	6	ABO27511	Abo27511 Human sec
717	35	54.7	455	6	ABM29002	Abm29002 Human sec
718	35	54.7	455	6	ABM06978	Abm06978 Human sec
719	35	54.7	455	6	ABM21072	Abm21072 Human sec
720	35	54.7	455	6	ABM09418	Abm09418 Human sec
721	35	54.7	455	6	ABO41288	Abo41288 Human sec
722	35	54.7	455	6	ABO36103	Abo36103 Human PRO
723	35	54.7	455	6	ABO43632	Abo43632 Human PRO
724	35	54.7	455	6	ABM76332	Abm76332 Human sec
725	35	54.7	455	6	ABM76028	Abm76028 Human sec
726	35	54.7	455	6	ABM25647	Abm25647 Human sec
727	35	54.7	455	6	ABM25952	Abm25952 Human sec
728	35	54.7	455	6	ABO03305	Abo03305 Human sec
729	35	54.7	455	6	ABO02390	Abo02390 Human sec
730	35	54.7	455	6	ABO44240	Abo44240 Human sec
731	35	54.7	455	6	ABR90561	Abr90561 Human sec
732	35	54.7	455	6	ABR73629	Abr73629 Human sec
733	35	54.7	455	6	ABO16881	Abo16881 Human sec
734	35	54.7	455	6	ABR94306	Abr94306 Human sec
735	35	54.7	455	6	ABR75813	Abr75813 Human sec
736	35	54.7	455	6	ABR71189	Abr71189 Human sec
737	35	54.7	455	6	ABR93086	Abr93086 Human sec
738	35	54.7	455	6	ABR93391	Abr93391 Human sec
739	35	54.7	455	6	ABR87816	Abr87816 Human sec
740	35	54.7	455	6	ABO27816	Abo27816 Human sec
741	35	54.7	455	6	ABO29951	Abo29951 Human sec
742	35	54.7	455	6	ABO33160	Abo33160 Human PRO
743	35	54.7	455	6	ABM04848	Abm04848 Human sec
744	35	54.7	455	6	ABM08808	Abm08808 Human sec
745	35	54.7	455	6	ABO36408	Abo36408 Human sec
746	35	54.7	455	6	ABO35493	Abo35493 Human PRO
747	35	54.7	455	6	ABO39458	Abo39458 Human sec
748	35	54.7	455	6	ABM10333	Abm10333 Human sec
749	35	54.7	455	6	ABM11858	Abm11858 Human sec
750	35	54.7	455	6	ABO52004	Abo52004 Human PRO
751	35	54.7	455	6	ABO52309	Abo52309 Human PRO
752	35	54.7	455	6	ADA19866	Ada19866 Novel hum
753	35	54.7	455	6	ABO23627	Abo23627 Human sec
754	35	54.7	455	6	ADB17249	Adb17249 Human tra
755	35	54.7	455	6	ABR97113	Abr97113 Human sec
756	35	54.7	455	6	ABR86901	Abr86901 Human sec
757	35	54.7	455	6	ABM10943	Abm10943 Human sec
758	35	54.7	455	6	ABM28087	Abm28087 Human sec
759	35	54.7	455	6	ABO32086	Abo32086 Human sec
760	35	54.7	455	6	ABM15213	Abm15213 Human sec
761	35	54.7	455	6	ABM06368	Abm06368 Human sec
762	35	54.7	455	6	ABM04179	Abm04179 Human sec
763	35	54.7	455	6	ABM22292	Abm22292 Human sec
764	35	54.7	455	6	ABM07588	Abm07588 Human sec
765	35	54.7	455	6	ABO40678	Abo40678 Human sec
766	35	54.7	455	6	ABM35325	Abm35325 Human sec
767	35	54.7	455	6	ABM33088	Abm33088 Human sec
768	35	54.7	455	6	ABO52614	Abo52614 Human PRO
769	35	54.7	455	6	ABO50174	Abo50174 Human sec
770	35	54.7	455	6	ABU99168	Abu99168 Human sec
771	35	54.7	455	6	ABO04220	Abo04220 Human sec
772	35	54.7	455	6	ABO05850	Abo05850 Human sec
773	35	54.7	455	6	ABM18390	Abm18390 Human sec
774	35	54.7	455	6	ABR97418	Abr97418 Human sec
775	35	54.7	455	6	ABR80518	Abr80518 Human sec
776	35	54.7	455	6	ABM01129	Abm01129 Human sec
777	35	54.7	455	6	ABR88731	Abr88731 Human sec
778	35	54.7	455	6	ABM13383	Abm13383 Human sec
779	35	54.7	455	6	ABM20767	Abm20767 Human sec
780	35	54.7	455	6	ABO41898	Abo41898 Human sec
781	35	54.7	455	6	ABO42508	Abo42508 Human sec
782	35	54.7	455	6	ABM10028	Abm10028 Human sec
783	35	54.7	455	6	ABO38543	Abo38543 Human sec
784	35	54.7	455	6	ABM32783	Abm32783 Human sec
785	35	54.7	455	6	ABM22597	Abm22597 Human sec
786	35	54.7	455	6	ABM74808	Abm74808 Human sec
787	35	54.7	455	6	ADA79558	Ada79558 Human sec
788	35	54.7	455	6	ADA24969	Ada24969 Novel hum
789	35	54.7	455	6	ABR96198	Abr96198 Human sec
790	35	54.7	455	6	ABM02349	Abm02349 Human sec
791	35	54.7	455	6	ABR86291	Abr86291 Human sec
792	35	54.7	455	6	ABR86596	Abr86596 Human sec
793	35	54.7	455	6	ABM16560	Abm16560 Human sec
794	35	54.7	455	6	ABM29612	Abm29612 Human sec
795	35	54.7	455	6	ABO29036	Abo29036 Human sec
796	35	54.7	455	6	ABM23817	Abm23817 Human sec
797	35	54.7	455	6	ABM23207	Abm23207 Human sec
798	35	54.7	455	6	ABM21987	Abm21987 Human sec
799	35	54.7	455	6	ABO37628	Abo37628 Human sec
800	35	54.7	455	6	ABM28392	Abm28392 Human sec
801	35	54.7	455	6	ABM28697	Abm28697 Human sec
802	35	54.7	455	6	ABM66341	Abm66341 Human sec
803	35	54.7	455	6	ABM75723	Abm75723 Human sec
804	35	54.7	455	6	ABM34003	Abm34003 Human sec
805	35	54.7	455	6	ABM34308	Abm34308 Human sec
806	35	54.7	455	6	ABO19708	Abo19708 Novel hum
807	35	54.7	455	6	ABO20239	Abo20239 Human sec
808	35	54.7	455	6	ABO21154	Abo21154 Human sec
809	35	54.7	455	6	ABO22069	Abo22069 Human sec
810	35	54.7	455	6	ADA12630	Ada12630 Human sec
811	35	54.7	455	6	ADA20038	Ada20038 Novel hum
812	35	54.7	455	6	ABO34168	Abo34168 Human sec
813	35	54.7	455	6	ABR96503	Abr96503 Human sec
814	35	54.7	455	6	ABR85681	Abr85681 Human sec
815	35	54.7	455	6	ABR99663	Abr99663 Human sec
816	35	54.7	455	6	ABM00519	Abm00519 Human sec
817	35	54.7	455	6	ABM00214	Abm00214 Human sec
818	35	54.7	455	6	ABO29646	Abo29646 Human sec
819	35	54.7	455	6	ABM23512	Abm23512 Human sec
820	35	54.7	455	6	ABM29307	Abm29307 Human sec
821	35	54.7	455	6	ABO38238	Abo38238 Human sec
822	35	54.7	455	6	ABO45538	Abo45538 Human PRO
823	35	54.7	455	6	ABM20462	Abm20462 Human sec
824	35	54.7	455	6	ADA81285	Ada81285 Human sec
825	35	54.7	455	6	ABO16576	Abo16576 Human sec
826	35	54.7	455	6	ABO18202	Abo18202 Human sec
827	35	54.7	455	6	ABO22629	Abo22629 Human PRO

828	35	54.7	455	6	ABO22934	Abo22934 Human PRO	901	35	54.7	455	6	ABR88121	Abr88121 Human sec			
829	35	54.7	455	6	ABR92476	Abr92476 Human sec	902	35	54.7	455	6	ADA00335	Ada00335 Human sec			
830	35	54.7	455	6	ABR81433	Abr81433 Human sec	903	35	54.7	455	6	ABM26867	Abm26867 Human sec			
831	35	54.7	455	6	ABM77857	Abm77857 Human sec	904	35	54.7	455	6	ABM03264	Abm03264 Human sec			
832	35	54.7	455	6	ABR89646	Abr89646 Human sec	905	35	54.7	455	7	ABO39763	Abo39763 Human sec			
833	35	54.7	455	6	ABM26562	Abm26562 Human sec	906	35	54.7	455	7	ABO49869	Abo49869 Human sec			
834	35	54.7	455	6	ABM13688	Abm13688 Human sec	907	35	54.7	455	7	ABO50784	Abo50784 Human sec			
835	35	54.7	455	6	ABO28426	Abo28426 Human sec	908	35	54.7	455	7	ABO05240	Abo05240 Human sec			
836	35	54.7	455	6	ABO30256	Abo30256 Human sec	909	35	54.7	455	7	ABR74544	Abr74544 Human sec			
837	35	54.7	455	6	ABM07283	Abm07283 Human sec	910	35	54.7	455	7	ABR77023	Abr77023 Human sec			
838	35	54.7	455	6	ABM03874	Abm03874 Human sec	911	35	54.7	455	7	ABM17780	Abm17780 Human sec			
839	35	54.7	455	6	ABO37018	Abo37018 Human sec	912	35	54.7	455	7	ABR95831	Abr95831 Human sec			
840	35	54.7	455	6	ABO41593	Abo41593 Human sec	913	35	54.7	455	7	ABO21764	Abo21764 Human sec			
841	35	54.7	455	6	ABO35188	Abo35188 Human PRO	914	35	54.7	455	7	ABO19934	Abo19934 Human sec			
842	35	54.7	455	6	ABM25037	Abm25037 Human sec	915	35	54.7	455	7	ABO24237	Abo24237 Human sec			
843	35	54.7	455	6	ABO47429	Abo47429 Human sec	916	35	54.7	455	7	ABR85986	Abr85986 Human sec			
844	35	54.7	455	6	ABO47734	Abo47734 Human sec	917	35	54.7	455	7	ABM10638	Abm10638 Human sec			
845	35	54.7	455	6	ABO48344	Abo48344 Human sec	918	35	54.7	455	7	ABM76637	Abm76637 Human sec			
846	35	54.7	455	6	ABO51394	Abo51394 Human PRO	919	35	54.7	455	7	ABR89341	Abr89341 Human sec			
847	35	54.7	455	6	ABO51699	Abo51699 Human PRO	920	35	54.7	455	7	ABM12468	Abm12468 Human sec			
848	35	54.7	455	6	ABO50479	Abo50479 Human sec	921	35	54.7	455	7	ABM05758	Abm05758 Human sec			
849	35	54.7	455	6	ABR79603	Abr79603 Human sec	922	35	54.7	455	7	ABO34883	Abo34883 Human PRO			
850	35	54.7	455	6	ABM16865	Abm16865 Human sec	923	35	54.7	455	7	ABM02959	Abm02959 Human sec			
851	35	54.7	455	6	ABO17897	Abo17897 Human sec	924	35	54.7	455	7	ABM18937	Abm18937 Human sec			
852	35	54.7	455	6	ABO20849	Abo20849 Human sec	925	35	54.7	455	7	ABM19242	Abm19242 Human sec			
853	35	54.7	455	6	ABR96808	Abr96808 Human sec	926	35	54.7	455	7	ABO46453	Abo46453 Human PRO			
854	35	54.7	455	6	ABM12163	Abm12163 Human sec	927	35	54.7	455	7	ABO48954	Abo48954 Human sec			
855	35	54.7	455	6	ABM16255	Abm16255 Human sec	928	35	54.7	455	7	ABR68997	Abr68997 Human sec			
856	35	54.7	455	6	ABM24122	Abm24122 Human sec	929	35	54.7	455	7	ABR89036	Abr89036 Human sec			
857	35	54.7	455	6	ABM14603	Abm14603 Human sec	930	35	54.7	455	7	ABR72409	Abr72409 Human sec			
858	35	54.7	455	6	ABM04484	Abm04484 Human sec	931	35	54.7	455	7	ABR74239	Abr74239 Human sec			
859	35	54.7	455	6	ABM06673	Abm06673 Human sec	932	35	54.7	455	7	ABO18507	Abo18507 Human sec			
860	35	54.7	455	6	ABM09113	Abm09113 Human sec	933	35	54.7	455	7	ABR80213	Abr80213 Human sec			
861	35	54.7	455	6	ABO39153	Abo39153 Human sec	934	35	54.7	455	7	ABM01434	Abm01434 Human sec			
862	35	54.7	455	6	ABM75418	Abm75418 Human sec	935	35	54.7	455	7	ABM02044	Abm02044 Human sec			
863	35	54.7	455	6	ABM25342	Abm25342 Human sec	936	35	54.7	455	7	ABR87206	Abr87206 Human sec			
864	35	54.7	455	6	ABM19852	Abm19852 Human sec	937	35	54.7	455	7	ABM12773	Abm12773 Human sec			
865	35	54.7	455	6	ABO46758	Abo46758 Human PRO	938	35	54.7	455	7	ABM30527	Abm30527 Human sec			
866	35	54.7	455	6	ABO47063	Abo47063 Human PRO	939	35	54.7	455	7	ABM24427	Abm24427 Human sec			
867	35	54.7	455	6	ADA83083	Ada83083 Human sec	940	35	54.7	455	7	ABO29341	Abo29341 Human sec			
868	35	54.7	455	6	ABR71494	Abr71494 Human sec	941	35	54.7	455	7	ABO31171	Abo31171 Human sec			
869	35	54.7	455	6	ABR72104	Abr72104 Human sec	942	35	54.7	455	7	ABM14298	Abm14298 Human sec			
870	35	54.7	455	6	ABR98443	Abr98443 Human sec	943	35	54.7	455	7	ABM09723	Abm09723 Human sec			
871	35	54.7	455	6	ABO06813	Abo06813 Human sec	944	35	54.7	455	7	ABO38848	Abo38848 Human sec			
872	35	54.7	455	6	ABR84766	Abr84766 Human sec	945	35	54.7	455	7	ABM34613	Abm34613 Human sec			
873	35	54.7	455	6	ABR73324	Abr73324 Human sec	946	35	54.7	455	7	ABO51089	Abo51089 Human sec			
874	35	54.7	455	6	ABR76418	Abr76418 Human sec	947	35	54.7	455	7	ABO03915	Abo03915 Human sec			
875	35	54.7	455	6	ABR73019	Abr73019 Human sec	948	35	54.7	455	7	ABO10385	Abo10385 Human PRO			
876	35	54.7	455	6	ABM18085	Abm18085 Human sec	949	35	54.7	455	7	ABR77628	Abr77628 Human sec			
877	35	54.7	455	6	ABO20544	Abo20544 Human sec	950	35	54.7	455	7	ABR78838	Abr78838 Human sec			
878	35	54.7	455	6	ABO25287	Abo25287 Human PRO	951	35	54.7	455	7	ABO23932	Abo23932 Human sec			
879	35	54.7	455	6	ABO25592	Abo25592 Human PRO	952	35	54.7	455	7	ABR93696	Abr93696 Human sec			
880	35	54.7	455	6	ABR94001	Abr94001 Human sec	953	35	54.7	455	7	ABM01739	Abm01739 Human sec			
881	35	54.7	455	6	ABR79908	Abr79908 Human sec	954	35	54.7	455	7	ABM78162	Abm78162 Human sec			
882	35	54.7	455	6	ABM11248	Abm11248 Human sec	955	35	54.7	455	7	ABR89951	Abr89951 Human sec			
883	35	54.7	455	6	ABO32855	Abo32855 Human PRO	956	35	54.7	455	7	ABM27477	Abm27477 Human sec			
884	35	54.7	455	6	ABO30561	Abo30561 Human sec	957	35	54.7	455	7	ABM13078	Abm13078 Human sec			
885	35	54.7	455	6	ABO30866	Abo30866 Human sec	958	35	54.7	455	7	ABO31781	Abo31781 Human sec			
886	35	54.7	455	6	ABM27172	Abm27172 Human sec	959	35	54.7	455	7	ABM13993	Abm13993 Human sec			
887	35	54.7	455	6	ABM29917	Abm29917 Human sec	960	35	54.7	455	7	ABM08198	Abm08198 Human sec			
888	35	54.7	455	6	ABM05453	Abm05453 Human sec	961	35	54.7	455	7	ABO40068	Abo40068 Human sec			
889	35	54.7	455	6	ABM15518	Abm15518 Human sec	962	35	54.7	455	7	ABM74503	Abm74503 Human sec			
890	35	54.7	455	6	ABM08503	Abm08503 Human sec	963	35	54.7	455	7	ABM33698	Abm33698 Human sec			
891	35	54.7	455	6	ABO42203	Abo42203 Human sec	964	35	54.7	455	7	ABM20157	Abm20157 Human sec			
892	35	54.7	455	6	ABO37933	Abo37933 Human sec	965	35	54.7	455	7	ABO48649	Abo48649 Human sec			
893	35	54.7	455	6	ABO45843	Abo45843 Human PRO	966	35	54.7	455	7	ABR72714	Abr72714 Human sec			
894	35	54.7	455	6	ABM66646	Abm66646 Human sec	967	35	54.7	455	7	ABO15356	Abo15356 Human sec			
895	35	54.7	455	6	ADB20126	Adb20126 Human sec	968	35	54.7	455	7	ABR85071	Abr85071 Human sec			
896	35	54.7	455	6	ABM19547	Abm19547 Human sec	969	35	54.7	455	7	ABO15051	Abo15051 Human sec			
897	35	54.7	455	6	ABO49259	Abo49259 Human sec	970	35	54.7	455	7	ABO17186	Abo17186 Human sec			
898	35	54.7	455	6	ABO49564	Abo49564 Human sec	971	35	54.7	455	7	ABM17475	Abm17475 Human sec			
899	35	54.7	455	6	ADA78378	Ada78378 Human sec	972	35	54.7	455	7	ABR85376	Abr85376 Human sec			
900	35	54.7	455	6	ABO19599	Abo19599 Novel hum	973	35	54.7	455	7	ABM76942	Abm76942 Human sec			

974	35	54.7	455	7	ABO28121	Abo28121 Human sec
975	35	54.7	455	7	ABM22902	Abm22902 Human sec
976	35	54.7	455	7	ABM30222	Abm30222 Human sec
977	35	54.7	455	7	ABM21682	Abm21682 Human sec
978	35	54.7	455	7	ABM21377	Abm21377 Human sec
979	35	54.7	455	7	ABM14908	Abm14908 Human sec
980	35	54.7	455	7	ABO40983	Abo40983 Human sec
981	35	54.7	455	7	ABO36713	Abo36713 Human sec
982	35	54.7	455	7	ABO37323	Abo37323 Human sec
983	35	54.7	455	7	ABM75113	Abm75113 Human sec
984	35	54.7	455	7	ABM33393	Abm33393 Human sec
985	35	54.7	455	7	ABO46148	Abo46148 Human PRO
986	35	54.7	455	7	ADA82449	Ada82449 Human sec
987	35	54.7	455	7	ADB85577	Adb85577 Novel hum
988	35	54.7	455	7	ABM31747	Abm31747 Human sec
989	35	54.7	455	7	ABM31137	Abm31137 Human sec
990	35	54.7	455	7	ADB73936	Adb73936 Human PRO
991	35	54.7	455	7	ADB85757	Adb85757 Human sec
992	35	54.7	455	7	ABM32052	Abm32052 Human sec
993	35	54.7	455	7	ABM32357	Abm32357 Human sec
994	35	54.7	455	7	ADB68256	Adb68256 Human PRO
995	35	54.7	455	7	ADB68063	Adb68063 Human PRO
996	35	54.7	455	7	ABM31442	Abm31442 Human sec
997	35	54.7	455	7	ABM30832	Abm30832 Human sec
998	35	54.7	455	7	ADB90880	Adb90880 Novel hum
999	35	54.7	455	7	ADB76652	Adb76652 Human PRO
1000	35	54.7	455	7	ADC44078	Adc44078 Human sec

ALIGNMENTS

RESULT 1
AAR97318
ID AAR97318 standard; peptide; 10 AA.
XX
AC AAR97318;
XX
DT 15-OCT-1996 (first entry)
XX
DE Humanised monoclonal antibody heavy chain CDR.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Mus musculus.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Claim 5; Page 39; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. This sequence is a murine derived CDR region which corresponds
CC to CDR 3 in the heavy chain of the humanised MAb. See AAR97313-97333
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 64; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
||||||||||
Db 1 LYFGFPWFAY 10

RESULT 2
ADM95107
ID ADM95107 standard; peptide; 10 AA.
XX
AC ADM95107;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 MAb heavy chain variable region CDR3.
XX
KW non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW complementarity determining region; pancreatic cancer; breast cancer;
KW ovarian cancer.
XX
OS Mus sp.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-364813/34.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Claim 6; SEQ ID NO 25; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the CDR3 of
CC the murine MN-14 antibody heavy chain variable region and used to
CC generate the humanised/chimeric antibody of the invention.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 64; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 LYFGFPWFAY 10
              ||||||||||
Db          1 LYFGFPWFAY 10


RESULT 3
ADM98316
ID   ADM98316 standard; peptide; 10 AA.
XX
AC   ADM98316;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 antibody heavy chain variable region CDR3 peptide.
XX
KW   carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; humanised;
KW   murine; mouse; antibody; MN-14; non-medullary thyroid carcinoma;
KW   medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW   hepatocellular carcinoma; breast cancer; lung cancer;
KW   antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW   apoptosis.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   WO2004032857-A2.
XX
PD   22-APR-2004.
XX
PF   08-OCT-2003; 2003WO-US031801.
XX
PR   08-OCT-2002; 2002US-0416531P.
PR   11-OCT-2002; 2002WO-US032307.
PR   02-MAY-2003; 2003US-0467161P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Goldenberg DM,  Hansen HJ;
XX
DR   WPI; 2004-340797/31.
XX
PT   Treating non-medullary or medullary thyroid carcinoma, involves
PT   administering to subject, either concurrently or sequentially, anti-
PT   carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS   Claim 8; Page 76; 122pp; English.
XX
CC   This invention relates to methods for treating cancers that express
CC   carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC   therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC   antibodies that can be used following administration of an agent that
CC   will increase antibody effector functions or following administration of
CC   an amount of interferon effective to upregulate CEA expression in tumour
CC   cells. The present invention describes the anti-CEA antibody as a class
CC   III humanised murine monoclonal antibody that retains specificity for CEA
CC   binding and is preferably an MN-14 antibody or fragment thereof.
CC   Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC   composition useful for the treatment of non-medullary or medullary
CC   thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC   carcinoma, as well as breast or lung cancer. Furthermore, it can
CC   stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC   mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC   cell growth and angiogenesis. This peptide sequence is a CDR region of
CC   the humanised murine MN-14 antibody of the invention.
XX
SQ   Sequence 10 AA;

  Query Match             100.0%;  Score 64;  DB 8;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.002;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db          1 LYFGFPWFAY 10


RESULT 4
ABR42755
ID   ABR42755 standard; protein; 118 AA.
XX
AC   ABR42755;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14 VH region.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Disclosure; Fig 12; 62pp; English.
XX
CC   The present sequence is the protein sequence of the heavy chain variable
CC   region of anti-carcinoembryonic antigen (CEA) humanized monoclonal
CC   antibody hMN-14. scFv constructs comprising the hMN-14 VH and Vkappa
CC   regions are used in novel multivalent, monospecific binding proteins
CC   (diabody, triabody and tetrabody) of the invention (see also ABR42754,
CC   ABR42757 and ABR42758). Claimed binding proteins are specific for a
CC   tumour-associated antigen, and are used in the diagnosis and treatment of
CC   a tumour, carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma,
CC   lymphoma or myeloma, or a cancer selected from acute lymphoblastic
CC   leukaemia, acute myelogenous leukaemia, biliary, breast, cervical,
CC   chronic lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 118 AA;

  Query Match             100.0%;  Score 64;  DB 6;  Length 118;
  Best Local Similarity   100.0%;  Pred. No. 0.023;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 5
AAR97336
ID   AAR97336 standard; protein; 119 AA.
XX
```

```
AC   AAR97336;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Humanised antibody variable heavy chain (MN14HuVH).
XX
KW   Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW   complementary determining region; anti-carcinoembryonic antigen; CEA;
KW   diagnosis; imaging; therapy; immune response.
XX
OS   Mus musculus.
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    31. .35
FT                   /label= CDR 1.
FT   Binding-site    50. .66
FT                   /label= CDR 2.
FT   Binding-site    99. .108
FT                   /label= CDR 3.
XX
PN   WO9611013-A1.
XX
PD   18-APR-1996.
XX
PF   28-SEP-1995;   95WO-US011964.
XX
PR   05-OCT-1994;   94US-00318157.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Hansen HJ,  Armour KL;
XX
DR   WPI; 1996-209653/21.
DR   N-PSDB; AAT29012.
XX
PT   New humanised anti-CEA monoclonal antibody - having engrafted murine
PT   CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS   Disclosure; Fig 7; 62pp; English.
XX
CC   New humanised monoclonal antibodies (MAbs) comprising the complementary
CC   determining regions (CDRs) of a parental murine class III anti-
CC   carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC   heterologous antibody which can be derived from any species including
CC   human, retain the anti-CEA binding specificity of the parental murine MAb
CC   but are less immunogenic in a human subject than the parental MAb. The
CC   humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC   -producing cancers and patients receiving the humanised antibodies and
CC   conjugates show improved therapeutic results, decreased immune responses
CC   and decreased immune-mediated adverse effects compared to the parent
CC   antibody. See AAR97313-97333 for the CDR sequence and framework regions
CC   of the humanised MAbs
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 64;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.023;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 6
AAR97334
ID   AAR97334 standard; protein; 119 AA.
XX
AC   AAR97334;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Murine NEWM MN-14 variable region heavy chain.
XX
KW   Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW   complementary determining region; anti-carcinoembryonic antigen; CEA;
KW   diagnosis; imaging; therapy; immune response.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Binding-site    31. .35
FT                   /label= CDR 1.
FT   Binding-site    50. .66
FT                   /label= CDR 2.
FT   Binding-site    99. .108
FT                   /label= CDR 3.
XX
PN   WO9611013-A1.
XX
PD   18-APR-1996.
XX
PF   28-SEP-1995;   95WO-US011964.
XX
PR   05-OCT-1994;   94US-00318157.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Hansen HJ,  Armour KL;
XX
DR   WPI; 1996-209653/21.
DR   N-PSDB; AAT29010.
XX
PT   New humanised anti-CEA monoclonal antibody - having engrafted murine
PT   CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS   Example 5; Fig 1; 62pp; English.
XX
CC   New humanised monoclonal antibodies (MAbs) comprising the complementary
CC   determining regions (CDRs) of a parental murine class III anti-
CC   carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC   heterologous antibody which can be derived from any species including
CC   human, retain the anti-CEA binding specificity of the parental murine MAb
CC   but are less immunogenic in a human subject than the parental MAb. The
CC   humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC   -producing cancers and patients receiving the humanised antibodies and
CC   conjugates show improved therapeutic results, decreased immune responses
CC   and decreased immune-mediated adverse effects compared to the parent
CC   antibody. See AAR97313-97333 for the CDR sequence and framework regions
CC   of the humanised MAbs
XX
SQ   Sequence 119 AA;

  Query Match             100.0%;  Score 64;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.023;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 7
ADM95101
ID   ADM95101 standard; protein; 119 AA.
XX
AC   ADM95101;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Humanised murine MN-14 MAb heavy chain variable region coding sequence.
XX
KW   non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW   complementarity determining region; pancreatic cancer; breast cancer;
KW   ovarian cancer.
```

XX
OS Mus sp.
OS Homo sapiens.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-364813/34.
DR N-PSDB; ADM95099.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Claim 14; Fig 16B; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the humanised
CC murine MN-14 antibody heavy chain variable region.
XX
SQ Sequence 119 AA;

```
  Query Match             100.0%;  Score 64;  DB 8;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.023;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108
```

RESULT 8
ADM95095
ID ADM95095 standard; protein; 119 AA.
XX
AC ADM95095;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 MAb heavy chain variable region.
XX
KW non-medullary thyroid carcinoma; carcinoembryonic antigen; antibody;
KW complementarity determining region; pancreatic cancer; breast cancer;
KW ovarian cancer.
XX
OS Mus sp.
XX
PN WO2004032962-A1.
XX
PD 22-APR-2004.
XX
PF 11-OCT-2002; 2002WO-US032307.
XX
PR 08-OCT-2002; 2002US-0416531P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX
DR WPI; 2004-364813/34.
XX
PT Treating non-medullary thyroid carcinoma or medullary thyroid carcinoma
PT comprises administering, either concurrently or sequentially, Class III
PT anti-CEA (carcinoembryonic antigen) monoclonal antibody or fragment and
PT therapeutic agent(s).
XX
PS Disclosure; Fig 11A-B; 88pp; English.
XX
CC The invention relates to a method of treating a non-medullary thyroid
CC carcinoma or treating medullary thyroid carcinoma involves administering
CC to a subject, either concurrently or sequentially, a Class III anti-CEA
CC (carcinoembryonic antigen) monoclonal antibody or its fragment and at
CC least one therapeutic agent. The antibody or its fragment comprises the
CC complementarity-determining regions (CDRs) of a murine MN-14 monoclonal
CC antibody. (I) is useful for treating medullary thyroid carcinoma or non-
CC medullary thyroid carcinoma such as pancreatic cancer, breast cancer,
CC ovarian cancer, in a subject. This sequence corresponds to the murine MN-
CC 14 antibody heavy chain variable region.
XX
SQ Sequence 119 AA;

```
  Query Match             100.0%;  Score 64;  DB 8;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.023;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108
```

RESULT 9
ADM98324
ID ADM98324 standard; protein; 119 AA.
XX
AC ADM98324;
XX
DT 15-JUL-2004 (first entry)
XX
DE Humanised murine MN-14 antibody heavy chain variable region protein.
XX
KW carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW antibody; MN-14; non-medullary thyroid carcinoma;
KW medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW hepatocellular carcinoma; breast cancer; lung cancer;
KW antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW apoptosis; humanised.
XX
OS Mus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 33. .34
FT /note= "Encoded by TGGGATAGCAGTACGATTAACTATGCGATG"
FT Misc-difference 53. .62
FT /note= "Encoded by CCACCG"
XX
PN WO2004032857-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031801.
XX
PR 08-OCT-2002; 2002US-0416531P.
PR 11-OCT-2002; 2002WO-US032307.
PR 02-MAY-2003; 2003US-0467161P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;

XX
DR WPI; 2004-340797/31.
DR N-PSDB; ADM98323.
XX
PT Treating non-medullary or medullary thyroid carcinoma, involves
PT administering to subject, either concurrently or sequentially, anti-
PT carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS Disclosure; Fig 23b; 122pp; English.
XX
CC This invention relates to methods for treating cancers that express
CC carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC antibodies that can be used following administration of an agent that
CC will increase antibody effector functions or following administration of
CC an amount of interferon effective to upregulate CEA expression in tumour
CC cells. The present invention describes the anti-CEA antibody as a class
CC III humanised murine monoclonal antibody that retains specificity for CEA
CC binding and is preferably an MN-14 antibody or fragment thereof.
CC Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC composition useful for the treatment of non-medullary or medullary
CC thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC carcinoma, as well as breast or lung cancer. Furthermore, it can
CC stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC cell growth and angiogenesis. This polypeptide sequence is the humanised
CC murine MN-14 antibody heavy chain variable region protein of the
CC invention.
XX
SQ Sequence 119 AA;

Query Match 100.0%; Score 64; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
||||||||||
Db 99 LYFGFPWFAY 108

RESULT 10
ADM98318
ID ADM98318 standard; protein; 119 AA.
XX
AC ADM98318;
XX
DT 15-JUL-2004 (first entry)
XX
DE Murine MN-14 antibody heavy chain variable region protein.
XX
KW carcinoembryonic antigen; CEA; antibody therapy; anti-CEA; murine; mouse;
KW antibody; MN-14; non-medullary thyroid carcinoma;
KW medullary thyroid carcinoma; colorectal cancer; gastric cancer;
KW hepatocellular carcinoma; breast cancer; lung cancer;
KW antibody-dependent cell-mediated cytotoxicity; complement-mediated lysis;
KW apoptosis.
XX
OS Mus sp.
XX
PN WO2004032857-A2.
XX
PD 22-APR-2004.
XX
PF 08-OCT-2003; 2003WO-US031801.
XX
PR 08-OCT-2002; 2002US-0416531P.
PR 11-OCT-2002; 2002WO-US032307.
PR 02-MAY-2003; 2003US-0467161P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Goldenberg DM, Hansen HJ;
XX

DR WPI; 2004-340797/31.
DR N-PSDB; ADM98317.
XX
PT Treating non-medullary or medullary thyroid carcinoma, involves
PT administering to subject, either concurrently or sequentially, anti-
PT carcinoembryonic antigen antibody or its fragment and therapeutic agent.
XX
PS Disclosure; Fig 11; 122pp; English.
XX
CC This invention relates to methods for treating cancers that express
CC carcinoembryonic antigens (CEAs). Specifically, it refers to antibody
CC therapy and in particular anti-carcinoembryonic antigen (anti-CEA)
CC antibodies that can be used following administration of an agent that
CC will increase antibody effector functions or following administration of
CC an amount of interferon effective to upregulate CEA expression in tumour
CC cells. The present invention describes the anti-CEA antibody as a class
CC III humanised murine monoclonal antibody that retains specificity for CEA
CC binding and is preferably an MN-14 antibody or fragment thereof.
CC Accordingly, hMN-14 can be formulated into a cytostatic pharmaceutical
CC composition useful for the treatment of non-medullary or medullary
CC thyroid carcinoma, colorectal cancer, gastric cancer, hepatocellular
CC carcinoma, as well as breast or lung cancer. Furthermore, it can
CC stimulate antibody-dependent cell-mediated cytotoxicity, complement-
CC mediated lysis and apoptosis as well as inhibit cell cycle progression,
CC cell growth and angiogenesis. This polypeptide sequence is murine MN-14
CC antibody heavy chain variable region protein of the invention.
XX
SQ Sequence 119 AA;

Query Match 100.0%; Score 64; DB 8; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
||||||||||
Db 99 LYFGFPWFAY 108

RESULT 11
ABG76489
ID ABG76489 standard; protein; 138 AA.
XX
AC ABG76489;
XX
DT 13-MAY-2003 (first entry)
XX
DE Heavy chain variable, VH, region of antibody hMN14.
XX
KW CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW human; zeta signalling chain; CD8alpha hinge; humanised antibody;
KW heavy chain variable region; VH.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1. .19
FT /label= Signal_peptide
FT Protein 20. .138
FT /label= Mature_VH_of_hMN14
XX
PN US2002165360-A1.
XX
PD 07-NOV-2002.
XX
PF 10-DEC-2001; 2001US-00006771.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250090P.
XX

```
PA   (JUNG/) JUNGHANS R P.
XX
PI   Junghans RP;
XX
DR   WPI; 2003-298705/29.
DR   N-PSDB; ABX13169.
XX
PT   New chimeric molecule from humanized antibody against carcinoembryonic
PT   antigen and having signaling molecules of T cells and other effector
PT   cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS   Disclosure; Page 9; 20pp; English.
XX
CC   The invention relates to a chimaeric molecule comprising the
CC   carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC   as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC   chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC   which the cysteine residues have been mutated, with the IgTCR molecule
CC   occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC   appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC   NK (not defined) or other effector cells are useful in treating patients
CC   with cancers expressing the CEA antigen, together with other or with
CC   heterologous constructs to engage additional stimulatory and functional
CC   properties of the effector cells to enhance the anti-tumour therapeutic
CC   efficacy. The cancer disorder includes colorectal, breast and lung
CC   cancers. The present sequence represents the heavy chain variable, VH,
CC   region of antibody hMN14. The VH protein is humanised (complementarity
CC   determining region-grafted) and has a leader peptide
XX
SQ   Sequence 138 AA;

  Query Match             100.0%;  Score 64;  DB 6;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. 0.027;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        118 LYFGFPWFAY 127


RESULT 12
ABR42757
ID   ABR42757 standard; protein; 256 AA.
XX
AC   ABR42757;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-0.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-0;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; triabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .256
FT                   /label= hMN-14-0
FT   Region          142. .250
FT                   /label= hMN-14Vkappa
FT   Region          251. .256
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
DR   N-PSDB; ACC58722.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 39; Fig 13; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-0, which is
CC   designed to form an hMN-14 triabody. The hMN-14-0 polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa without a peptide linker. The use of the zero linker enables the
CC   secreted polypeptide to form a triabody, forming 3 binding sites for CEA.
CC   The polypeptide also includes a pelB signal peptide, which precedes the
CC   VH moiety to facilitate synthesis of the polypeptide in the periplasmic
CC   space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific triabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 256 AA;

  Query Match             100.0%;  Score 64;  DB 6;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 0.049;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        122 LYFGFPWFAY 131


RESULT 13
ABR42758
ID   ABR42758 standard; protein; 257 AA.
XX
AC   ABR42758;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-1G.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-1G;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; tetrabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
```

```
FT   Peptide          1. .23
FT                    /label= Signal_peptide
FT                    /note= "pelB"
FT   Region           23. .141
FT                    /label= hMN-14VH
FT   Protein          24. .257
FT                    /label= hMN-14-0
FT   Region           142
FT                    /label= 1G_linker
FT   Region           143. .251
FT                    /label= hMN-14Vkappa
FT   Region           252. .257
FT                    /label= 6xHis_tag
FT
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 48; Fig 14; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-1G, which is
CC   designed to form an hMN-14 tetrabody. The hMN-14-1G polypeptide comprises
CC   the C-terminal end of anti-carcinoembryonic antigen (CEA) humanized
CC   monoclonal antibody hMN-14 VH joined to the N-terminal part of hMN-14
CC   Vkappa via a single glycine residues. Use of the 1G linker enables some
CC   of the the secreted polypeptide to form a tetrabody with 4 binding sites
CC   for CEA. The polypeptide also includes a pelB signal peptide, which
CC   precedes the VH moiety to facilitate synthesis of the polypeptide in the
CC   periplasmic space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. This monospecific tetrabody is an example of claimed
CC   multivalent binding proteins specific for a tumour-associated antigen.
CC   The binding proteins are used in the diagnosis and treatment of a tumour,
CC   carcinoma, melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma
CC   or myeloma, or a cancer selected from acute lymphoblastic leukaemia,
CC   acute myelogenous leukaemia, biliary, breast, cervical, chronic
CC   lymphocytic leukaemia, chronic myelogenous leukaemia, colorectal,
CC   endometrial, oesophageal, gastric, head and neck, Hodgkin's lymphoma,
CC   lung, medullary thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic,
CC   prostate and bladder
XX
SQ   Sequence 257 AA;

  Query Match             100.0%;  Score 64;  DB 6;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 0.049;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        122 LYFGFPWFAY 131


RESULT 14
ABR42289
ID   ABR42289 standard; protein; 261 AA.
XX
AC   ABR42289;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Diabody 679-scFv-L5 polypeptide (VH-I3Q/C101S mutant).
XX
KW   Diabody; antibody; 679-scFv-L5; histamine-succinyl-glycyl; HSG;
KW   affinity enhancement system; tumour; targeting; mutant; mutein.
XX
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB signal peptide"
FT   Misc-difference 3
FT                   /note= "wild-type Ile substituted by Gln"
FT   Protein         23. .268
FT                   /label= 679-scFv-L5
FT   Region          23. .142
FT                   /label= 679VH(I3Q/C101S)
FT   Misc-difference 101
FT                   /note= "wild-type Cys substituted by Ser"
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .260
FT                   /label= 679Vk
FT   Region          261. .268
FT                   /label= 6His_tag
FT
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57803.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Disclosure; Fig 28; 87pp; English.
XX
CC   The present sequence is the protein sequence of a 679 mutant diabody in
CC   which antibody 679 VH has a Gln for Ile amino acid substitution at
CC   position 3 and a Ser for Gln amino acid substitution at position 101.
CC   Murine monoclonal antibody 679 binds with high affinity to molecules
CC   containing the moiety histamine-succinyl-glycyl (HSG). The present
CC   polypeptide comprises: 679 VH(I3Q) linked to 679 Vk via a peptide linker
CC   (enables the secreted polypeptide to dimerise into a diabody, forming 2
CC   sites for HSG); a pelB leader signal peptide (facilitates transport of
CC   the polypeptide into the periplasmic space of Escherichia coli); and 6
CC   His residues (allows purification by IMAC). The 679 diabody was expressed
CC   in E. coli at a level of 10 ug/l of culture, compared with 1 ug/l for the
CC   non-mutant polypeptide. The invention provides a bispecific diabody
CC   comprising an HSG binding site and a carcinoembryonic antigen (CEA)
CC   binding site. The HSG antigen binding site may comprise the VH and Vk
CC   polypeptides of 679 MAb. These diabodies are produced via recombinant DNA
CC   technology and create a novel affinity enhancement system that shows
```

```
CC   specific affinity for HSG and CEA. They pre-target CEA positive tumours
CC   for subsequent specific delivery of therapeutic radioisotopes carried by
CC   HSG-carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 261 AA;

  Query Match            100.0%;  Score 64;  DB 6;  Length 261;
  Best Local Similarity  100.0%;  Pred. No. 0.05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        122 LYFGFPWFAY 131


RESULT 15
ABR42754
ID   ABR42754 standard; protein; 261 AA.
XX
AC   ABR42754;
XX
DT   26-AUG-2003  (first entry)
XX
DE   Anti-CEA humanized monoclonal antibody hMN-14-scFv-L5.
XX
KW   Humanized; monoclonal antibody; antibody; hMN-14-scFv-15;
KW   carcinoembryonic antigen; CEA; tumour; cytostatic; diabody.
XX
OS   Homo sapiens.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .23
FT                   /label= Signal_peptide
FT                   /note= "pelB"
FT   Region          23. .141
FT                   /label= hMN-14VH
FT   Protein         24. .261
FT                   /label= hMN-14-scFv-L5
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .255
FT                   /label= hMN-14Vkappa
FT   Region          256. .261
FT                   /label= 6xHis_tag
XX
PN   WO2003033654-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032718.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
PR   08-JAN-2002; 2002US-0345641P.
PR   22-AUG-2002; 2002US-0404919P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg DM;
XX
DR   WPI; 2003-513460/48.
DR   N-PSDB; ACC58721.
XX
PT   New multivalent, monospecific binding protein comprising two or more
PT   binding sites having affinity for the same single target antigen, where
PT   each binding site is associated with scFv fragments, useful for
PT   diagnosing or treating tumor.
XX
PS   Claim 31; Fig 11; 62pp; English.
XX
CC   The present sequence is the protein sequence of hMN-14-scFv-L5, which was
CC   designed to form an hMN-14 diabody. The hMN-14-scFv-L5 polypeptide
CC   comprises the C-terminal end of anti-carcinoembryonic antigen (CEA)
CC   humanized monoclonal antibody hMN-14 VH linked to the N-terminal part of
CC   hMN-14 Vkappa by a peptide linker that enables the secreted polypeptide
CC   to dimerize into a diabody, forming 2 binding sites for CEA. The
CC   polypeptide also includes a pelB signal peptide, which precedes the VH
CC   moiety to facilitate synthesis of the polypeptide in the periplasmic
CC   space of Escherichia coli, and a 6xHis C-terminal tag to aid
CC   purification. In the claimed monospecific diabody, each scFv comprises
CC   the present sequence. The diabody is an example of claimed multivalent
CC   binding proteins specific for a tumour-associated antigen. The binding
CC   proteins are used in the diagnosis and treatment of a tumour, carcinoma,
CC   melanoma, sarcoma, neuroblastoma, leukaemia, glioma, lymphoma or myeloma,
CC   or a cancer selected from acute lymphoblastic leukaemia, acute
CC   myelogenous leukaemia, biliary, breast, cervical, chronic lymphocytic
CC   leukaemia, chronic myelogenous leukaemia, colorectal, endometrial,
CC   oesophageal, gastric, head and neck, Hodgkin's lymphoma, lung, medullary
CC   thyroid, non-Hodgkin's lymphoma, ovarian, pancreatic, prostate and
CC   bladder
XX
SQ   Sequence 261 AA;

  Query Match            100.0%;  Score 64;  DB 6;  Length 261;
  Best Local Similarity  100.0%;  Pred. No. 0.05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        122 LYFGFPWFAY 131


RESULT 16
ABR83645
ID   ABR83645 standard; protein; 261 AA.
XX
AC   ABR83645;
XX
DT   16-OCT-2003  (first entry)
XX
DE   hMN14-scFv-L5 amino acid sequence.
XX
KW   Multispecific binding protein; multivalent; target antigen; cytostatic;
KW   immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW   immunotherapy; autoimmune disease; infectious disease;
KW   cardiovascular disease; inflammatory disease.
XX
OS   Escherichia coli.
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO2003057829-A2.
XX
PD   17-JUL-2003.
XX
PF   26-DEC-2002; 2002WO-US038985.
XX
PR   26-DEC-2001; 2001US-0342103P.
XX
PA   (ROSS/) ROSSI E.
XX
PI   Rossi E,  Chang CK,  Goldenberg D;
XX
DR   WPI; 2003-607997/57.
DR   N-PSDB; ACF57430.
XX
PT   Novel multivalent, multi-specific binding protein useful for treating
PT   cancer, has first binding site having affinity towards hapten group and
PT   second and third binding sites each having affinity towards target
PT   antigen.
XX
```

```
PS   Claim 11; Fig 6; 43pp; English.
XX
CC   The present invention describes a multivalent, multi-specific binding
CC   protein (I) comprising a first binding site having an affinity towards a
CC   hapten group and a second and a third binding sites each having affinity
CC   towards a target antigen, which may be the same or a different target
CC   antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC   and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC   useful for delivering a diagnostic agent, a therapeutic agent, or its
CC   combination to a target, which involves administering (I) to a subject,
CC   waiting for a sufficient amount of time for an amount of the non-binding
CC   protein to clear the subject's blood stream, and administering to the
CC   subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC   agent, or its combination, that binds to a binding site of the binding
CC   protein. (I) is also useful for detecting or treating a human disorder,
CC   preferably cancer, autoimmune diseases, infectious diseases,
CC   cardiovascular diseases and inflammatory diseases. The present sequence
CC   represents a hMN14-scFv-L5 amino acid sequence, which is used in the
CC   exemplification of the present invention
XX
SQ   Sequence 261 AA;

  Query Match             100.0%;  Score 64;  DB 6;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 0.05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        122 LYFGFPWFAY 131


RESULT 17
ABR42292
ID   ABR42292 standard; protein; 267 AA.
XX
AC   ABR42292;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .267
FT                   /label= BSI_polypeptide#1
FT   Region          24. .141
FT                   /label= hMN14_VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .259
FT                   /label= 679_Vk
FT   Region          262. .267
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57806.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 31; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of a
CC   novel bispecific diabody comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen. The bispecific diabody can be produced using
CC   recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC   a novel affinity enhancement system that shows specific affinity for HSG
CC   and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC   subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC   carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC   cardiovascular diseases and inflammatory diseases can be detected or
CC   treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             100.0%;  Score 64;  DB 6;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 0.051;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        122 LYFGFPWFAY 131


RESULT 18
ABR42299
ID   ABR42299 standard; protein; 267 AA.
XX
AC   ABR42299;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS1.5H polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .262
FT                   /label= BS1.5H_polypeptide#2
FT   Region          24. .142
FT                   /label= hMN14_VH
FT   Region          143. .147
FT                   /label= Linker
FT   Region          148. .254
```

```
FT                   /label= h679_Vk
FT   Region          257. .262
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57813.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 38; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of novel
CC   bispecific diabody BS1.5H comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). A humanised version of its VH and Vk sequences
CC   have been used in BS1.5H. Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC   using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC   provides a novel affinity enhancement system that shows specific affinity
CC   for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC   tumours for subsequent specific delivery of therapeutic radioisotopes
CC   carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC   disease, cardiovascular diseases and inflammatory diseases can be
CC   detected or treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             100.0%;  Score 64;  DB 6;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 0.051;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        122 LYFGFPWFAY 131


RESULT 19
ABR42296
ID   ABR42296 standard; protein; 267 AA.
XX
AC   ABR42296;
XX
DT   11-AUG-2003  (first entry)
XX
DE   Bispecific diabody BS2 polypeptide #2.
XX
KW   Diabody; antibody; carcinoembryonic antigen; CEA;
KW   histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW   targeting; mutant; mutein.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Escherichia coli.
OS   Synthetic.
OS   Chimeric.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .22
FT                   /label= Signal_peptide
FT                   /note= "pelB leader peptide"
FT   Protein         23. .267
FT                   /label= BS2_polypeptide#2
FT   Region          24. .141
FT                   /label= hMN14-VH
FT   Region          142. .146
FT                   /label= Linker
FT   Region          147. .259
FT                   /label= 679_Vk
FT   Region          262. .267
FT                   /label= His_tag
XX
PN   WO2003033653-A2.
XX
PD   24-APR-2003.
XX
PF   15-OCT-2002; 2002WO-US032717.
XX
PR   15-OCT-2001; 2001US-0328835P.
PR   21-DEC-2001; 2001US-0341881P.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
PA   (IBCP-) IBC PHARM.
XX
PI   Chang CK,  Rossi E;
XX
DR   WPI; 2003-393513/37.
DR   N-PSDB; ACC57810.
XX
PT   New kit comprising a multivalent, multi-specific binding protein and a
PT   carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT   for treating cancer, and cardiovascular, immune, inflammatory, or
PT   infectious diseases.
XX
PS   Claim 14; Fig 35; 87pp; English.
XX
CC   The present sequence is the protein sequence for polypeptide #2 of novel
CC   bispecific diabody BS2 comprising the VH region of monoclonal antibody
CC   hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC   binds with high affinity to molecules containing the moiety histamine-
CC   succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC   carcinoembryonic antigen (CEA). The bispecific diabody can be produced
CC   using recombinant DNA methods, e.g. in Escherichia coli host cells. It
CC   provides a novel affinity enhancement system that shows specific affinity
CC   for HSG and CEA. Such bispecific diabodies pre-target CEA positive
CC   tumours for subsequent specific delivery of therapeutic radioisotopes
CC   carried by HSG-carrying peptides. Cancer, autoimmune diseases, infectious
CC   disease, cardiovascular diseases and inflammatory diseases can be
CC   detected or treated using the methods of the invention
XX
SQ   Sequence 267 AA;

  Query Match             100.0%;  Score 64;  DB 6;  Length 267;
  Best Local Similarity   100.0%;  Pred. No. 0.051;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        122 LYFGFPWFAY 131


RESULT 20
ABR42294
ID   ABR42294 standard; protein; 267 AA.
XX
AC   ABR42294;
XX
DT   11-AUG-2003  (first entry)
XX
```

DE Bispecific diabody BS1.5 polypeptide #2.
XX
KW Diabody; antibody; carcinoembryonic antigen; CEA;
KW histamine-succinyl-glycyl; affinity enhancement system; tumour;
KW targeting; mutant; mutein.
XX
OS Homo sapiens.
OS Mus sp.
OS Escherichia coli.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1. .22
FT /label= Signal_peptide
FT /note= "pelB leader peptide"
FT Protein 23. .267
FT /label= BS1.5_polypeptide#2
FT Region 24. .141
FT /label= hMN14_VH
FT Region 142. .146
FT /label= Linker
FT Region 147. .259
FT /label= 679_Vk(I3Q)
FT Region 261. .267
FT /label= His_tag
XX
PN WO2003033653-A2.
XX
PD 24-APR-2003.
XX
PF 15-OCT-2002; 2002WO-US032717.
XX
PR 15-OCT-2001; 2001US-0328835P.
PR 21-DEC-2001; 2001US-0341881P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (IBCP-) IBC PHARM.
XX
PI Chang CK, Rossi E;
XX
DR WPI; 2003-393513/37.
DR N-PSDB; ACC57808.
XX
PT New kit comprising a multivalent, multi-specific binding protein and a
PT carrier molecule, useful for delivering a diagnostic/therapeutic agent
PT for treating cancer, and cardiovascular, immune, inflammatory, or
PT infectious diseases.
XX
PS Claim 14; Fig 33; 87pp; English.
XX
CC The present sequence is the protein sequence for polypeptide #2 of a
CC novel bispecific diabody comprising the VH region of monoclonal antibody
CC hMN14 and the Vk region of monoclonal antibody 679. Mouse antibody 679
CC binds with high affinity to molecules containing the moiety histamine-
CC succinyl-glycyl (HSG). Humanised antibody hMN14 binds specifically to
CC carcinoembryonic antigen. The bispecific diabody can be produced using
CC recombinant DNA methods, e.g. in Escherichia coli host cells. It provides
CC a novel affinity enhancement system that shows specific affinity for HSG
CC and CEA. Such bispecific diabodies pre-target CEA positive tumours for
CC subsequent specific delivery of therapeutic radioisotopes carried by HSG-
CC carrying peptides. Cancer, autoimmune diseases, infectious disease,
CC cardiovascular diseases and inflammatory diseases can be detected or
CC treated using the methods of the invention
XX
SQ Sequence 267 AA;

Query Match 100.0%; Score 64; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
||||||||||
Db 122 LYFGFPWFAY 131

RESULT 21
ADU26571
ID ADU26571 standard; protein; 358 AA.
XX
AC ADU26571;
XX
DT 27-JAN-2005 (first entry)
XX
DE Chimeric hBS14 polypeptide 2.
XX
KW cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW neoplasm; fungal infection; viral infection; bacterial infection;
KW mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW autoimmune disease; myocardial infarction; ischemic heart disease;
KW atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
OS Synthetic.
XX
PN WO2004094613-A2.
XX
PD 04-NOV-2004.
XX
PF 22-APR-2004; 2004WO-US012662.
XX
PR 22-APR-2003; 2003US-0464532P.
PR 24-NOV-2003; 2003US-0525391P.
XX
PA (IBCP-) IBC PHARM.
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Rossi EA, Chang C, Mcbride WJ;
XX
DR WPI; 2004-795560/78.
DR N-PSDB; ADU26573.
XX
PT Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT chains having immunoglobulin variable domains, to form complex having
PT three antigen binding sites.
XX
PS Example 2; SEQ ID NO 12; 148pp; English.
XX
CC The invention relates to a polyvalent protein complex (PPC) (I),
CC comprising a first and second polypeptide chains having immunoglobulin
CC variable domains, where the first and second polypeptide chains form a
CC complex having three antigen binding sites, and where each binding site
CC comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC useful in pretargeting method of treating or diagnosing, or treating and
CC diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC also useful for diagnosing a non-neoplastic disease or disorder where the
CC disease or disorder is caused by a fungus, a virus, a bacterium, a
CC mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC infarction, ischemic heart disease, atherosclerotic plaques, graft
CC rejection, Alzheimer's disease or inflammation caused by accretion of
CC activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC site of inflammation (caused by infectious agent). (I) is useful in
CC antibody dependent enzyme prodrug therapy (ADEPT), for detecting target

```
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric hBS14 polypeptide 2 containing heavy and light chain variable
CC   regions.
XX
SQ   Sequence 358 AA;

  Query Match             100.0%;  Score 64;  DB 8;  Length 358;
  Best Local Similarity   100.0%;  Pred. No. 0.069;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        213 LYFGFPWFAY 222


RESULT 22
ADU26561
ID   ADU26561 standard; protein; 363 AA.
XX
AC   ADU26561;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric BS14hp polypeptide 2.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .6
FT                   /note= "signal peptide"
FT   Protein         7. .363
FT                   /note= "mature protein"
FT   Region          30. .40
FT                   /note= "CDR1hMN14Vk"
FT   Region          56. .62
FT                   /note= "CDR2hMN14Vk"
FT   Region          95. .102
FT                   /note= "CDR3hMN14Vk"
FT   Region          114. .119
FT                   /note= "linker region"
FT   Region          150. .154
FT                   /note= "CDR1hMN14Vh"
FT   Region          169. .185
FT                   /note= "CDR2hMN14Vh"
FT   Region          218. .227
FT                   /note= "CDR3hMN14Vh"
FT   Region          238. .242
FT                   /note= "linker region"
FT   Region          266. .282
FT                   /note= "CDR1h679Vk"
FT   Region          298. .304
FT                   /note= "CDR2h679Vk"
FT   Region          337. .344
FT                   /note= "CDR3h679Vk"
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26569.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 1; SEQ ID NO 2; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
CC   activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC   site of inflammation (caused by infectious agent). (I) is useful in
CC   antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric BS14HP polypeptide 2 containing heavy and light chain variable
CC   regions. The encoded polypeptide is designated alpha-factor-hMN-14Vk-
CC   GGGGS-hMN-14Vh-LEGGGS-h679Vk-6-His where the hMN14 is from a humanized
CC   antibody that binds specifically to the carcinoembryonic antigen and the
CC   h679 is a monoclonal antibody that binds the tri-peptide moiety histamine
CC   -succinyl-glycyl (HSG).
XX
SQ   Sequence 363 AA;

  Query Match             100.0%;  Score 64;  DB 8;  Length 363;
  Best Local Similarity   100.0%;  Pred. No. 0.07;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        218 LYFGFPWFAY 227


RESULT 23
ADU26570
ID   ADU26570 standard; protein; 364 AA.
XX
AC   ADU26570;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric hBS14 polypeptide 1.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
```

```
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26572.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
PT   bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT   chains having immunoglobulin variable domains, to form complex having
PT   three antigen binding sites.
XX
PS   Example 2; SEQ ID NO 11; 148pp; English.
XX
CC   The invention relates to a polyvalent protein complex (PPC) (I),
CC   comprising a first and second polypeptide chains having immunoglobulin
CC   variable domains, where the first and second polypeptide chains form a
CC   complex having three antigen binding sites, and where each binding site
CC   comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC   useful in pretargeting method of treating or diagnosing, or treating and
CC   diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC   lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC   malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC   also useful for diagnosing a non-neoplastic disease or disorder where the
CC   disease or disorder is caused by a fungus, a virus, a bacterium, a
CC   mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC   infarction, ischemic heart disease, atherosclerotic plaques, graft
CC   rejection, Alzheimer's disease or inflammation caused by accretion of
CC   activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC   site of inflammation (caused by infectious agent). (I) is useful in
CC   antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC   molecule, and immunostaining technique. This sequence corresponds to the
CC   chimeric hBS14 polypeptide 1 containing heavy and light chain variable
CC   regions.
XX
SQ   Sequence 364 AA;

  Query Match             100.0%;  Score 64;  DB 8;  Length 364;
  Best Local Similarity   100.0%;  Pred. No. 0.07;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        337 LYFGFPWFAY 346


RESULT 24
ADU26560
ID   ADU26560 standard; protein; 370 AA.
XX
AC   ADU26560;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Chimeric  BS14HP polypeptide 1.
XX
KW   cytostatic; fungicide; virucide; antibacterial; antimalarial;
KW   immunosuppressive; muscular-gen.; neuroprotective; antiinflammatory;
KW   dermatological; antipyretic; antirheumatic; antidiabetic; anabolic;
KW   hypertensive; antiarthritic; antiulcer; gastrointestinal-gen.;
KW   nephrotropic; hepatotropic; thyromimetic; antiallergic; vasotropic;
KW   antianemic; antipsoriatic; nephrotropic; antitubercular; tuberculostatic;
KW   cardiant; antiarteriosclerotic; nootropic; antibody engineering;
KW   cardiovascular disease; immunoglobulin; heavy chain variable domain;
KW   neoplasm; fungal infection; viral infection; bacterial infection;
KW   mycoplasma infection; parasitic infection; malaria; Plasmodium infection;
KW   autoimmune disease; myocardial infarction; ischemic heart disease;
KW   atherosclerosis; graft rejection; Alzheimer's disease; inflammation;
KW   antibody dependent enzyme prodrug therapy; immunosensor.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Chimeric.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .7
FT                   /note= "signal peptide"
FT   Protein         8. .370
FT                   /note= "mature protein"
FT   Region          38. .42
FT                   /note= "CDR1h679Vh"
FT   Region          57. .68
FT                   /note= "CDR2h679Vh"
FT   Region          106. .115
FT                   /note= "CDR3h679Vh"
FT   Region          127. .131
FT                   /note= "linker region"
FT   Region          155. .165
FT                   /note= "CDR1hMN14Vk"
FT   Region          181. .187
FT                   /note= "CDR2hMN14Vk"
FT   Region          220. .227
FT                   /note= "CDR3hMN14Vk"
FT   Region          239. .244
FT                   /note= "linker region"
FT   Region          275. .279
FT                   /note= "CDR1hMN14Vh"
FT   Region          294. .310
FT                   /note= "CDR2hMN14Vh"
FT   Region          343. .352
FT                   /note= "CDR3hMN14Vh"
XX
PN   WO2004094613-A2.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-US012662.
XX
PR   22-APR-2003; 2003US-0464532P.
PR   24-NOV-2003; 2003US-0525391P.
XX
PA   (IBCP-) IBC PHARM.
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Rossi EA,  Chang C,  Mcbride WJ;
XX
DR   WPI; 2004-795560/78.
DR   N-PSDB; ADU26568.
XX
PT   Polyvalent protein complex for treating B-cell malignancy, Anthrax
```

PT bacillus, Alzheimer's disease, reovirus, Microsporum, has polypeptide
PT chains having immunoglobulin variable domains, to form complex having
PT three antigen binding sites.
XX
PS Example 1; SEQ ID NO 1; 148pp; English.
XX
CC The invention relates to a polyvalent protein complex (PPC) (I),
CC comprising a first and second polypeptide chains having immunoglobulin
CC variable domains, where the first and second polypeptide chains form a
CC complex having three antigen binding sites, and where each binding site
CC comprises an immunoglobulin heavy and light chain variable domain. (I) is
CC useful in pretargeting method of treating or diagnosing, or treating and
CC diagnosing a neoplastic condition such as carcinomas, sarcomas, gliomas,
CC lymphomas, leukemias or melanomas. (I) is useful for treating B-cell
CC malignancy, or B-cell immune or autoimmune disorder in a subject. (I) is
CC also useful for diagnosing a non-neoplastic disease or disorder where the
CC disease or disorder is caused by a fungus, a virus, a bacterium, a
CC mycoplasma, a parasite e.g. malaria, an autoimmune disease, myocardial
CC infarction, ischemic heart disease, atherosclerotic plaques, graft
CC rejection, Alzheimer's disease or inflammation caused by accretion of
CC activated granulocytes, monocytes, lymphoid cells or macrophages at the
CC site of inflammation (caused by infectious agent). (I) is useful in
CC antibody dependent enzyme prodrug therapy (ADEPT), for detecting target
CC molecule, and immunostaining technique. This sequence corresponds to the
CC chimeric BS14HP polypeptide 1 containing heavy and light chain variable
CC regions. The encoded polypeptide is designated alpha-factor-h679Vh-GGGGS-
CC hMN-14Vk-LEGGGS-hMN-14Vh-6-His where the hMN14 is from a humanized
CC antibody that binds specifically to the carcinoembryonic antigen and the
CC h679 is a monoclonal antibody that binds the tri-peptide moiety histamine
CC -succinyl-glycyl (HSG).
XX
SQ Sequence 370 AA;

Query Match 100.0%; Score 64; DB 8; Length 370;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
||||||||||
Db 343 LYFGFPWFAY 352

RESULT 25
ABR83648
ID ABR83648 standard; protein; 415 AA.
XX
AC ABR83648;
XX
DT 16-OCT-2003 (first entry)
XX
DE TS1 VH chain amino acid sequence.
XX
KW Multispecific binding protein; multivalent; target antigen; cytostatic;
KW immunosuppressive; antimicrobial; cardiant; antiinflammatory; cancer;
KW immunotherapy; autoimmune disease; infectious disease;
KW cardiovascular disease; inflammatory disease.
XX
OS Escherichia coli.
OS Homo sapiens.
OS Synthetic.
XX
PN WO2003057829-A2.
XX
PD 17-JUL-2003.
XX
PF 26-DEC-2002; 2002WO-US038985.
XX
PR 26-DEC-2001; 2001US-0342103P.
XX
PA (ROSS/) ROSSI E.
XX
PI Rossi E, Chang CK, Goldenberg D;
XX
DR WPI; 2003-607997/57.
DR N-PSDB; ACF57433.
XX
PT Novel multivalent, multi-specific binding protein useful for treating
PT cancer, has first binding site having affinity towards hapten group and
PT second and third binding sites each having affinity towards target
PT antigen.
XX
PS Claim 48; Fig 8A-B; 43pp; English.
XX
CC The present invention describes a multivalent, multi-specific binding
CC protein (I) comprising a first binding site having an affinity towards a
CC hapten group and a second and a third binding sites each having affinity
CC towards a target antigen, which may be the same or a different target
CC antigen. (I) has cytostatic, immunosuppressive, antimicrobial, cardiant
CC and antiinflammatory activities, and can be used in immunotherapy. (I) is
CC useful for delivering a diagnostic agent, a therapeutic agent, or its
CC combination to a target, which involves administering (I) to a subject,
CC waiting for a sufficient amount of time for an amount of the non-binding
CC protein to clear the subject's blood stream, and administering to the
CC subject a carrier molecule comprising a diagnostic agent, a therapeutic
CC agent, or its combination, that binds to a binding site of the binding
CC protein. (I) is also useful for detecting or treating a human disorder,
CC preferably cancer, autoimmune diseases, infectious diseases,
CC cardiovascular diseases and inflammatory diseases. The present sequence
CC represents the TS1 VH chain amino acid sequence, which is used in the
CC exemplification of the present invention
XX
SQ Sequence 415 AA;

Query Match 100.0%; Score 64; DB 6; Length 415;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
||||||||||
Db 122 LYFGFPWFAY 131

RESULT 26
ABG76488
ID ABG76488 standard; protein; 443 AA.
XX
AC ABG76488;
XX
DT 13-MAY-2003 (first entry)
XX
DE Humanised anti-CEA antibody, hMN14.
XX
KW CEA; carcinoembryonic antigen; IgTCR; T-cell receptor; cancer; tumour;
KW colorectal cancer; breast cancer; lung cancer; hMN14; cytostatic; mouse;
KW human; zeta signalling chain; CD8alpha hinge; humanised antibody.
XX
OS Homo sapiens.
OS Mus sp.
OS Synthetic.
OS Chimeric.
XX
PN US2002165360-A1.
XX
PD 07-NOV-2002.
XX
PF 10-DEC-2001; 2001US-00006771.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250090P.
XX
PA (JUNG/) JUNGHANS R P.
XX
PI Junghans RP;
XX
DR WPI; 2003-298705/29.
DR N-PSDB; ABX13168.

XX
PT New chimeric molecule from humanized antibody against carcinoembryonic
PT antigen and having signaling molecules of T cells and other effector
PT cells, useful for the treatment of colorectal, breast and lung cancers.
XX
PS Disclosure; Page 7-8; 20pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the
CC carcinoembryonic antigen (CEA) binding domain of humanised antibody MN14
CC as a single chain antibody with a (GGSGS)3 linker, the zeta signaling
CC chain of the T cell receptor (TCR) and an intervening CD8alpha hinge in
CC which the cysteine residues have been mutated, with the IgTCR molecule
CC occupying nucleotides 2426-3766 of the retroviral vector sequence.
CC appearing as ABX13168. The new chimaeric molecule expressed in T cells,
CC NK (not defined) or other effector cells are useful in treating patients
CC with cancers expressing the CEA antigen, together with other or with
CC heterologous constructs to engage additional stimulatory and functional
CC properties of the effector cells to enhance the anti-tumour therapeutic
CC efficacy. The cancer disorder includes colorectal, breast and lung
CC cancers. The present sequence represents the chimaeric molecule of the
CC invention
XX
SQ Sequence 443 AA;

Query Match 100.0%; Score 64; DB 6; Length 443;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
||||||||||
Db 240 LYFGFPWFAY 249

RESULT 27
ABG74240
ID ABG74240 standard; protein; 443 AA.
XX
AC ABG74240;
XX
DT 23-OCT-2003 (revised)
DT 22-APR-2003 (first entry)
XX
DE Chimaeric hMN14/T-cell receptor.
XX
KW Retroviral vector; T-cell receptor; hMN14; antibody; IgTCR; receptor;
KW cytostatic; dermatological; neuroprotective; immunostimulant; GD3;
KW ganglioside antigen; MB3.6; PSMA; tumour; 3D8; 4D4; 3E11;
KW prostate-specific membrane antigen; zeta signalling chain; human; cancer;
KW melanoma; neuroendocrine tumour; prostate cancer; small cell lung cancer;
KW mouse; CD8alpha hinge.
XX
OS Homo sapiens.
OS Mus sp.
OS Chimeric.
XX
PN US2002132983-A1.
XX
PD 19-SEP-2002.
XX
PF 10-DEC-2001; 2001US-00006773.
XX
PR 30-NOV-2000; 2000US-0250087P.
PR 30-NOV-2000; 2000US-0250089P.
XX
PA (JUNG/) JUNGHANS R P.
XX
PI Junghans RP;
XX
DR WPI; 2003-208946/20.
DR N-PSDB; ABX16565.
XX
PT New chimeric molecule useful in treating patients with disorders, such as
PT melanoma, neuroendocrine disorders, prostate and small cell lung cancer
PT comprises GD3 and/or PSMA binding domains of antibody.
XX
PS Disclosure; Page 7-8; 35pp; English.
XX
CC The invention relates to a chimaeric molecule comprising the GD3
CC (ganglioside antigen) binding domain of antibody MB3.6, with any of 3
CC variable gene sequences, or the PSMA (prostate-specific membrane antigen)
CC binding domain of antibody 3D8, 4D4 and 3E11, with variable gene
CC sequences, the zeta signalling chain of the T cell receptor and an
CC intervening CD8alpha hinge in which cysteine residues have been mutated.
CC The chimaeric molecules expressed in T cells or NK cells or other
CC effector cells are useful in treating patients with cancers expressing
CC the GD3 (MB3.6 derivatives) or PSMA antigen (3D8, 4D4, 3E11 derivatives),
CC and/or together with each other or with heterologous constructs to engage
CC additional stimulatory and functional properties of the effector cells to
CC enhance the antitumour therapeutic efficacy (claimed). They are
CC particularly useful in disorders including melanoma, neuroendocrine
CC tumours and prostate and small cell lung cancer. The present sequence is
CC a hMN14 antibody (specific to CEA antigen) in a fusion protein with the
CC modified CD8alpha hinge and the T-cell receptor zeta chain (IgTCR)
CC encoded by a retroviral vector. The hMN14 antibody coding region is
CC replaced with the MB3.6, 3D8, 4D4 or 3E11 genes of the invention.
CC (Updated on 23-OCT-2003 to standardise OS field)
XX
SQ Sequence 443 AA;

Query Match 100.0%; Score 64; DB 6; Length 443;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
||||||||||
Db 240 LYFGFPWFAY 249

RESULT 28
ADE64201
ID ADE64201 standard; protein; 468 AA.
XX
AC ADE64201;
XX
DT 29-JAN-2004 (first entry)
XX
DE MN14HCF protein related to a novel antibody library.
XX
KW antibody library; retroviral vector; antibody light chain;
KW antibody heavy chain; human therapy; multiplicity of infection; MOI;
KW plasmid; GATEWAY vector; MN14HCF.
XX
OS Unidentified.
XX
PN WO2003083077-A2.
XX
PD 09-OCT-2003.
XX
PF 28-MAR-2003; 2003WO-US009662.
XX
PR 28-MAR-2002; 2002US-0368808P.
PR 10-APR-2002; 2002US-0371299P.
PR 28-MAR-2003; 2003US-00371299.
XX
PA (GALA-) GALA DESIGN INC.
XX
PI Bremel RD, Eakle K, Imboden M;
XX
DR WPI; 2003-804051/75.
DR N-PSDB; ADE64206.
XX
PT New antibody library comprising cells comprising at least one integrated
PT retroviral vector expressing an antibody light or heavy chain, useful in
PT preparing a composition for diagnosing or treating disorders.
XX
PS Disclosure; Fig 6; 57pp; English.

XX
CC This invention relates to a new antibody library which comprises at least
CC 100 cells, each of which comprises at least one integrated retroviral
CC vector expressing an antibody light or heavy chain. Antibodies are of
CC increasing importance in human therapy, assay procedures and diagnostic
CC methods and a need exists for efficient methods of generating and
CC screening antibody libraries containing large numbers of antibodies. The
CC antibody library of the invention addresses this need, with the
CC additional advantage of strict control over multiplicity of infection
CC (MOI), and is useful in preparing a composition for diagnosing or
CC treating a wide variety of disorders. The present sequence is the amino
CC acid sequence of the MN14HCF protein, which was encoded by the Gateway
CC retroviral vectors used in the exemplification of the invention.
XX
SQ Sequence 468 AA;

Query Match 100.0%; Score 64; DB 7; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
||||||||||
Db 118 LYFGFPWFAY 127

RESULT 29
ADF60815
ID ADF60815 standard; protein; 468 AA.
XX
AC ADF60815;
XX
DT 12-FEB-2004 (first entry)
XX
DE hMN-14 heavy chain amino acid sequence.
XX
KW Immunomodulatory; antidiabetic; immunosuppressive; cardiovascular;
KW neuroprotective; nootropic; fungicide; virucide; antimalarial;
KW antihelmintic; antiparasitic; haemostatic; muscular; antiinflammatory;
KW dermatological; antipyretic; antirheumatic; cytostatic; mutant;
KW bispecific antibody; immunoglobulin G; IgG; scFvs; Fvs; CH2 domain;
KW immune; autoimmune; disease; organ graft rejection; cardiovascular;
KW neurological; Alzheimer's disease; graft vs host disease;
KW systemic lupus erythematosus; diabetes mellitus.
XX
OS Homo sapiens.
XX
PN WO2003074569-A2.
XX
PD 12-SEP-2003.
XX
PF 03-MAR-2003; 2003WO-GB000871.
XX
PR 01-MAR-2002; 2002US-0361037P.
XX
PA (IMMU-) IMMUNOMEDICS INC.
PA (MCCA/) MCCALL J D.
XX
PI Qu Z, Hansen H, Goldenberg DM;
XX
DR WPI; 2003-902725/82.
DR N-PSDB; ADF60814.
XX
PT Mutant bispecific antibody which is rapidly cleared from a patient's
PT body, useful as a pretargeting agent in methods for diagnosing or
PT treating diseases, such as autoimmune disease, and disease caused by
PT infectious agents.
XX
PS Example; Fig 1; 68pp; English.
XX
CC The invention relates to a mutant bispecific antibody (mbAb1) comprising
CC at least a human hinge constant region from immunoglobulin G (IgG), two
CC single chain variable fragments (scFvs), and two variable fragments
CC (Fvs), where the constant region contains one or more amino acid
CC mutations in the heavy chain 2 (CH2) domain. The methods and antibody of
CC the invention are used to diagnose or treat an immune dysregulation
CC disease, an autoimmune disease, organ graft rejection, cardiovascular
CC disease, neurological disease (Alzheimer's disease) or graft vs. host
CC disease. The methods are also useful for treating a disease caused by a
CC fungus, virus, parasite, or bacterium. The methods may also be used for
CC intraoperative or endoscopic diagnosis to identify diseased tissue. The
CC autoimmune diseases that may be diagnosed or treated include acute or
CC chronic idiopathic thrombocytopenic purpura, dermatomyositis, Sydenham's
CC chorea, myasthenia gravis, systemic lupus erythematosus, lupus nephritis,
CC rheumatic fever, polyglandular syndromes and diabetes mellitus. The
CC current sequence represents the hMN-14 heavy chain amino acid sequence.
XX
SQ Sequence 468 AA;

Query Match 100.0%; Score 64; DB 7; Length 468;
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
||||||||||
Db 118 LYFGFPWFAY 127

RESULT 30
ADY97271
ID ADY97271 standard; protein; 669 AA.
XX
AC ADY97271;
XX
DT 16-JUN-2005 (first entry)
XX
DE Exemplary antibody fusion protein SEQ ID NO:3.
XX
KW antibody engineering; fusion protein; cytostatic; antimicrobial;
KW virucide; antibacterial; cancer; infection.
XX
OS Synthetic.
XX
PN US2005069552-A1.
XX
PD 31-MAR-2005.
XX
PF 28-JUL-2004; 2004US-00900928.
XX
PR 28-JUL-2003; 2003US-0490569P.
XX
PA (BLEC/) BLECK G T.
PA (YORK/) YORK D.
PA (COLL/) COLLINS I.
XX
PI Bleck GT, York D, Collins I;
XX
DR WPI; 2005-261600/27.
DR N-PSDB; ADY97269.
XX
PT Composition useful as cancer vaccine, comprises polypeptide having
PT antibody heavy chain fused to antibody light chain, or multivalent
PT antibody having two polypeptides with antibody heavy chain fused to
PT antibody light chain.
XX
PS Disclosure; SEQ ID NO 3; 101pp; English.
XX
CC The invention describes a composition (I) comprising: (a) a polypeptide
CC comprising at least one antibody heavy chain fused to at least one
CC antibody light chain; or (b) a multivalent antibody comprising at least
CC two polypeptides, where each of the polypeptides comprises at least one
CC antibody heavy chain fused to at least one antibody light chain. Also
CC described: (1) a composition (II) comprising a nucleic acid comprising at
CC least one antibody heavy chain gene and at least one antibody light chain
CC gene, where the nucleic acid encodes a polypeptide comprising at least
CC one antibody heavy chain fused to at least one antibody light chain; (2)
CC a method (M1) of binding an antigen, involves providing a polypeptide

CC comprising at least one antibody heavy chain fused to at least one
CC antibody light chain, and contacting the polypeptide with a sample having
CC an antigen under conditions such that the polypeptide binds to the
CC antigen; (3) a method (M2), which involves providing a vector comprising
CC a bicistronic expression construct comprising genes encoding an antibody
CC heavy chain gene and an antibody light chain gene, and altering the
CC nucleic acid sequence of a splice acceptor sequence or a splice donor
CC sequence in the antibody light chain gene or the antibody heavy chain
CC gene under conditions such that splicing is prevented at the splice
CC acceptor sequence or donor sequence; (4) a nucleic acid sequence produced
CC by (M2); (5) a vector (III) comprising a modified antibody heavy or light
CC gene, where modification eliminates a splice donor or acceptor sequence
CC in antibody heavy or light chain gene; and (6) a host cell comprising
CC (III). (I) is useful in in vitro binding assays for identifying antigens
CC in a mixture or determining the presence or absence of expression of a
CC particular protein. (I) is also useful as vaccine for treating cancer and
CC infections caused by pathogens e.g. virus or bacteria. The present
CC sequence represents an exemplary antibody fusion protein from the present
CC invention.
XX
SQ Sequence 669 AA;

Query Match 100.0%; Score 64; DB 9; Length 669;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
||||||||||
Db 99 LYFGFPWFAY 108

RESULT 31
AAR72599
ID AAR72599 standard; protein; 253 AA.
XX
AC AAR72599;
XX
DT 25-MAR-2003 (revised)
DT 03-JUL-1996 (first entry)
XX
DE Anti-dansyl single chain antibody.
XX
KW Single chain antibody; dansyl; SCAB; bispecific; tetravalent;
KW immunoglobulin; heavy chain; light chain; primer.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 126. .140
FT /note= "Flexible linker"
XX
PN WO9509917-A1.
XX
PD 13-APR-1995.
XX
PF 07-OCT-1994; 94WO-US011411.
XX
PR 07-OCT-1993; 93US-00134556.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Morrison SL, Coloma MJ;
XX
DR WPI; 1995-155258/20.
DR N-PSDB; AAQ86755.
XX
PT Prodn. of bi:specific, tetra:valent antibodies - by recombinant
PT expression of DNA encoding variable heavy and light immunoglobulin
PT chains.
XX
PS Example 1; Page 19; 33pp; English.
XX
CC The anti-dansyl single chain antibody was produced using PCR to join two
CC variable regions by overlap extension. A flexible linker region
CC consisting of three gly-gly-gly-gly-ser repeats was used to connect the C
CC -terminus of the heavy chain variable region (Vh) and the N-terminus of
CC the light chain variable region (Vl) in order to maximise flexibility
CC while minimising steric hindrance during protein folding. For the PCR
CC reaction, the 3' primer for Vh (AAQ86751) and the 5' primer for Vl
CC (AAQ86752) were designed to have a complementary region in the linker
CC portion. The Vh and Vl regions were independently amplified, followed by
CC a second PCR reaction in which these products were used as templates. The
CC complementary sequences in the linker were hybridised, joining the V
CC regions and two primers (AAQ86753, AAQ86754) were then used to amplify
CC the single chain antibody. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 253 AA;

Query Match 75.0%; Score 48; DB 2; Length 253;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
:|: :|||||
Db 105 IYYHYPWFAY 114

RESULT 32
AAB10040
ID AAB10040 standard; protein; 2210 AA.
XX
AC AAB10040;
XX
DT 02-NOV-2000 (first entry)
XX
DE LCMV L protein.
XX
KW Glycoprotein; gag gene; pol gene; GP-1; GP-2; anti-HIV; cytostatic;
KW gene therapy; treatment; infectious disease; HIV; AIDS; neoplasm;
KW carcinoma; melanoma; L protein.
XX
OS Lymphocytic choriomeningitis virus.
XX
PN EP1006196-A2.
XX
PD 07-JUN-2000.
XX
PF 25-NOV-1999; 99EP-00250415.
XX
PR 26-NOV-1998; 98DE-01056463.
XX
PA (PETT-) PETTE INST HEINRICH.
XX
PI Von Laer MD;
XX
DR WPI; 2000-378268/33.
DR N-PSDB; AAA40295.
XX
PT New retroviral packing cell useful as pharmaceutical carrier in gene
PT therapy for treatment of HIV and neoplasms, comprises retroviral genes
PT and glycoproteins.
XX
PS Disclosure; Page 22-26; 69pp; German.
XX
CC This invention describes a novel retroviral packing cell (I), comprising
CC the retroviral genes gag, pol and glycoproteins GP-1 and GP-2 of the LCMV
CC coding gene gp, or a part of these. The products of the invention have
CC anti-HIV and cytostatic activity and can be used for gene therapy. (I) is
CC useful for in vitro infection of cells, especially hematopoietic stem
CC cells, for expression of transgenes in cells and as a pharmaceutical
CC carrier for gene therapy. (I) is therefore useful in the treatment of
CC infectious diseases (HIV or AIDS), neoplasms (carcinomas), melanomas and
CC other diseases. This sequence represents a Lymphocytic choriomeningitis
CC virus (LCMV) L-protein which is described in the method of the invention
XX

```
SQ   Sequence 2210 AA;

  Query Match            68.8%;  Score 44;  DB 3;  Length 2210;
  Best Local Similarity  70.0%;  Pred. No. 5.7e+02;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              | ||| ||:|
Db       1901 LQFGFGWFSY 1910


RESULT 33
AAW04592
ID   AAW04592 standard; protein; 116 AA.
XX
AC   AAW04592;
XX
DT   27-AUG-2003  (revised)
DT   11-AUG-1997  (first entry)
XX
DE   Anti-DNA antibody 10f4 heavy chain variable region.
XX
KW   Heavy chain; variable region; anti-DNA; monoclonal; antibody; MAb 10f4;
KW   hairpin; diagnosis; inflammatory glomerulonephritis;
KW   systemic lupus erythematosus; screening; treatment; prevention; SLE;
KW   disease.
XX
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .22
FT                   /label= framework_I
FT   Region          23. .27
FT                   /label= CDR_I
FT   Region          28. .41
FT                   /label= framework_II
FT   Region          42. .58
FT                   /label= CDR_II
FT   Region          59. .90
FT                   /label= framework_III
FT   Region          91. .105
FT                   /label= CDR_III
FT   Region          106. .116
FT                   /label= J_region
XX
PN   WO9636361-A1.
XX
PD   21-NOV-1996.
XX
PF   16-MAY-1996;   96WO-US007113.
XX
PR   18-MAY-1995;   95US-00443540.
XX
PA   (UNMI ) UNIV MICHIGAN.
XX
PI   Glick GD,  Swanson PC;
XX
DR   WPI; 1997-011854/01.
DR   N-PSDB; AAT43736.
XX
PT   Anti-DNA antibody which specifically binds DNA hairpin - useful to
PT   develop prods. for diagnosis and treatment of disorders, e.g.
PT   glomerulonephritis or systemic lupus erythematosus.
XX
PS   Example; Fig 7; 102pp; English.
XX
CC   The present sequence is the heavy chain variable region of the anti-DNA
CC   monoclonal antibody (MAb) 10f4, which has a high affinity for single
CC   stranded DNA, low or no affinity for double stranded DNA and specifically
CC   binds a DNA hairpin. The MAb can be used diagnose disorders associated
CC   with the pathological complexation of DNA, e.g. inflammatory
CC   glomerulonephritis and systemic lupus erythematosus. It can also be used
CC   to generate reagents to screen for pharmaceutical agents, and treat
CC   and/or prevent an above disorder. Calf thymus DNA was used to immunise a
CC   MRL-1pr mouse, spleen cells from which were then fused with Sp2/0 myeloma
CC   cells to give hybridomas producing the anti-DNA MAb. 10f4 was found to
CC   react strongly with single stranded DNA and poly(dT), moderately with
CC   poly(dG) and weakly with poly(dI). (Updated on 27-AUG-2003 to correct OS
CC   field.)
XX
SQ   Sequence 116 AA;

  Query Match            67.2%;  Score 43;  DB 2;  Length 116;
  Best Local Similarity  66.7%;  Pred. No. 44;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              |  :|||||
Db         97 YSNYPWFAY 105


RESULT 34
AEB39735
ID   AEB39735 standard; protein; 812 AA.
XX
AC   AEB39735;
XX
DT   08-SEP-2005  (first entry)
XX
DE   L. pneumophila protein SEQ ID NO 4067.
XX
KW   detection; infection; Antibacterial; Vaccine.
XX
OS   Legionella pneumophila.
XX
PN   WO2005049642-A2.
XX
PD   02-JUN-2005.
XX
PF   23-SEP-2004; 2004WO-IB003578.
XX
PR   21-NOV-2003; 2003FR-00013687.
XX
PA   (INSP ) INST PASTEUR.
PA   (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
PA   (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Buchrieser C,  Tichit M,  Etienne J,  Ma L,  Cazalet C,  Glaser P;
PI   Rusniok C,  Bouchier C,  Zidane N,  Magnier A,  Kunst F,  Vandenesch F;
PI   Jarraud S;
XX
DR   WPI; 2005-388305/40.
XX
PT   New genome of Legionella pneumophila Paris strain and derived
PT   polypeptides, useful for detection or identification of the strain and
PT   for treatment and prevention of infections.
XX
PS   Claim 3; SEQ ID NO 4067; 660pp; English.
XX
CC   The invention relates to an isolated or purified nucleotide sequences (I)
CC   from Legionella pneumophila Paris strain. (I), and their related
CC   sequences or fragments, are useful as primers and probes for detection
CC   and amplification, including differentiation between the Paris and
CC   Philadelphia strains of Legionella pneumophila and to prepare recombinant
CC   (hybrid) polypeptides (II). (II) are also useful for preparation of
CC   specific antibodies (Ab), also used for detection/identification of
CC   Legionella, and some (I), specifically those involved in synthesis of
CC   surface proteins, are targets for identification of inhibitors. (II), or
CC   vectors that contain (I), are useful as vaccines and immunogenic
CC   compositions, for treatment and prevention of infections by L.
CC   pneumophila. The present squence represents the amino acid sequence of a
CC   L. pneumophila protein.
XX
SQ   Sequence 812 AA;
```

Query Match 67.2%; Score 43; DB 9; Length 812;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YFGFPW 7
||||||
Db 40 YFGFPW 45

RESULT 35
AEB36318
ID AEB36318 standard; protein; 812 AA.
XX
AC AEB36318;
XX
DT 08-SEP-2005 (first entry)
XX
DE L. pneumophila protein SEQ ID NO 650.
XX
KW detection; infection; Antibacterial; Vaccine.
XX
OS Legionella pneumophila.
XX
PN WO2005049642-A2.
XX
PD 02-JUN-2005.
XX
PF 23-SEP-2004; 2004WO-IB003578.
XX
PR 21-NOV-2003; 2003FR-00013687.
XX
PA (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P;
PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
PI Jarraud S;
XX
DR WPI; 2005-388305/40.
XX
PT New genome of Legionella pneumophila Paris strain and derived
PT polypeptides, useful for detection or identification of the strain and
PT for treatment and prevention of infections.
XX
PS Claim 3; SEQ ID NO 650; 660pp; English.
XX
CC The invention relates to an isolated or purified nucleotide sequences (I)
CC from Legionella pneumophila Paris strain. (I), and their related
CC sequences or fragments, are useful as primers and probes for detection
CC and amplification, including differentiation between the Paris and
CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
CC (hybrid) polypeptides (II). (II) are also useful for preparation of
CC specific antibodies (Ab), also used for detection/identification of
CC Legionella, and some (I), specifically those involved in synthesis of
CC surface proteins, are targets for identification of inhibitors. (II), or
CC vectors that contain (I), are useful as vaccines and immunogenic
CC compositions, for treatment and prevention of infections by L.
CC pneumophila. The present squence represents the amino acid sequence of a
CC L. pneumophila protein.
XX
SQ Sequence 812 AA;

Query Match 67.2%; Score 43; DB 9; Length 812;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YFGFPW 7
||||||
Db 40 YFGFPW 45

RESULT 36
AAR83375
ID AAR83375 standard; peptide; 12 AA.
XX
AC AAR83375;
XX
DT 24-MAY-1996 (first entry)
XX
DE Kbm1-binding random peptide, H6.
XX
KW MHC; Kb; major histocompatibility complex; terminal; identification;
KW investigation; random.
XX
OS Synthetic.
XX
PN WO9527901-A1.
XX
PD 19-OCT-1995.
XX
PF 10-APR-1995; 95WO-US004509.
XX
PR 11-APR-1994; 94US-00227101.
XX
PA (IXSY-) IXSYS INC.
XX
PI Gay DA;
XX
DR WPI; 1995-366462/47.
XX
PT Identifying peptide(s) which bind MHC molecules - using a library of
PT random peptide(s) expressed as fusion proteins and obtaining terminal
PT octamers or nonamers.
XX
PS Disclosure; Fig 6; 46pp; English.
XX
CC AAR83351-R83391 are random MHC binding peptides which are identified from
CC a library of random peptides expressed as fusion proteins on the surface
CC of a cell or virus. These peptides are isolated using the murine MHC
CC molecule Kbm1. The identification method rapidly identifies MHC binding
CC motifs, provides sequence information on neighbouring amino acids and
CC relationships between amino acids within the peptides and reveals a
CC preference for several amino acids at peptide positions previously
CC thought to be indiscriminate
XX
SQ Sequence 12 AA;

Query Match 65.6%; Score 42; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 6.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FGFPWFAY 10
||:||| |
Db 3 FGWPWFDY 10

RESULT 37
ABP02212
ID ABP02212 standard; protein; 117 AA.
XX
AC ABP02212;
XX
DT 25-JUN-2002 (first entry)
XX
DE Human ORFX protein sequence SEQ ID NO:4406.
XX
KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
KW hypertension; hypothyroidism; cholesterol ester storage disease;
KW immune deficiency; immune disorder; infectious disease;
KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
KW myasthenia gravis.

XX
OS Homo sapiens.
XX
PN WO200192523-A2.
XX
PD 06-DEC-2001.
XX
PF 29-MAY-2001; 2001WO-US010836.
XX
PR 30-MAY-2000; 2000US-0206132P.
PR 29-AUG-2000; 2000US-0228716P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach MD;
XX
DR WPI; 2002-106308/14.
DR N-PSDB; ABN17964.
XX
PT Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders.
XX
PS Disclosure; SEQ ID NO 4406; 1037pp; English.
XX
CC The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated
CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage. N.B. The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 117 AA;

Query Match 65.6%; Score 42; DB 5; Length 117;
Best Local Similarity 77.8%; Pred. No. 63;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LYFGFPWFA 9
|| |||:||
Db 40 LYIGFPYFA 48

RESULT 38
AAW01585
ID AAW01585 standard; protein; 119 AA.
XX
AC AAW01585;
XX
DT 22-AUG-1997 (first entry)
XX
DE Lead binding MAb 11D11 heavy chain variable region.
XX
KW Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic;
KW pharmaceutical; health care; skin treatment; pesticide; herbicide;
KW heavy metal.
XX
OS Mus musculus.
XX
PN WO9639518-A1.
XX
PD 12-DEC-1996.
XX
PF 05-JUN-1996; 96WO-US009258.
XX
PR 05-JUN-1995; 95US-00462798.
PR 10-OCT-1995; 95US-00541373.
XX
PA (BION-) BIONEBRASKA INC.
XX
PI Wylie DE, Lopez O, Murray PJ;
XX
DR WPI; 1997-043140/04.
DR N-PSDB; AAT58259.
XX
PT DNA encoding heavy metal binding polypeptide sequences - used for
PT detecting, removing, adding or neutralising heavy metals, such as lead
PT cations.
XX
PS Claim 12; Page 73; 125pp; English.
XX
CC The present sequence represents the heavy chain variable region for
CC monoclonal antibody (MAb) 11D11, which immunoreacts with a lead cation.
CC The sequence was derived from RNA isolated from mouse hybridoma cells.
CC The protein can be used for binding heavy metals, such as lead cations.
CC It can be used for detecting, removing, adding or neutralising the heavy
CC metals in biological and inanimate systems. It can be used in e.g.
CC aqueous liquid systems, in biological or environmental systems or in such
CC compositions as perfumes, cosmetics, pharmaceuticals, health care
CC products, skin treatment products, pesticides, herbicides, solvents used
CC in the production of semi-conductor and integrated circuit components and
CC production materials for electronic components. The products can provide
CC for applications involving minute amounts of specific heavy metals
XX
SQ Sequence 119 AA;

Query Match 65.6%; Score 42; DB 2; Length 119;
Best Local Similarity 60.0%; Pred. No. 64;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
:|:| ||||
Db 99 IYYGHLWFAY 108

RESULT 39
AAU10305
ID AAU10305 standard; protein; 153 AA.
XX
AC AAU10305;
XX
DT 25-JAN-2002 (first entry)
XX
DE G-protein coupled receptor (GCREC) #6.
XX
KW G-protein coupled receptor; GCREC; vaccine; gene therapy;
KW cell proliferation disorder; cancer; arteriosclerosis;
KW neurological disorder; epilepsy; stroke; cardiovascular disorder;
KW hypertension; ischaemic heart disease; gastrointestinal disorder;
KW anorexia; peptic ulcer; autoimmune disorder; inflammatory disorder;
KW diabetes; osteoporosis; psoriasis; metabolic disorder; obesity;
KW schizophrenic disorder; neuroskeletal disorder.
XX
OS Homo sapiens.
XX
PN WO200166742-A2.
XX
PD 13-SEP-2001.

XX
PF 01-MAR-2001; 2001WO-US006814.
XX
PR 03-MAR-2000; 2000US-0186854P.
PR 10-MAR-2000; 2000US-0188384P.
PR 17-MAR-2000; 2000US-0190453P.
PR 20-MAR-2000; 2000US-0190730P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Tang YT, Patterson C, Yao MG, Shih LL, Tribouley CM;
PI Lu DAM, Yue H, Khan FA, Policky JL, Au-Young J, Yang J, Harland L;
PI Walsh RT, Lo TP, Borowsky ML;
XX
DR WPI; 2001-656776/75.
DR N-PSDB; AAS15902.
XX
PT Novel G-protein coupled receptor polypeptides, for treating and
PT preventing autoimmune/inflammatory disorders, neurological disorders,
PT cell proliferative disorders, cardiovascular disorders and viral
PT infections.
XX
PS Claim 1; Page 118; 141pp; English.
XX
CC The invention describes a novel isolated polypeptide, selected from a
CC group of 21 G-protein coupled receptor polypeptides (GCREC) and useful in
CC vaccines and gene therapy. The polypeptide (I) is useful for screening
CC for agonist or antagonist of (I), compounds specifically binding to (I),
CC or compounds that modulate the activity of (I). The polynucleotide
CC encoding (1) is useful for screening a compound for effectiveness in
CC altering expression of a target polynucleotide comprising (II), by
CC exposing a sample comprising the target polynucleotide to a compound,
CC detecting altered expression of the target polynucleotide, and comparing
CC the expression of the target polynucleotide in the presence of varying
CC amounts of compound and in the absence of the compound. (I) and (II) are
CC useful for diagnosis, treatment and prevention of cell proliferative
CC disorders (e.g. cancers, arteriosclerosis, atherosclerosis), neurological
CC disorders (e.g. epilepsy, stroke, schizophrenic disorders and
CC neuroskeletal disorders), cardiovascular disorders (e.g. hypertension,
CC ischaemic heart disease), gastrointestinal disorders (e.g. anorexia,
CC peptic ulcer), autoimmune/inflammatory disorders (e.g. diabetes mellitus,
CC osteoporosis, psoriasis), and metabolic disorders such as obesity.
CC Furthermore, the polynucleotide is useful; as primers for detecting
CC single nucleotide polymorphisms; as elements in microarray, to monitor or
CC measure protein-protein interactions, drug-target interactions, and gene
CC expression profiles; to generate a transcript image of a tissue or cell
CC type, and to generate hybridisation probes useful in mapping the
CC naturally occurring genomic sequence. This is the G-protein coupled
CC receptor 6 (GCREC-6), one of 21 GCREC proteins described in the method of
CC the invention
XX
SQ Sequence 153 AA;

```
  Query Match             65.6%;  Score 42;  DB 4;  Length 153;
  Best Local Similarity   77.8%;  Pred. No. 82;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db         56 LYFAFHWFA 64
```

RESULT 40
ABP56821
ID ABP56821 standard; protein; 246 AA.
XX
AC ABP56821;
XX
DT 02-APR-2003 (first entry)
XX
DE Human glucocorticoid-induced receptor (GIR) protein SEQ ID NO:6.
XX
KW Glucocorticoid-induced receptor; GIR; stress reward disorder; antidote;
KW addiction reward disorder; neuroleptic; antialcoholic; gene therapy;
KW stress reward disorder susceptibility locus; polysubstance abuse;
KW drug addiction; nicotine addiction; alcohol addiction; cocaine addiction.
XX
OS Homo sapiens.
XX
PN WO2003004706-A1.
XX
PD 16-JAN-2003.
XX
PF 03-JUL-2002; 2002WO-US021149.
XX
PR 03-JUL-2001; 2001US-0302973P.
XX
PA (CHIL-) CHILDRENS HOSPITAL RES FOUND.
XX
PI Richtand N, Sallee FR, Wang D;
XX
DR WPI; 2003-201559/19.
DR N-PSDB; ABZ22786.
XX
PT Predicting a likelihood of developing a stress reward disorder for
PT treating stress related disorders, e.g., cocaine addiction, comprises
PT detecting in the DNA obtained from a subject a human glucocorticoid-
PT induced receptor gene.
XX
PS Claim 12; Page 92-94; 99pp; English.
XX
CC The present invention describes a method for predicting a patient's
CC likelihood of developing a stress reward disorder, comprising: (a)
CC obtaining DNA from a human subject; and (b) detecting in the DNA a human
CC glucocorticoid-induced receptor (GIR) gene, where the gene indicates a
CC potential susceptibility to an addiction reward disorder. GIR has
CC neuroleptic; antialcoholic; antidote. gene therapy. Other methods from
CC the present invention are used for detecting a human GIR receptor gene,
CC detecting a genetic potential susceptibility to a stress reward disorder,
CC detecting the presence of a stress reward disorder susceptibility locus,
CC genetically diagnosing an addiction reward disorder, treating an
CC individual phenotypically diagnosed with an addiction reward disorder,
CC diagnosing GIR receptor sensitisation, identifying a chemical compound
CC that specifically binds to a mammalian GIR receptor, determining whether
CC a mammalian compound is a mammalian GIR receptor agonist or antagonist,
CC and determining whether a chemical compound specifically binds to and
CC activates a mammalian GIR receptor. The method is useful for preparing a
CC composition for treating an individual afflicted with stress related
CC disorders, e.g., polysubstance abuse, or drug, nicotine, alcohol or
CC cocaine addiction. The present sequence represents human GIR, which is
CC used in the exemplification of the present invention
XX
SQ Sequence 246 AA;

```
  Query Match             65.6%;  Score 42;  DB 6;  Length 246;
  Best Local Similarity   77.8%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        149 LYFAFHWFA 157
```

RESULT 41
AAR48750
ID AAR48750 standard; protein; 349 AA.
XX
AC AAR48750;
XX
DT 07-JUN-1996 (first entry)
XX
DE G-protein coupled mouse glucocorticoid-induced receptor protein.
XX
KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
KW psychotic disorder; schizophrenia; dopamine; cAMP; adenosine; thrombin;
KW muscarinic acetylcholine; adrenergic; endothelin; bombesin; endocrine;

KW rhodopsin; opsin; odorant; cytomegalovirus.
XX
OS Mus musculus.
XX
PN WO9405695-A1.
XX
PD 17-MAR-1994.
XX
PF 09-SEP-1993; 93WO-US008528.
XX
PR 10-SEP-1992; 92US-00943236.
XX
PA (UYNY) UNIV NEW YORK STATE.
XX
PI Murphy RB, Schuster DI;
XX
DR WPI; 1994-101120/12.
XX
PT Polypeptides of G-coupled receptor proteins (GPRs) - useful for binding
PT GPR ligands or modulating GPR binding.
XX
PS Disclosure; Page 125-126; 160pp; English.
XX
CC Proteins AAR48685-R48758 represent a range of G-protein coupled receptor
CC proteins selected from cAMP, adenosine, muscarinic acetylcholine,
CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
CC odorant, cytomegaloviral and other G-protein coupled receptors. The
CC receptor proteins were used to design polypeptides, pref. based on the
CC transmembrane domains, for use in G-protein coupled receptor ligand
CC binding assays. The polypeptide fragments retain biological activity such
CC as binding a GPR ligand or modulating GPR ligand binding to a GPR (see
CC AAR48759-R48758, AAR50569-R50807 and AAR89189-R89195 for examples of
CC polypeptide fragments). The polypeptide fragments can be used in
CC compositions for treating subjects suffering from a pathology related to
CC a GPR abnormality e.g. a psychotic disorder such as schizophrenia
XX
SQ Sequence 349 AA;

Query Match 65.6%; Score 42; DB 2; Length 349;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LYFGFPWFA 9
||| | |||
Db 254 LYFAFHWFA 262

RESULT 42
AAW02722
ID AAW02722 standard; peptide; 349 AA.
XX
AC AAW02722;
XX
DT 25-MAR-2003 (revised)
DT 13-NOV-1996 (first entry)
XX
DE G-protein coupled mouse glucocorticoid-induced receptor.
XX
KW G-protein coupled receptor; ligand binding assay; transmembrane domain;
KW schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
KW muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
KW odorant; cytomegalovirus; serotonergic.
XX
OS Mus musculus.
XX
PN US5508384-A.
XX
PD 16-APR-1996.
XX
PF 09-SEP-1993; 93US-00118270.
XX
PR 10-SEP-1992; 92US-00943236.
XX
PA (UYNY) UNIV NEW YORK STATE.
XX
PI Schuster DI, Murphy RB;
XX
DR WPI; 1996-208785/21.
XX
PT New dopamine receptor peptide - useful as antipsychotic agent, e.g. for
PT treating schizophrenia.
XX
PS Disclosure; Col 163-166; 184pp; English.
XX
CC Proteins AAW02657-W02730 represent a range of G-protein coupled receptor
CC (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,
CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,
CC odorant, cytomegaloviral and other GPR proteins. The receptor proteins
CC were used to design polypeptides, pref. based on the transmembrane
CC domains, for use in G-protein coupled receptor ligand binding assays. The
CC polypeptide fragments retain biological activity such as binding a GPR
CC ligand or modulating GPR ligand binding to a GPR (see AAW02747-W02999 for
CC examples of polypeptide fragments). The polypeptide fragments can be used
CC in compositions for treating subjects suffering from a pathology related
CC to a GPR abnormality e.g. a psychotic disorder such as schizophrenia.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 349 AA;

Query Match 65.6%; Score 42; DB 2; Length 349;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LYFGFPWFA 9
||| | |||
Db 254 LYFAFHWFA 262

RESULT 43
AAB73388
ID AAB73388 standard; protein; 369 AA.
XX
AC AAB73388;
XX
DT 05-JUN-2001 (first entry)
XX
DE Anti-VHSV single chain antibody BU1.
XX
KW Anti-VHSV; single chain antibody BU1; ScAb; scFv;
KW monoclonal antibody 3F1H10; variable region; antiviral; anti-allergy;
KW human kappa light chain constant domain; vaccine; gene therapy;
KW rainbow trout TGF-beta signal peptide; transforming growth factor beta;
KW genetic prophylaxis.
XX
OS Oncorhynchus mykiss.
OS Mus musculus.
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
PN WO200121800-A1.
XX
PD 29-MAR-2001.
XX
PF 20-SEP-2000; 2000WO-GB003605.
XX
PR 20-SEP-1999; 99DK-00001329.
XX
PA (UYAB-) UNIV ABERDEEN.
PA (STAT-) STATENS VETERINAERE SERUMLABORATOTIUM.
XX
PI Secombes CJ, Cunningham C, Lorenzen N;
XX
DR WPI; 2001-257991/26.
DR N-PSDB; AAF73388.
XX

```
PT   New non-infectious nucleic acid construct encoding recombinant antibody
PT   molecule, useful for conferring protective immunity to infectious
PT   diseases, preventing allergic reactions or reactions caused by toxins in
PT   animals.
XX
PS   Example; Page; 29pp; English.
XX
CC   The invention relates to a non-infectious nucleic acid construct encoding
CC   a recombinant (e.g., single chain) antibody molecule. The nucleic acid
CC   construct is adapted for in vivo establishment of protective immunity to
CC   an infectious disease in an animal, or is formulated for in vivo
CC   prevention of an allergic reaction to an allergen or a reaction caused by
CC   the presence of a toxic substance in an animal. Constructs of the
CC   invention are thus useful for treating infectious disease caused by viral
CC   haemorrhagic septicaemia virus (VHSV) (fish), infectious haemotopoietic
CC   necrosis virus (fish), bovine viral diarrhoea virus, pseudorabies virus
CC   (pigs), plasmocytosis virus (mink), feline leukaemia virus, human
CC   immunodeficiency virus, and hepatitis A virus (human). Genetic
CC   prophylaxis methods using such constructs are useful for the transient
CC   protection of individuals against exposure to pathogens or toxins where
CC   no efficient vaccines are available, for inducing the synthesis of
CC   antibodies of a desired specificity for use in immunocompromised
CC   individuals, and for protecting an individual against an allergic
CC   reaction. In contrast to DNA vaccines, including anti- idiotype vaccines,
CC   administration of plasmid-borne genes do not involve specific activation
CC   of the immune system in the individual. Prophylaxis against infectious
CC   diseases takes place without any side effects such as the transfer of
CC   infectious diseases or induction of hypersensitivity following repeated
CC   administration. The single chain antibodies will be systemically
CC   distributed by the body fluids and protect the individual if infection
CC   with the pathogen occurs. The present sequence represents a portion of a
CC   construct of the invention which encodes a single chain antibody, BU1.
CC   BU1 is reactive to the fish pathogenic rhabdovirus, VHSV. BU1 is derived
CC   from the variable regions of the VHSV-reactive murine monoclonal antibody
CC   3F1H10, and also contains the rainbow trout transforming growth factor
CC   beta (TGF-beta) signal peptide at the N- terminus (to ensure secretion of
CC   the single chain antibody) and the human kappa light chain constant
CC   domain (used as a tag to facilitate detection) at the C-terminus. Note:
CC   The present sequence is not shown in the specification, but has been
CC   decoded from the corresponding nucleic acid sequence (AAF76338)
XX
SQ   Sequence 369 AA;

  Query Match             65.6%;  Score 42;  DB 4;  Length 369;
  Best Local Similarity   60.0%;  Pred. No. 2e+02;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              :|:|  ||||
Db        121 IYYGNDWFAY 130


RESULT 44
ABP56819
ID   ABP56819 standard; protein; 422 AA.
XX
AC   ABP56819;
XX
DT   02-APR-2003  (first entry)
XX
DE   Rat glucocorticoid-induced receptor (GIR) protein SEQ ID NO:2.
XX
KW   Glucocorticoid-induced receptor; GIR; stress reward disorder; antidote;
KW   addiction reward disorder; neuroleptic; antialcoholic; gene therapy;
KW   stress reward disorder susceptibility locus; polysubstance abuse;
KW   drug addiction; nicotine addiction; alcohol addiction; cocaine addiction.
XX
OS   Rattus norvegicus.
XX
PN   WO2003004706-A1.
XX
PD   16-JAN-2003.
XX
PF   03-JUL-2002; 2002WO-US021149.
XX
PR   03-JUL-2001; 2001US-0302973P.
XX
PA   (CHIL-) CHILDRENS HOSPITAL RES FOUND.
XX
PI   Richtand N,  Sallee FR,  Wang D;
XX
DR   WPI; 2003-201559/19.
DR   N-PSDB; ABZ22784.
XX
PT   Predicting a likelihood of developing a stress reward disorder for
PT   treating stress related disorders, e.g., cocaine addiction, comprises
PT   detecting in the DNA obtained from a subject a human glucocorticoid-
PT   induced receptor gene.
XX
PS   Claim 12; Fig 1A-C; 99pp; English.
XX
CC   The present invention describes a method for predicting a patient's
CC   likelihood of developing a stress reward disorder, comprising: (a)
CC   obtaining DNA from a human subject; and (b) detecting in the DNA a human
CC   glucocorticoid-induced receptor (GIR) gene, where the gene indicates a
CC   potential susceptibility to an addiction reward disorder. GIR has
CC   neuroleptic; antialcoholic; antidote. gene therapy. Other methods from
CC   the present invention are used for detecting a human GIR receptor gene,
CC   detecting a genetic potential susceptibility to a stress reward disorder,
CC   detecting the presence of a stress reward disorder susceptibility locus,
CC   genetically diagnosing an addiction reward disorder, treating an
CC   individual phenotypically diagnosed with an addiction reward disorder,
CC   diagnosing GIR receptor sensitisation, identifying a chemical compound
CC   that specifically binds to a mammalian GIR receptor, determining whether
CC   a mammalian compound is a mammalian GIR receptor agonist or antagonist,
CC   and determining whether a chemical compound specifically binds to and
CC   activates a mammalian GIR receptor. The method is useful for preparing a
CC   composition for treating an individual afflicted with stress related
CC   disorders, e.g., polysubstance abuse, or drug, nicotine, alcohol or
CC   cocaine addiction. The present sequence represents rat GIR, which is used
CC   in the exemplification of the present invention
XX
SQ   Sequence 422 AA;

  Query Match             65.6%;  Score 42;  DB 6;  Length 422;
  Best Local Similarity   77.8%;  Pred. No. 2.3e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        325 LYFAFHWFA 333


RESULT 45
AAW34512
ID   AAW34512 standard; protein; 423 AA.
XX
AC   AAW34512;
XX
DT   19-MAR-1998  (first entry)
XX
DE   G protein coupled receptor.
XX
KW   G protein coupled receptor; human; amygdaloid nucleus-derived protein;
KW   agonist identification; antagonist; gene therapy.
XX
OS   Homo sapiens.
XX
PN   EP789076-A2.
XX
PD   13-AUG-1997.
XX
PF   05-FEB-1997;   97EP-00101767.
XX
PR   07-FEB-1996;   96JP-00021562.
XX
```

```
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Hinuma S,  Sakamoto J,  Hosoya M;
XX
DR   WPI; 1997-395571/37.
DR   N-PSDB; AAT98796.
XX
PT   Human amygdaloid nucleus-derived G protein coupled receptor - useful for
PT   identifying (ant)agonists used in the treatment of, e.g., Alzheimer's
PT   disease, dementia, angina or epilepsy.
XX
PS   Claim 1; Page 30-31; 58pp; English.
XX
CC   This sequence represents the human amygdaloid nucleus-derived G protein
CC   coupled receptor of the invention. The protein and peptide can be used to
CC   identify agonists or antagonists useful for treating spinal injury,
CC   Alzheimer's disease, asthma, hyperphagia, neuropathy, dementia, pain,
CC   cerebral thrombosis, encephalitis, cerebral infarction, cerebrovascular
CC   spasm, spondylitis, angina, neurosis, drug dependence, drug and alcohol
CC   withdrawal symptoms, schizophrenia, phobia, stroke, anxiety, depression,
CC   respiratory distress syndrome, emesis, epilepsy, etc. The DNA encoding it
CC   can be used to produce the recombinant protein or peptide, to construct
CC   diagnostic probes and primers, and for gene therapy. An antibody directed
CC   against the G protein coupled receptor can be used in immunoassays for
CC   the protein
XX
SQ   Sequence 423 AA;

  Query Match             65.6%;  Score 42;  DB 2;  Length 423;
  Best Local Similarity   77.8%;  Pred. No. 2.3e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        326 LYFAFHWFA 334


RESULT 46
AAW32797
ID   AAW32797 standard; protein; 423 AA.
XX
AC   AAW32797;
XX
DT   22-APR-1998  (first entry)
XX
DE   Human derived long chain DNA novel protein.
XX
KW   Human; long chain DNA; antibody; nervous disorder; detection; inhibitor.
XX
OS   Homo sapiens.
XX
PN   WO9737018-A1.
XX
PD   09-OCT-1997.
XX
PF   19-MAR-1997;   97WO-JP000919.
XX
PR   03-APR-1996;   96JP-00081304.
XX
PA   (ASAH ) ASAHI KASEI KOGYO KK.
XX
PI   Takada Y,  Kato C;
XX
DR   WPI; 1997-503103/46.
DR   N-PSDB; AAT94563, AAT04564.
XX
PT   Human long chain DNA and antibodies which bind to the peptide(s) - is
PT   potentially useful in treating nervous disorders.
XX
PS   Claim 2; Page 89-91; 109pp; Japanese.
XX
CC   The present sequence represents a protein encoded by human derived long
CC   chain DNA comprising at least a peptide-encoding region. Peptides encoded
CC   by the human derived long chain DNA, may be used for detecting substances
CC   which bind to the peptides, and for detecting substances which suppress
CC   or inhibit binding to these peptides. The peptides and their inhibitors
CC   are potentially useful in treating nervous disorders
XX
SQ   Sequence 423 AA;

  Query Match             65.6%;  Score 42;  DB 2;  Length 423;
  Best Local Similarity   77.8%;  Pred. No. 2.3e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        326 LYFAFHWFA 334


RESULT 47
AAW81460
ID   AAW81460 standard; protein; 423 AA.
XX
AC   AAW81460;
XX
DT   27-JAN-1999  (first entry)
XX
DE   Human G-protein coupled receptor polypeptide HCEPT09.
XX
KW   G-protein coupled receptor; HCEPT09; gene therapy; immune response;
KW   vaccine; HIV-1; HIV-2; cancer; anorexia; bulimia; asthma; hypertension;
KW   Parkinson's disease; heart failure; hypotension; urinary retension;
KW   osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy;
KW   benign prostatic hypertrophy; psychotic disorder; neurological disorder;
KW   anxiety; schizophrenia; manic depression; delirium; dementia; human;
KW   mental retardation; dyskinesias; Huntington's disease; gene mapping;
KW   Gilles de la Tourette's syndrome; linkage analysis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 26
FT                   /note= "encoded by GAG"
FT   Misc-difference 28
FT                   /note= "encoded by AGC"
FT   Misc-difference 49
FT                   /note= "encoded by TTC"
FT   Misc-difference 91
FT                   /note= "encoded by CTG"
XX
PN   EP877083-A1.
XX
PD   11-NOV-1998.
XX
PF   09-APR-1998;   98EP-00302890.
XX
PR   07-MAY-1997;   97US-0045889P.
PR   05-SEP-1997;   97US-00924174.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Zhu Y,  Elshourbagy N,  Halsey WS,  Sathe G;
XX
DR   WPI; 1998-570539/49.
DR   N-PSDB; AAV69220.
XX
PT   New human G-protein coupled receptor polypeptides and polynucleotides -
PT   useful as diagnostic reagents and for prevention and treatment of HIV,
PT   cancer and Parkinson's disease.
XX
PS   Claim 11; Page 9; 24pp; English.
XX
CC   This represents a human G-protein coupled receptor (HCEPT09) polypeptide.
CC   The HCEPT09 polypeptide can be recombinantly produced by transforming a
CC   host cell with an expression vector comprising the HCEPT09 nucleic acid.
CC   HCEPT09 polypeptides and polynucleotides are useful for diagnosing
```

CC susceptibility to diseases by detecting mutations in the HCEPT09 gene
CC using probes containing the HCEPT09 nucleotide sequence, and can diagnose
CC diseases associated with HCEPT09 imbalance by determining HCEPT09
CC polypeptide or mRNA expression levels. HCEPT09 can be used to screen for
CC agonists and antagonists which bind the HCEPT09 polypeptide. These can be
CC used in treatment to activate or inhibit HCEPT09 activity, in addition to
CC direct administration of antisense sequences to prevent expression, or
CC HCEPT09 polypeptides to treat conditions associated with a lack of
CC HCEPT09 protein. Gene therapy may also be used to affect endogenous
CC HCEPT09 polypeptide production. HCEPT09 antibodies are useful for
CC inducing an immune response to immunise and prevent diseases, and for
CC isolating HCEPT09 clones or purifying the polypeptides by affinity
CC chromatography. HCEPT09 polypeptides can be administered directly or as a
CC vaccine to inoculate against disease. Diseases diagnosed, prevented or
CC treated include HIV-1 and -2; cancers; anorexia; bulimia; asthma;
CC Parkinson's disease; acute heart failure; hypotension; hypertension;
CC urinary retension; osteoporosis; angina pectoris; myocardial infarction;
CC ulcers; allergies; benign prostatic hypertrophy; neurological and
CC psychotic disorders, including anxiety, schizophrenia, manic depression,
CC delirium, dementia, severe mental retardation and dyskinesias, such as
CC Huntington's disease or Gilles de la Tourette's syndrome. The HCEPT09
CC polypeptide is also useful for mapping the gene to a chromosome, allowing
CC gene inheritance to be studied through linkage analysis
XX
SQ Sequence 423 AA;

Query Match 65.6%; Score 42; DB 2; Length 423;
Best Local Similarity 77.8%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LYFGFPWFA 9
||| | |||
Db 326 LYFAFHWFA 334

RESULT 48
AAE03740
ID AAE03740 standard; protein; 423 AA.
XX
AC AAE03740;
XX
DT 04-SEP-2001 (first entry)
XX
DE Mouse G-protein coupled receptor (GPCR) RP-23 protein.
XX
KW Mouse; G-protein coupled receptor; GPCR; RP-23; sphingosine-1-PO4;
KW sphingosine-1-phosphate; therapy; cardiovascular disease; cancer;
KW inflammatory disease; cell signalling.
XX
OS Mus sp.
XX
PN WO200144439-A2.
XX
PD 21-JUN-2001.
XX
PF 15-DEC-2000; 2000WO-SE002563.
XX
PR 17-DEC-1999; 99SE-00004660.
XX
PA (ASTR) ASTRAZENECA AB.
XX
PI Ahmad S, Lembo P, Walker P;
XX
DR WPI; 2001-398140/42.
DR N-PSDB; AAD08133.
XX
PT Determining modulator of binding of sphingosine-1-PO4 to RP-23 receptor,
PT involves incubating sphingosine-1-PO4 and RP-23 receptor with test
PT compound, determining the binding and comparing with a control.
XX
PS Disclosure; Fig 3; 25pp; English.
XX
CC The present sequence is mouse G-protein coupled receptor (GPCR) RP-23
CC protein. RP-23 is a ligand for sphingosine-1-phosphate (sphingosine-1-
CC PO4) which is formed by the breakdown of sphingolipids and is involved in
CC cell signalling. Sphingosine-1-PO4 causes an increase in receptor-
CC generated adenylyl cyclase activity and an increase in intracellular
CC calcium concentration. The present invention relates to methods for
CC determining whether a test compound modulates interactions between
CC sphingosine-1-PO4 and RP-23 a particular G-protein coupled receptor. The
CC method is useful for determining a modulator which binds sphingosine-1-
CC PO4 to an RP-23 receptor. The compounds identified are useful as
CC therapeutic agents for treating cardiovascular diseases, inflammatory
CC diseases and cancers
XX
SQ Sequence 423 AA;

Query Match 65.6%; Score 42; DB 4; Length 423;
Best Local Similarity 77.8%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LYFGFPWFA 9
||| | |||
Db 326 LYFAFHWFA 334

RESULT 49
AAE03739
ID AAE03739 standard; protein; 423 AA.
XX
AC AAE03739;
XX
DT 04-SEP-2001 (first entry)
XX
DE Human G-protein coupled receptor (GPCR) RP-23 protein.
XX
KW Human; G-protein coupled receptor; GPCR; RP-23; sphingosine-1-PO4;
KW sphingosine-1-phosphate; therapy; cardiovascular disease; cancer;
KW inflammatory disease; cell signalling.
XX
OS Homo sapiens.
XX
PN WO200144439-A2.
XX
PD 21-JUN-2001.
XX
PF 15-DEC-2000; 2000WO-SE002563.
XX
PR 17-DEC-1999; 99SE-00004660.
XX
PA (ASTR) ASTRAZENECA AB.
XX
PI Ahmad S, Lembo P, Walker P;
XX
DR WPI; 2001-398140/42.
DR N-PSDB; AAD08132.
XX
PT Determining modulator of binding of sphingosine-1-PO4 to RP-23 receptor,
PT involves incubating sphingosine-1-PO4 and RP-23 receptor with test
PT compound, determining the binding and comparing with a control.
XX
PS Claim 2; Fig 1; 25pp; English.
XX
CC The present sequence is human G-protein coupled receptor (GPCR) RP-23
CC protein. RP-23 is a ligand for sphingosine-1-phosphate (sphingosine-1-
CC PO4) which is formed by the breakdown of sphingolipids and is involved in
CC cell signalling. Sphingosine-1-PO4 causes an increase in receptor-
CC generated adenylyl cyclase activity and an increase in intracellular
CC calcium concentration. The present invention relates to methods for
CC determining whether a test compound modulates interactions between
CC sphingosine-1-PO4 and RP-23 a particular G-protein coupled receptor. The
CC method is useful for determining a modulator which binds sphingosine-1-
CC PO4 to an RP-23 receptor. The compounds identified are useful as
CC therapeutic agents for treating cardiovascular diseases, inflammatory
CC diseases and cancers
XX

```
SQ   Sequence 423 AA;

  Query Match            65.6%;  Score 42;  DB 4;  Length 423;
  Best Local Similarity   77.8%;  Pred. No. 2.3e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        326 LYFAFHWFA 334


RESULT 50
AAM51507
ID   AAM51507 standard; protein; 423 AA.
XX
AC   AAM51507;
XX
DT   02-JAN-2002  (first entry)
XX
DE   Mouse 5HT receptor.
XX
KW   Mouse; 5HT receptor; chimera; cDNA library preparation; serotonin;
KW   G protein-coupled receptor.
XX
OS   Mus musculus.
XX
PN   JP2001178476-A.
XX
PD   03-JUL-2001.
XX
PF   28-DEC-1999;   99JP-00373989.
XX
PR   28-DEC-1999;   99JP-00373989.
XX
PA   (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
PA   (KUBO/) KUBO Y.
PA   (KEIZ-) KEIZAI SANGYOSHO SANGYO GIJUTSU SOGO KEN.
XX
DR   WPI; 2001-599907/68.
DR   N-PSDB; AAI69851.
XX
PT   Preparing a chimera cDNA library comprises recombinantly expressing cDNA
PT   with a protein translation frame and a cDNA containing a carboxy terminal
PT   side from a stored region of a functional protein synthesized.
XX
PS   Example 7; Fig 6; 24pp; Japanese.
XX
CC   The present sequence is provided in a specification relating to the
CC   preparation of a chimera cDNA library containing a cDNA encoding a
CC   functional protein. The specification describes the preparation of a
CC   serotonin-related cDNA library, and the preparation of a G protein-
CC   coupled receptor chimera cDNA library from which an orphan G protein-
CC   coupled receptor cDNA was isolated
XX
SQ   Sequence 423 AA;

  Query Match            65.6%;  Score 42;  DB 4;  Length 423;
  Best Local Similarity   77.8%;  Pred. No. 2.3e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        326 LYFAFHWFA 334


Search completed: March 23, 2006, 01:53:50
Job time : 115.986 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:54:26 ; Search time 13.8356 Seconds
(without alignments)
69.543 Million cell updates/sec

Title: US-10-755-382-25
Perfect score: 64
Sequence: 1 LYFGFPWPAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	48	75.0	170	2	A35944	Ig gamma-2a chain
2	44	68.8	2210	1	RRXPLC	genome polyprotein
3	42	65.6	381	2	A40470	glucocorticoid-ind
4	42	65.6	423	2	B40470	glucocorticoid-ind
5	42	65.6	443	2	D40470	glucocorticoid-ind
6	42	65.6	453	2	D69829	Na+/H+-exchanging
7	42	65.6	491	2	C40470	glucocorticoid-ind
8	42	65.6	519	2	T24784	hypothetical prote
9	41.5	64.8	218	2	G81391	amino-acid ABC tra
10	41	64.1	222	2	H90730	hypothetical membr
11	41	64.1	247	2	D91066	hypothetical membr
12	41	64.1	252	2	D85910	unknown protein en
13	40	62.5	107	2	S14506	Ig heavy chain V r
14	40	62.5	286	2	H88175	protein T24H7.1 [i
15	40	62.5	442	2	H85096	hypothetical prote
16	40	62.5	442	2	F84618	probable flavonol
17	40	62.5	447	2	E96672	Similar to Flavono
18	40	62.5	452	2	F96672	Similar to Flavono
19	40	62.5	2167	2	S19444	hypothetical prote
20	39	60.9	129	2	F70676	hypothetical prote
21	39	60.9	187	2	C81803	CDPdiacylglycerol-
22	39	60.9	187	2	F81065	CDP-diacylglycerol
23	39	60.9	256	2	D90055	hypothetical prote
24	39	60.9	256	2	S42926	hypothetical membr
25	39	60.9	421	2	D82500	hypothetical prote
26	39	60.9	433	2	S77508	srrA protein - Syn
27	39	60.9	1075	2	S54067	probable membrane
28	38	59.4	107	2	S14492	Ig heavy chain V r
29	38	59.4	107	2	S14493	Ig heavy chain V r
30	38	59.4	107	2	S14491	Ig heavy chain V r
31	38	59.4	142	2	C34903	Ig heavy chain pre
32	38	59.4	226	2	C69760	amino acid ABC tra
33	38	59.4	275	2	A82578	glycerol uptake fa
34	38	59.4	292	2	H70677	hypothetical prote
35	38	59.4	318	2	B82447	conserved hypothet
36	38	59.4	345	2	T16869	hypothetical prote
37	38	59.4	424	2	JC5891	omega 6 desaturase
38	38	59.4	529	2	F90447	amino acid transpo
39	38	59.4	687	1	B32382	ubiquinol-cytochro
40	38	59.4	972	2	A87321	TonB-dependent rec
41	38	59.4	1091	2	S57112	JSN1 protein - yea
42	37.5	58.6	894	2	T27007	hypothetical prote
43	37	57.8	139	2	S64949	probable membrane
44	37	57.8	367	2	C44102	di-N-acetylchitobi
45	37	57.8	400	2	S32879	lipA protein - Nei
46	37	57.8	415	2	C83544	probable MFS trans
47	37	57.8	427	2	T02381	hypothetical prote
48	37	57.8	485	1	F71275	probable periplasm
49	37	57.8	515	2	AD2349	hypothetical prote
50	37	57.8	704	2	D81240	capsule polysaccha
51	37	57.8	704	2	H82012	capsule polysaccha
52	37	57.8	712	2	AD0274	probable toxin tra
53	37	57.8	733	2	T24977	hypothetical prote
54	37	57.8	764	2	T07608	chloride channel p
55	37	57.8	780	2	T02939	chloride channel p
56	37	57.8	804	2	H75549	glycogen debranchi
57	36.5	57.0	71	2	G72226	hypothetical prote
58	36	56.2	126	2	S74493	thioredoxin M-2 -
59	36	56.2	158	2	JC7522	nucleoside deoxyri
60	36	56.2	190	2	T39622	probable phosphate
61	36	56.2	214	2	C95195	hypothetical prote
62	36	56.2	242	2	H97768	hypothetical prote
63	36	56.2	274	2	T16977	pectinesterase (EC
64	36	56.2	282	2	H81358	probable signal pe
65	36	56.2	292	2	E96910	probable Co/Zn/Cd
66	36	56.2	295	2	JE0174	frizzled protein-2
67	36	56.2	298	2	S46996	B-cell receptor-as
68	36	56.2	309	2	T31123	hypothetical prote
69	36	56.2	312	2	AH2476	permease protein o
70	36	56.2	315	2	T16976	pectinesterase (EC
71	36	56.2	315	2	T16975	pectinesterase (EC
72	36	56.2	318	2	C70636	probable echA13 pr
73	36	56.2	350	2	D39364	GDF-1 embryonic gr
74	36	56.2	355	2	T13864	NADH2 dehydrogenas
75	36	56.2	355	2	T11597	NADH2 dehydrogenas
76	36	56.2	355	2	T11598	NADH2 dehydrogenas
77	36	56.2	355	2	T11599	NADH2 dehydrogenas
78	36	56.2	355	2	T11600	NADH2 dehydrogenas
79	36	56.2	355	2	T12100	NADH2 dehydrogenas
80	36	56.2	355	2	T13831	NADH2 dehydrogenas
81	36	56.2	355	2	T13830	NADH2 dehydrogenas
82	36	56.2	355	2	T14016	NADH2 dehydrogenas
83	36	56.2	355	2	T11734	NADH2 dehydrogenas
84	36	56.2	355	2	T14009	NADH2 dehydrogenas
85	36	56.2	355	2	T14012	NADH2 dehydrogenas
86	36	56.2	355	2	T14011	NADH2 dehydrogenas
87	36	56.2	355	2	T11737	NADH2 dehydrogenas
88	36	56.2	355	2	T13989	NADH2 dehydrogenas
89	36	56.2	355	2	T14010	NADH2 dehydrogenas
90	36	56.2	355	2	T11752	NADH2 dehydrogenas
91	36	56.2	355	2	T11760	NADH2 dehydrogenas
92	36	56.2	355	2	T14013	NADH2 dehydrogenas
93	36	56.2	355	2	T11733	NADH2 dehydrogenas
94	36	56.2	355	2	T11762	NADH2 dehydrogenas
95	36	56.2	355	2	T14014	NADH2 dehydrogenas
96	36	56.2	355	2	T11754	NADH2 dehydrogenas
97	36	56.2	355	2	T13988	NADH2 dehydrogenas
98	36	56.2	355	2	T14008	NADH2 dehydrogenas
99	36	56.2	355	2	T11739	NADH2 dehydrogenas
100	36	56.2	355	2	T14120	NADH2 dehydrogenas
101	36	56.2	355	2	T14098	NADH2 dehydrogenas
102	36	56.2	355	2	T13832	NADH2 dehydrogenas

103	36	56.2	355	2	T13904	NADH2 dehydrogenas
104	36	56.2	355	2	T13861	NADH2 dehydrogenas
105	36	56.2	355	2	T13862	NADH2 dehydrogenas
106	36	56.2	355	2	T13977	NADH2 dehydrogenas
107	36	56.2	355	2	T13894	NADH2 dehydrogenas
108	36	56.2	355	2	T13925	NADH2 dehydrogenas
109	36	56.2	355	2	T12118	NADH2 dehydrogenas
110	36	56.2	355	2	T14030	NADH2 dehydrogenas
111	36	56.2	355	2	T14028	NADH2 dehydrogenas
112	36	56.2	355	2	T14036	NADH2 dehydrogenas
113	36	56.2	355	2	T14044	NADH2 dehydrogenas
114	36	56.2	355	2	T14051	NADH2 dehydrogenas
115	36	56.2	355	2	T14048	NADH2 dehydrogenas
116	36	56.2	355	2	T14131	NADH2 dehydrogenas
117	36	56.2	355	2	T14134	NADH2 dehydrogenas
118	36	56.2	355	2	T14111	NADH2 dehydrogenas
119	36	56.2	355	2	T14107	NADH2 dehydrogenas
120	36	56.2	355	2	T14115	NADH2 dehydrogenas
121	36	56.2	355	2	T14121	NADH2 dehydrogenas
122	36	56.2	355	2	T14123	NADH2 dehydrogenas
123	36	56.2	355	2	T14060	NADH2 dehydrogenas
124	36	56.2	355	2	T14062	NADH2 dehydrogenas
125	36	56.2	355	2	T14089	NADH2 dehydrogenas
126	36	56.2	355	2	T14061	NADH2 dehydrogenas
127	36	56.2	355	2	T14090	NADH2 dehydrogenas
128	36	56.2	355	2	T13846	NADH2 dehydrogenas
129	36	56.2	355	2	T11602	NADH2 dehydrogenas
130	36	56.2	355	2	T11601	NADH2 dehydrogenas
131	36	56.2	355	2	T12029	NADH2 dehydrogenas
132	36	56.2	355	2	T12032	NADH2 dehydrogenas
133	36	56.2	355	2	T12031	NADH2 dehydrogenas
134	36	56.2	355	2	T12023	NADH2 dehydrogenas
135	36	56.2	355	2	T12028	NADH2 dehydrogenas
136	36	56.2	355	2	T12114	NADH2 dehydrogenas
137	36	56.2	355	2	T12111	NADH2 dehydrogenas
138	36	56.2	355	2	T12104	NADH2 dehydrogenas
139	36	56.2	355	2	T12033	NADH2 dehydrogenas
140	36	56.2	355	2	T12112	NADH2 dehydrogenas
141	36	56.2	355	2	T12025	NADH2 dehydrogenas
142	36	56.2	355	2	T12154	NADH2 dehydrogenas
143	36	56.2	355	2	T12027	NADH2 dehydrogenas
144	36	56.2	355	2	T12026	NADH2 dehydrogenas
145	36	56.2	355	2	T12109	NADH2 dehydrogenas
146	36	56.2	355	2	T12030	NADH2 dehydrogenas
147	36	56.2	355	2	T12107	NADH2 dehydrogenas
148	36	56.2	355	2	T13842	NADH2 dehydrogenas
149	36	56.2	355	2	T13844	NADH2 dehydrogenas
150	36	56.2	355	2	T14099	NADH2 dehydrogenas
151	36	56.2	355	2	T13843	NADH2 dehydrogenas
152	36	56.2	355	2	T13841	NADH2 dehydrogenas
153	36	56.2	355	2	T13865	NADH2 dehydrogenas
154	36	56.2	355	2	T13875	NADH2 dehydrogenas
155	36	56.2	355	2	T14093	NADH2 dehydrogenas
156	36	56.2	355	2	T14092	NADH2 dehydrogenas
157	36	56.2	355	2	T13873	NADH2 dehydrogenas
158	36	56.2	355	2	T13871	NADH2 dehydrogenas
159	36	56.2	355	2	T13872	NADH2 dehydrogenas
160	36	56.2	355	2	T13876	NADH2 dehydrogenas
161	36	56.2	355	2	T13870	NADH2 dehydrogenas
162	36	56.2	355	2	T13869	NADH2 dehydrogenas
163	36	56.2	355	2	T13868	NADH2 dehydrogenas
164	36	56.2	355	2	T14091	NADH2 dehydrogenas
165	36	56.2	355	2	T13874	NADH2 dehydrogenas
166	36	56.2	355	2	T14097	NADH2 dehydrogenas
167	36	56.2	355	2	T13866	NADH2 dehydrogenas
168	36	56.2	355	2	T14095	NADH2 dehydrogenas
169	36	56.2	355	2	T14094	NADH2 dehydrogenas
170	36	56.2	355	2	T13867	NADH2 dehydrogenas
171	36	56.2	355	2	T13901	NADH2 dehydrogenas
172	36	56.2	355	2	T13902	NADH2 dehydrogenas
173	36	56.2	355	2	T13896	NADH2 dehydrogenas
174	36	56.2	355	2	T13895	NADH2 dehydrogenas
175	36	56.2	355	2	T14109	NADH2 dehydrogenas
176	36	56.2	355	2	T13903	NADH2 dehydrogenas
177	36	56.2	355	2	T13897	NADH2 dehydrogenas
178	36	56.2	355	2	T13898	NADH2 dehydrogenas
179	36	56.2	355	2	T13899	NADH2 dehydrogenas
180	36	56.2	355	2	T13911	NADH2 dehydrogenas
181	36	56.2	355	2	T13906	NADH2 dehydrogenas
182	36	56.2	355	2	T13914	NADH2 dehydrogenas
183	36	56.2	355	2	T13910	NADH2 dehydrogenas
184	36	56.2	355	2	T14113	NADH2 dehydrogenas
185	36	56.2	355	2	T14112	NADH2 dehydrogenas
186	36	56.2	355	2	T13913	NADH2 dehydrogenas
187	36	56.2	355	2	T13909	NADH2 dehydrogenas
188	36	56.2	355	2	T13912	NADH2 dehydrogenas
189	36	56.2	355	2	T13907	NADH2 dehydrogenas
190	36	56.2	355	2	T13908	NADH2 dehydrogenas
191	36	56.2	355	2	T13915	NADH2 dehydrogenas
192	36	56.2	355	2	T14116	NADH2 dehydrogenas
193	36	56.2	355	2	T13918	NADH2 dehydrogenas
194	36	56.2	355	2	T13919	NADH2 dehydrogenas
195	36	56.2	355	2	T14117	NADH2 dehydrogenas
196	36	56.2	355	2	T13972	NADH2 dehydrogenas
197	36	56.2	355	2	T13971	NADH2 dehydrogenas
198	36	56.2	355	2	T37191	NADH2 dehydrogenas
199	36	56.2	355	2	T13986	NADH2 dehydrogenas
200	36	56.2	355	2	T13983	NADH2 dehydrogenas
201	36	56.2	355	2	T13981	NADH2 dehydrogenas
202	36	56.2	355	2	T14126	NADH2 dehydrogenas
203	36	56.2	355	2	T13987	NADH2 dehydrogenas
204	36	56.2	355	2	T14125	NADH2 dehydrogenas
205	36	56.2	355	2	T13982	NADH2 dehydrogenas
206	36	56.2	355	2	T14127	NADH2 dehydrogenas
207	36	56.2	355	2	T13985	NADH2 dehydrogenas
208	36	56.2	355	2	T13984	NADH2 dehydrogenas
209	36	56.2	355	2	T13833	NADH2 dehydrogenas
210	36	56.2	355	2	T12119	NADH2 dehydrogenas
211	36	56.2	385	2	A44102	di-N-acetylchitobi
212	36	56.2	408	2	T47585	hypothetical prote
213	36	56.2	424	2	A55089	vasopressin V3 rec
214	36	56.2	435	2	D71857	hypothetical prote
215	36	56.2	435	2	B64658	hypothetical prote
216	36	56.2	468	2	T21535	hypothetical prote
217	36	56.2	475	2	B64120	killing factor kic
218	36	56.2	477	2	F86670	lysine specific pe
219	36	56.2	482	2	S15748	nitrogenase (EC 1.
220	36	56.2	530	2	C38497	G1 protein - vacci
221	36	56.2	550	2	JC4112	P-methyltransferas
222	36	56.2	558	2	T47851	hypothetical prote
223	36	56.2	591	2	F42511	G1L protein - vacc
224	36	56.2	591	2	T37346	probable 68K prote
225	36	56.2	591	2	S33078	G1L protein - vari
226	36	56.2	591	2	T28501	hypothetical prote
227	36	56.2	591	2	E72158	I1L protein - vari
228	36	56.2	594	2	T12995	pectinesterase hom
229	36	56.2	646	2	B70396	histidine kinase s
230	36	56.2	718	2	A99195	hypothetical prote
231	36	56.2	734	2	D95856	conserved hypothet
232	36	56.2	777	2	AE0462	probable exported
233	36	56.2	878	2	I51940	gene VAV2 protein
234	35.5	55.5	248	2	JQ1338	TraX protein - Esc
235	35.5	55.5	538	2	E72561	probable thermosta
236	35	54.7	54	2	T07541	hypothetical prote
237	35	54.7	101	2	H37262	Ig heavy chain V r
238	35	54.7	104	2	S56386	hypothetical 12.6K
239	35	54.7	111	2	PH0994	Ig heavy chain V r
240	35	54.7	123	2	A69884	cell wall protein
241	35	54.7	167	2	T32353	hypothetical prote
242	35	54.7	179	2	C82240	hypothetical prote
243	35	54.7	246	2	C97177	C-terminal domain
244	35	54.7	259	2	G84685	probable DOF zinc
245	35	54.7	271	2	AE3150	dehydrogenase Atu4
246	35	54.7	271	2	D98137	2,5-dichloro-2,5-c
247	35	54.7	281	2	B81894	hypothetical prote
248	35	54.7	281	2	G81126	conserved hypothet

249	35	54.7	281	2	C71698	hypothetical prote
250	35	54.7	281	2	S55646	hypothetical prote
251	35	54.7	290	2	D71921	signal peptidase I
252	35	54.7	290	2	H64591	signal peptidase I
253	35	54.7	306	2	D83992	proline oxidase (p
254	35	54.7	322	2	G95244	hypothetical prote
255	35	54.7	328	2	C89769	hypothetical prote
256	35	54.7	331	2	G75035	iron (iii) abc tra
257	35	54.7	331	2	A71128	probable iron (III
258	35	54.7	341	2	H48563	G1 protein - fowlp
259	35	54.7	344	2	T33264	hypothetical prote
260	35	54.7	418	2	JC7872	stearoyl-CoA 9-des
261	35	54.7	424	2	AC2975	oxidoreductase ord
262	35	54.7	424	2	H98307	probable oxidoredu
263	35	54.7	425	2	B95389	probable oxidoredu
264	35	54.7	465	1	XYECMB	5-methylcytosine-s
265	35	54.7	469	2	T41465	hypothetical prote
266	35	54.7	473	2	S58537	photosystem II chl
267	35	54.7	473	2	H69761	conserved hypothet
268	35	54.7	475	2	AE0855	conserved hypothet
269	35	54.7	475	2	H91077	probable 4-hydroxy
270	35	54.7	475	2	T44997	probable 4-hydroxy
271	35	54.7	475	2	A85923	probable 4-hydroxy
272	35	54.7	522	2	H64060	apolipoprotein N-a
273	35	54.7	526	2	AH0601	probable membrane
274	35	54.7	527	2	E90740	probable enzyme [i
275	35	54.7	527	2	G85590	probable enzyme yb
276	35	54.7	527	2	G64818	probable membrane
277	35	54.7	548	2	B90446	ABC transporter, p
278	35	54.7	583	2	T20291	hypothetical prote
279	35	54.7	585	1	F64159	hypothetical prote
280	35	54.7	591	2	F69837	asparagine synthas
281	35	54.7	593	2	T30658	hypothetical prote
282	35	54.7	615	2	D83838	asparagine synthet
283	35	54.7	717	2	E86812	sugar hydrolase [i
284	35	54.7	731	2	A95307	probable amino aci
285	35	54.7	944	2	T03826	cytochrome b245 be
286	35	54.7	977	2	D96665	protein F22C12.18
287	34.5	53.9	124	2	PH1404	Ig heavy chain V r
288	34.5	53.9	124	2	AG2789	hypothetical prote
289	34.5	53.9	177	2	AH2393	hypothetical prote
290	34.5	53.9	308	2	B84133	hypothetical prote
291	34	53.1	9	2	I46023	growth hormone rec
292	34	53.1	64	2	C69939	hypothetical prote
293	34	53.1	80	2	G96841	hypothetical prote
294	34	53.1	83	2	H81188	hypothetical prote
295	34	53.1	88	2	AF3586	hypothetical prote
296	34	53.1	98	2	AC2369	hypothetical prote
297	34	53.1	123	2	AF3251	quorum sensing Tra
298	34	53.1	134	2	AC0665	probable cytochrom
299	34	53.1	152	2	H83813	hypothetical prote
300	34	53.1	188	2	B85737	cytochrome b(561)
301	34	53.1	188	2	G90881	cytochrome b(561)
302	34	53.1	188	2	E64893	cytochrome b561 -
303	34	53.1	216	2	G75128	hypothetical prote
304	34	53.1	216	2	F71002	hypothetical prote
305	34	53.1	239	2	T31881	hypothetical prote
306	34	53.1	245	2	H70438	aminodeoxychorisma
307	34	53.1	245	2	JC7893	prostate-specific
308	34	53.1	246	1	C86566	probable phosphoes
309	34	53.1	246	1	H72057	probable phosphoes
310	34	53.1	251	1	QQECF	Replication initia
311	34	53.1	251	1	QQECR7	gene E protein - E
312	34	53.1	259	2	F83825	hypothetical prote
313	34	53.1	269	2	AF3097	hypothetical prote
314	34	53.1	269	2	C98189	ABC transporter, p
315	34	53.1	282	2	AB1929	hypothetical prote
316	34	53.1	285	2	T39644	conserved hypothet
317	34	53.1	287	2	C90290	hypothetical prote
318	34	53.1	302	2	T50737	bacteriochlorophyl
319	34	53.1	302	2	C64311	Na+/Ca2+-exchangin
320	34	53.1	334	2	B83785	ferrichrome ABC tr
321	34	53.1	337	2	AH2719	delta-aminolevulin
322	34	53.1	337	2	T25153	hypothetical prote
323	34	53.1	356	2	C83041	hypothetical prote
324	34	53.1	360	2	D97501	porphobilinogen sy
325	34	53.1	364	2	G69377	bacteriochlorophyl
326	34	53.1	379	2	H81741	cell shape-determi
327	34	53.1	387	2	JU0461	sarcosine oxidase
328	34	53.1	389	2	T44248	sarcosine oxidase
329	34	53.1	389	2	A83229	hypothetical prote
330	34	53.1	390	2	I39975	sarcosine oxidase
331	34	53.1	393	2	C89961	hypothetical prote
332	34	53.1	400	2	C70837	hypothetical prote
333	34	53.1	419	2	G02232	G protein-coupled
334	34	53.1	419	2	S48077	K(ATP) channel - r
335	34	53.1	420	2	G95215	xanthine permease
336	34	53.1	420	2	E98079	nucleobase,cation
337	34	53.1	430	2	B70813	hypothetical prote
338	34	53.1	433	2	T28805	hypothetical prote
339	34	53.1	439	2	E70371	apolipoprotein N-a
340	34	53.1	457	2	G72053	translocase - Chla
341	34	53.1	457	2	B86569	translocase [impor
342	34	53.1	462	2	B81613	preprotein translo
343	34	53.1	475	2	E83450	cytochrome-c oxida
344	34	53.1	477	2	H91123	probable oxidoredu
345	34	53.1	477	2	G85968	probable oxidoredu
346	34	53.1	477	2	C65096	hypothetical 52.1
347	34	53.1	482	2	A32422	dihydrolipoamide S
348	34	53.1	488	2	A41961	chitinase (EC 3.2.
349	34	53.1	500	1	A23874	nitrogenase (EC 1.
350	34	53.1	515	1	NIZJAM	nitrogenase (EC 1.
351	34	53.1	517	2	G83521	probable coenzyme
352	34	53.1	532	2	T30764	hypothetical prote
353	34	53.1	561	2	JE0158	dwarf protein, OSD
354	34	53.1	564	2	A48141	ferric reductase (
355	34	53.1	598	2	S75728	hypothetical prote
356	34	53.1	602	2	G97784	hypothetical prote
357	34	53.1	610	2	F83384	probable asparagin
358	34	53.1	634	2	S33339	somatotropin recep
359	34	53.1	638	2	S12136	somatotropin recep
360	34	53.1	638	2	B28176	somatotropin recep
361	34	53.1	638	2	A33505	somatotropin recep
362	34	53.1	638	2	S54418	fibronectin-bindin
363	34	53.1	655	2	T16538	hypothetical prote
364	34	53.1	659	2	S40043	adhesin - Streptoc
365	34	53.1	675	2	D48492	kpsC protein - Esc
366	34	53.1	702	2	C84111	hypothetical prote
367	34	53.1	706	2	T20052	hypothetical prote
368	34	53.1	712	2	AG0175	probable membrane
369	34	53.1	849	2	D88368	protein F19H8.4 [i
370	34	53.1	865	2	A25104	band 3 protein, no
371	34	53.1	868	2	E89897	conserved hypothet
372	34	53.1	934	2	C81298	probable formate d
373	34	53.1	939	2	S18213	formate dehydrogen
374	34	53.1	1111	2	T05646	hypothetical prote
375	34	53.1	1185	2	T19212	hypothetical prote
376	34	53.1	1234	2	A34911	band 3-related pro
377	34	53.1	1237	2	A56764	band 3-related pro
378	34	53.1	1237	2	A31789	band 3-related pro
379	34	53.1	1240	2	S21086	anion exchange pro
380	34	53.1	1559	2	T30535	calcium channel al
381	34	53.1	1852	2	A37860	calcium channel pr
382	34	53.1	1873	2	A55645	calcium channel, v
383	34	53.1	1873	2	A30063	dihydropyridine re
384	34	53.1	3106	1	S53868	laminin alpha-2 ch
385	33.5	52.3	289	1	MFIHPC	E1 membrane glycop
386	33.5	52.3	387	2	B55164	scn1 protein - fis
387	33.5	52.3	465	2	JC5184	glutamate synthase
388	33.5	52.3	1707	2	S01865	genome polyprotein
389	33	51.6	86	2	F86294	hypothetical prote
390	33	51.6	114	2	A72607	hypothetical prote
391	33	51.6	121	2	S76514	hypothetical prote
392	33	51.6	157	2	B69221	conserved hypothet
393	33	51.6	161	2	T16344	hypothetical prote
394	33	51.6	186	1	D69206	conserved hypothet

395	33	51.6	188	2	T33623	hypothetical prote
396	33	51.6	209	2	H70189	probable CDPdiacyl
397	33	51.6	211	2	PS0045	nitrogenase (EC 1.
398	33	51.6	242	2	F84788	hypothetical prote
399	33	51.6	244	1	F71508	probable phosphoes
400	33	51.6	245	2	AD3104	conserved hypothet
401	33	51.6	245	2	G98182	hypothetical prote
402	33	51.6	248	2	T00300	traX protein - Esc
403	33	51.6	248	2	JQ1340	traX protein - Esc
404	33	51.6	265	2	JH0430	transformation com
405	33	51.6	269	2	S74024	hypothetical prote
406	33	51.6	270	2	T48780	hypothetical prote
407	33	51.6	271	2	F71490	hypothetical prote
408	33	51.6	276	2	AF1960	hypothetical prote
409	33	51.6	280	2	G72428	oligopeptide ABC t
410	33	51.6	292	2	E90180	conserved hypothet
411	33	51.6	294	2	S75135	hypothetical prote
412	33	51.6	307	2	G97575	probable permease
413	33	51.6	307	2	AG2796	hypothetical prote
414	33	51.6	307	2	D70651	hypothetical prote
415	33	51.6	308	2	H70767	hypothetical prote
416	33	51.6	311	2	H75411	conserved hypothet
417	33	51.6	316	2	E70538	probable ephC prot
418	33	51.6	317	2	JE0175	frezzled protein-1
419	33	51.6	321	2	F86571	methionyl tRNA for
420	33	51.6	321	2	B72051	methionyl tRNA for
421	33	51.6	321	2	F81615	methionyl-tRNA for
422	33	51.6	322	2	T50494	hypothetical prote
423	33	51.6	329	2	AG3190	conserved hypothet
424	33	51.6	333	2	H89961	hypothetical prote
425	33	51.6	337	2	T16323	hypothetical prote
426	33	51.6	338	2	T23260	hypothetical prote
427	33	51.6	340	2	AC0459	porphobilinogen sy
428	33	51.6	341	2	S40612	myosin-related pro
429	33	51.6	343	2	A35639	G protein-coupled
430	33	51.6	346	2	A70144	hypothetical prote
431	33	51.6	355	2	T12034	NADH2 dehydrogenas
432	33	51.6	358	2	G90456	conserved hypothet
433	33	51.6	359	2	H70876	hypothetical prote
434	33	51.6	359	2	A95277	hypothetical prote
435	33	51.6	371	2	AI0298	probable sarcosine
436	33	51.6	372	2	A31564	casein kinase II (
437	33	51.6	391	2	C96031	probable ureashort
438	33	51.6	392	2	AB2873	hypothetical prote
439	33	51.6	392	2	D97649	probable permease
440	33	51.6	404	2	S27339	F-antigen - Tetrah
441	33	51.6	410	2	F88978	protein F37B4.4 [i
442	33	51.6	413	2	AH2933	N-carbamoyl-beta-a
443	33	51.6	414	2	AB1291	sugar ABC transpor
444	33	51.6	414	2	AH1662	sugar ABC transpor
445	33	51.6	415	2	T39080	hypothetical prote
446	33	51.6	429	2	B83826	hypothetical prote
447	33	51.6	432	2	C97258	sugar-binding peri
448	33	51.6	441	2	G98348	n-carbamoyl-beta-a
449	33	51.6	447	2	T05070	hypothetical prote
450	33	51.6	448	2	C96542	hypothetical prote
451	33	51.6	457	2	S44484	secY protein - Chl
452	33	51.6	457	2	D71505	probable transloca
453	33	51.6	463	2	S36565	L2 protein - human
454	33	51.6	467	2	H82711	cardiolipin syntha
455	33	51.6	469	2	D81017	chloride channel p
456	33	51.6	474	2	T01347	pectinesterase hom
457	33	51.6	474	2	AB2161	hypothetical prote
458	33	51.6	482	1	XUBOLA	dihydrolipoamide S
459	33	51.6	489	2	T11622	extensin class 1 p
460	33	51.6	492	1	NIAVMA	nitrogenase (EC 1.
461	33	51.6	494	1	JQ2156	nitrogenase (EC 1.
462	33	51.6	499	2	S41599	cytochrome P450 77
463	33	51.6	504	2	A41783	tachykinin recepto
464	33	51.6	514	2	G97118	levanase [imported
465	33	51.6	514	2	B84290	hypothetical prote
466	33	51.6	525	2	AF3274	hypothetical prote
467	33	51.6	530	2	S74038	probable L-lactate
468	33	51.6	532	2	AF3498	apolipoprotein N-a
469	33	51.6	538	2	AG2902	conserved hypothet
470	33	51.6	540	2	T08662	probable signaling
471	33	51.6	550	2	H97677	hypothetical prote
472	33	51.6	554	2	T43466	hypothetical prote
473	33	51.6	555	2	T31158	hypothetical prote
474	33	51.6	559	2	G86238	protein T10O24.13
475	33	51.6	566	2	T03855	hypothetical prote
476	33	51.6	574	2	B86005	probable transport
477	33	51.6	574	2	D91159	probable transport
478	33	51.6	574	2	E65135	hypothetical 64.6K
479	33	51.6	589	2	H64829	ycaO protein - Esc
480	33	51.6	589	2	AE0613	conserved hypothet
481	33	51.6	589	2	B85616	hypothetical prote
482	33	51.6	589	2	D90752	hypothetical prote
483	33	51.6	605	2	S46833	hypothetical prote
484	33	51.6	646	2	I38049	cell surface glyco
485	33	51.6	650	2	JC7093	Fas associated fac
486	33	51.6	670	2	JC5887	signaling mediator
487	33	51.6	682	2	G84639	hypothetical prote
488	33	51.6	698	2	AG2219	hypothetical prote
489	33	51.6	756	2	JC5886	signaling mediator
490	33	51.6	836	2	T18460	hypothetical prote
491	33	51.6	844	2	T05227	hypothetical prote
492	33	51.6	877	2	T01271	serine/threonine-s
493	33	51.6	1050	2	T39780	probable membrane
494	33	51.6	1072	2	A38457	integrin alpha-6 c
495	33	51.6	1155	2	T39040	hypothetical prote
496	33	51.6	1462	2	T50338	probable guanine-n
497	33	51.6	2291	2	S11238	polymerase - Berne
498	32.5	50.8	178	2	JC2022	enhancer factor I
499	32.5	50.8	290	2	H97791	hypothetical prote
500	32.5	50.8	299	2	S56749	junctional adhesio
501	32.5	50.8	351	2	G70137	phospho-N-acetylmu
502	32.5	50.8	459	2	C85017	probable CAAX pren
503	32.5	50.8	1356	2	T09107	DNA (cytosine-5-)-
504	32	50.0	47	2	E72258	hypothetical prote
505	32	50.0	61	2	E84772	hypothetical prote
506	32	50.0	70	2	F69818	hypothetical prote
507	32	50.0	75	2	PQ0805	core protein - hep
508	32	50.0	91	2	H86701	hypothetical prote
509	32	50.0	100	2	S61013	probable membrane
510	32	50.0	108	2	S41348	genome polyprotein
511	32	50.0	109	2	PL0233	Ig heavy chain V r
512	32	50.0	112	2	PL0232	Ig heavy chain V r
513	32	50.0	131	2	A27472	Ig heavy chain pre
514	32	50.0	132	2	S67165	probable membrane
515	32	50.0	133	2	G45893	T-cell receptor al
516	32	50.0	137	2	G72666	hypothetical prote
517	32	50.0	143	2	H90037	hypothetical prote
518	32	50.0	147	2	C95274	hypothetical prote
519	32	50.0	151	2	AF0014	conserved hypothet
520	32	50.0	156	2	T49529	hypothetical prote
521	32	50.0	157	2	E83761	hypothetical prote
522	32	50.0	162	2	AG3586	hypothetical membr
523	32	50.0	163	2	F81339	probable membrane
524	32	50.0	167	1	WMVZF2	hepatic lectin hom
525	32	50.0	168	2	B72635	hypothetical prote
526	32	50.0	179	2	T51570	hypothetical prote
527	32	50.0	192	1	IVRTA1	interferon alpha-I
528	32	50.0	206	2	AH0466	threonine efflux p
529	32	50.0	268	2	AI3189	hypothetical prote
530	32	50.0	271	2	C69407	phosphoribosylform
531	32	50.0	276	2	A49853	ammonia monooxygen
532	32	50.0	279	2	T14332	homeotic protein -
533	32	50.0	286	2	F87075	membrane transport
534	32	50.0	288	2	A05235	hypothetical prote
535	32	50.0	290	2	AD2870	ABC transporter, m
536	32	50.0	290	2	F97646	probable aliphatic
537	32	50.0	295	2	S46413	hypothetical prote
538	32	50.0	295	2	A99489	arabinose ABC tran
539	32	50.0	297	2	T30613	hypothetical prote
540	32	50.0	299	2	S66007	yyaK protein - Bac

541	32	50.0	304	2	E69323	ribose-phosphate p
542	32	50.0	308	1	A34082	branched-chain-ami
543	32	50.0	308	2	AI0474	branched-chain-ami
544	32	50.0	308	2	AF1990	hypothetical prote
545	32	50.0	309	1	XNECV	branched-chain-ami
546	32	50.0	309	2	AD0924	branched-chain ami
547	32	50.0	309	2	A86063	branched-chain ami
548	32	50.0	309	2	H91216	branched-chain ami
549	32	50.0	310	1	KIBETH	thymidine kinase (
550	32	50.0	317	2	S72851	hypothetical prote
551	32	50.0	319	2	C83892	proline dehydrogen
552	32	50.0	319	2	G82374	branched-chain ami
553	32	50.0	320	2	B99254	formate hydrogenly
554	32	50.0	323	2	T07734	homeotic protein V
555	32	50.0	331	2	JT0589	pectinesterase (EC
556	32	50.0	332	2	A85062	probable fatty aci
557	32	50.0	343	2	T29547	hypothetical prote
558	32	50.0	345	2	S36959	dopamine receptor
559	32	50.0	347	2	T20472	hypothetical prote
560	32	50.0	347	2	F22845	hypothetical prote
561	32	50.0	350	1	KIBEFC	thymidine kinase (
562	32	50.0	351	2	T18066	hypothetical prote
563	32	50.0	352	2	C84603	probable pectinest
564	32	50.0	353	2	T34059	hypothetical prote
565	32	50.0	355	2	C90144	terminal oxidase,
566	32	50.0	361	2	S59814	UFD1 protein - yea
567	32	50.0	363	2	AI0184	probable sugar ABC
568	32	50.0	365	2	AE2782	transcription regu
569	32	50.0	365	2	F97561	hypothetical prote
570	32	50.0	379	2	S27502	hypothetical prote
571	32	50.0	388	2	G75375	hypothetical prote
572	32	50.0	398	2	C81729	Mtr/TnaB/TyrO perm
573	32	50.0	407	2	D90705	probable resistanc
574	32	50.0	407	2	G85555	probable resistanc
575	32	50.0	412	2	D95941	conserved hypothet
576	32	50.0	414	2	D69895	conserved hypothet
577	32	50.0	415	2	C71467	probable tyrosine
578	32	50.0	423	2	AE1138	PTS system, Galact
579	32	50.0	423	2	AD1496	PTS system, Galact
580	32	50.0	425	2	AC2909	MFS permease [impo
581	32	50.0	430	2	T41958	hypothetical prote
582	32	50.0	432	2	AH1934	periplasmic sugar-
583	32	50.0	435	2	T33206	hypothetical prote
584	32	50.0	440	1	OXRTGU	L-gulonolactone ox
585	32	50.0	442	1	DYXLD2	dopamine receptor
586	32	50.0	443	1	DYHUD2	dopamine receptor
587	32	50.0	444	1	DYBOD2	dopamine receptor
588	32	50.0	444	1	DYMSD2	dopamine receptor
589	32	50.0	444	1	S08146	dopamine receptor
590	32	50.0	452	2	A83734	PTS system, n-acet
591	32	50.0	454	2	AH0469	probable 4-alpha-L
592	32	50.0	455	2	T34155	hypothetical prote
593	32	50.0	456	2	AH0551	proline-specific p
594	32	50.0	457	2	B64769	proline transport
595	32	50.0	457	2	D90685	proline permease t
596	32	50.0	457	2	H85535	proline permease t
597	32	50.0	474	1	G2MS11	Ig gamma-2b chain
598	32	50.0	475	2	C72538	probable cysteinyl
599	32	50.0	476	2	A83387	probable transport
600	32	50.0	487	2	B97684	probable tartrate
601	32	50.0	500	2	B95318	nitrogenase (EC 1.
602	32	50.0	512	2	AG0583	apolipoprotein N-a
603	32	50.0	512	2	S18194	apolipoprotein N-a
604	32	50.0	512	2	G90715	apolipoprotein N-a
605	32	50.0	512	2	B85566	apolipoprotein N-a
606	32	50.0	514	2	D56849	dopamine receptor-
607	32	50.0	515	2	AD0319	probable apolipopr
608	32	50.0	532	1	RRBPBG	RNA-directed RNA p
609	32	50.0	546	2	F84900	hypothetical prote
610	32	50.0	561	2	S71189	Dwarf1 protein - A
611	32	50.0	572	2	F96755	hypothetical prote
612	32	50.0	578	2	T35537	cytochrome-c oxida
613	32	50.0	580	2	JC7502	choline transporte
614	32	50.0	588	2	B65168	probable adenine d
615	32	50.0	588	2	B91204	probable adenine d
616	32	50.0	588	2	D86050	probable adenine d
617	32	50.0	593	2	A70887	probable acyl Co-A
618	32	50.0	598	2	AC0154	probable membrane
619	32	50.0	598	2	D84242	hypothetical prote
620	32	50.0	600	2	C82126	conserved hypothet
621	32	50.0	622	2	A32499	apical membrane an
622	32	50.0	622	2	B44986	apical membrane an
623	32	50.0	622	2	A44986	apical membrane an
624	32	50.0	622	2	D44986	apical membrane an
625	32	50.0	622	2	C44986	apical membrane an
626	32	50.0	638	2	JC2139	phenylethylamine o
627	32	50.0	665	1	VCMVKA	env polyprotein pr
628	32	50.0	665	1	VCMVVR	env polyprotein pr
629	32	50.0	681	2	T16353	hypothetical prote
630	32	50.0	684	2	A56102	amine oxidase (cop
631	32	50.0	709	2	T00096	DNA replication-re
632	32	50.0	711	2	S67293	probable membrane
633	32	50.0	711	2	S38063	ferric reductase (
634	32	50.0	721	2	F82198	probable toxin sec
635	32	50.0	731	2	T17002	probable beta-gala
636	32	50.0	751	2	D83418	probable Orn/Arg/L
637	32	50.0	763	2	A47563	glucose-6-phosphat
638	32	50.0	783	2	T00354	hypothetical prote
639	32	50.0	787	2	B70643	probable sulfatase
640	32	50.0	789	2	T29461	hypothetical prote
641	32	50.0	800	2	E97935	phenylalanine-tRNA
642	32	50.0	801	2	F95067	phenylalanyl-tRNA
643	32	50.0	809	2	AE0374	probable permease
644	32	50.0	844	2	S61112	regulatory protein
645	32	50.0	922	2	T03854	hypothetical prote
646	32	50.0	932	2	S09151	suvar(3)7 protein
647	32	50.0	934	2	G86548	polymorphic outer
648	32	50.0	934	2	A72075	polymorphic outer
649	32	50.0	952	2	D81593	polymorphic membra
650	32	50.0	956	2	A89153	protein C24B5.3 [i
651	32	50.0	1013	2	S65195	probable membrane
652	32	50.0	1092	2	T45095	probable arabinosy
653	32	50.0	1111	2	A86922	probable arabinosy
654	32	50.0	1114	2	T30819	RNA-directed RNA p
655	32	50.0	1116	2	T30828	RNA-directed RNA p
656	32	50.0	1141	2	T24176	hypothetical prote
657	32	50.0	1143	2	T22952	hypothetical prote
658	32	50.0	1584	1	JN0114	kinesin-related pr
659	32	50.0	1584	2	T15822	kinesin-like prote
660	32	50.0	1695	2	A56921	kinesin family pro
661	32	50.0	1876	2	E97944	zinc metalloprotei
662	31.5	49.2	137	2	F29380	Ig heavy chain pre
663	31.5	49.2	157	2	D75058	hypothetical prote
664	31.5	49.2	243	2	D75092	hypothetical prote
665	31.5	49.2	406	2	AH3485	argininosuccinate
666	31.5	49.2	407	2	AB2904	argininosuccinate
667	31.5	49.2	431	1	RGECFR	sensor kinase (EC
668	31.5	49.2	431	2	AE0551	phosphate regulon
669	31.5	49.2	431	2	F85535	hypothetical prote
670	31.5	49.2	431	2	B90685	hypothetical prote
671	31.5	49.2	431	2	B44753	sensor kinase (EC
672	31.5	49.2	458	2	G69123	conserved hypothet
673	31.5	49.2	460	2	D97679	argininosuccinate
674	31.5	49.2	469	2	B75039	hypothetical prote
675	31.5	49.2	469	2	S73404	MG061 homolog R02_
676	31.5	49.2	488	2	G69727	biosynthesis of te
677	31.5	49.2	489	1	C64984	lysine-specific pe
678	31.5	49.2	489	2	AH0782	lysine-specific pe
679	31.5	49.2	489	2	H91009	lysine-specific pe
680	31.5	49.2	489	2	B85854	lysine-specific pe
681	31.5	49.2	496	2	D71089	hypothetical prote
682	31.5	49.2	503	2	AH0159	probable lysine-sp
683	31.5	49.2	545	2	T39499	conserved hypothet
684	31.5	49.2	564	2	F85813	hypothetical prote
685	31.5	49.2	564	2	F90965	hypothetical prote
686	31.5	49.2	569	2	H64959	probable membrane

687	31.5	49.2	680	2	T35404	probable squalene-
688	31.5	49.2	731	2	JC7919	1,4-alpha-glucan b
689	31	48.4	16	2	T44936	calmodulin kinase
690	31	48.4	17	2	I53392	CD33 antigen homol
691	31	48.4	50	2	H82423	hypothetical prote
692	31	48.4	67	2	D84870	hypothetical prote
693	31	48.4	71	2	A24303	Na+/K+-exchanging
694	31	48.4	82	2	A41051	spore coat protein
695	31	48.4	98	2	S19974	Ig kappa chain V r
696	31	48.4	100	2	C72667	hypothetical prote
697	31	48.4	101	2	F82421	conserved hypothet
698	31	48.4	103	2	E70638	hypothetical prote
699	31	48.4	111	2	S40090	Ig heavy chain - m
700	31	48.4	117	2	C72511	hypothetical prote
701	31	48.4	118	1	G1YC	gene 1 protein - S
702	31	48.4	118	2	S49241	hypothetical prote
703	31	48.4	121	2	A41940	Ig heavy chain V r
704	31	48.4	121	2	G72768	hypothetical prote
705	31	48.4	123	2	A30540	Ig heavy chain V r
706	31	48.4	123	2	AC2234	hypothetical prote
707	31	48.4	124	2	B55257	Ig gamma heavy cha
708	31	48.4	127	2	S24366	probable Na+-trans
709	31	48.4	137	2	E29380	Ig heavy chain pre
710	31	48.4	146	2	T26379	hypothetical prote
711	31	48.4	153	2	AF2344	hypothetical prote
712	31	48.4	156	2	C81025	H+-transporting tw
713	31	48.4	167	2	G96684	hypothetical prote
714	31	48.4	169	2	G84112	hypothetical prote
715	31	48.4	187	2	AE3409	hypothetical membr
716	31	48.4	206	2	E71308	conserved hypothet
717	31	48.4	210	2	G72507	hypothetical prote
718	31	48.4	220	2	C75332	hypothetical prote
719	31	48.4	232	2	AB0741	exodeoxyribonuclea
720	31	48.4	234	2	H85613	leucyl, phenylalan
721	31	48.4	234	2	AI0610	leucyl/phenylalany
722	31	48.4	234	2	A36888	leucyl, phenylalan
723	31	48.4	234	2	B90750	leucyl, phenylalan
724	31	48.4	234	2	T46941	conjugal transfer
725	31	48.4	234	2	S25491	probable transcrip
726	31	48.4	234	2	S37463	regulatory protein
727	31	48.4	234	2	AD3244	transcriptional re
728	31	48.4	237	2	B87562	hypothetical prote
729	31	48.4	239	2	S37604	farnesyl cysteine
730	31	48.4	241	2	H81226	leucyl/phenylalany
731	31	48.4	243	2	S75432	hypothetical prote
732	31	48.4	244	2	S25988	hypothetical prote
733	31	48.4	245	2	T47501	dof6 zinc finger p
734	31	48.4	245	2	C30010	hypothetical ORF-6
735	31	48.4	246	2	T28166	hypothetical prote
736	31	48.4	247	1	E81667	probable phosphoes
737	31	48.4	250	2	F75219	hypothetical prote
738	31	48.4	256	2	C70394	ABC transporter (A
739	31	48.4	256	2	S42928	probable membrane-
740	31	48.4	256	2	S42932	probable transmemb
741	31	48.4	257	2	S78200	H+-transporting tw
742	31	48.4	259	2	C87287	inositol monophosp
743	31	48.4	260	2	T27819	hypothetical prote
744	31	48.4	261	2	S68134	cytochrome-c oxida
745	31	48.4	263	2	F84339	hypothetical prote
746	31	48.4	269	2	AG1126	conserved membrane
747	31	48.4	269	2	AD1487	conserved membrane
748	31	48.4	269	2	H75576	cobalamin synthase
749	31	48.4	269	2	A70134	flagellar biosynth
750	31	48.4	270	2	G70812	hypothetical prote
751	31	48.4	274	2	T23862	hypothetical prote
752	31	48.4	274	2	D89724	protein R03A10.6 [
753	31	48.4	280	2	E82099	phosphatidate cyti
754	31	48.4	282	1	JQ0347	cytochrome c1 - Rh
755	31	48.4	284	2	A87306	conserved hypothet
756	31	48.4	286	2	T39404	hypothetical prote
757	31	48.4	290	1	A39131	type IV prepilin p
758	31	48.4	290	2	T10488	pectinesterase (EC
759	31	48.4	290	2	T01130	hypothetical prote
760	31	48.4	292	2	E72576	probable ABC trans
761	31	48.4	294	2	T32170	hypothetical prote
762	31	48.4	296	2	T13885	NADH2 dehydrogenas
763	31	48.4	298	2	AB3293	tetratricopeptide
764	31	48.4	302	1	F70021	proline dehydrogen
765	31	48.4	304	2	G70392	thiosulfate sulfur
766	31	48.4	304	2	E90521	hypothetical prote
767	31	48.4	305	2	A25010	pectinesterase (EC
768	31	48.4	306	2	D70409	hypothetical prote
769	31	48.4	310	2	D75471	probable proline d
770	31	48.4	311	2	S23533	hypothetical prote
771	31	48.4	311	2	B70083	hypothetical prote
772	31	48.4	312	1	E69781	ABC transporter ho
773	31	48.4	312	2	G69978	probable ATPase yr
774	31	48.4	314	2	S72525	pectinesterase (EC
775	31	48.4	314	2	AI3190	hypothetical prote
776	31	48.4	316	2	C47099	lysR homolog, nac
777	31	48.4	316	2	C64963	transcription regu
778	31	48.4	316	2	E85823	transcription regu
779	31	48.4	316	2	G90976	transcription regu
780	31	48.4	320	2	S78456	pectinesterase (EC
781	31	48.4	321	2	E97314	pectin methylester
782	31	48.4	321	2	E86423	probable 60S ribos
783	31	48.4	328	2	H84061	ferrichrome ABC tr
784	31	48.4	336	2	T31882	hypothetical prote
785	31	48.4	337	2	JC5832	neurotransmitter r
786	31	48.4	343	2	T33945	hypothetical prote
787	31	48.4	346	2	A83686	hypothetical prote
788	31	48.4	347	2	T23944	hypothetical prote
789	31	48.4	348	2	T36890	probable iron-side
790	31	48.4	350	2	D86420	unknown protein [i
791	31	48.4	351	2	E81210	transaldolase NMB0
792	31	48.4	359	2	F81036	Mrp/NBP35 family p
793	31	48.4	359	2	S35157	Delta6 fatty acid
794	31	48.4	362	2	B57641	G protein-coupled
795	31	48.4	363	2	T34631	probable integral
796	31	48.4	367	2	AC0907	conserved hypothet
797	31	48.4	371	2	T49696	related to peroxis
798	31	48.4	372	2	C70590	probable nicT prot
799	31	48.4	374	2	S78041	pectinesterase (EC
800	31	48.4	374	2	E91250	probable proteinas
801	31	48.4	375	2	G81980	hypothetical prote
802	31	48.4	375	2	D90061	conserved hypothet
803	31	48.4	379	2	T04762	chitinase homolog
804	31	48.4	380	2	T10898	probable omega-3 f
805	31	48.4	387	2	T51225	related to INORGAN
806	31	48.4	389	2	S00629	pectinesterase (EC
807	31	48.4	390	2	D69757	multidrug-efflux t
808	31	48.4	396	1	B69851	cytochrome P450 yj
809	31	48.4	397	2	D71467	probable tyrosine
810	31	48.4	397	2	E97321	membrane associate
811	31	48.4	397	2	H71116	hypothetical prote
812	31	48.4	398	2	F84099	hypothetical prote
813	31	48.4	398	2	T32653	hypothetical prote
814	31	48.4	402	2	S47329	OXA1 protein precu
815	31	48.4	406	2	B81391	zinc proteinase-li
816	31	48.4	409	2	T50311	oxa1sp2 protein [i
817	31	48.4	409	2	T43703	respiratory protei
818	31	48.4	411	2	AD2359	hypothetical prote
819	31	48.4	412	2	T40899	probable proteinas
820	31	48.4	414	2	AG0075	probable sugar bin
821	31	48.4	415	2	A35773	translation elonga
822	31	48.4	418	2	B72565	hypothetical prote
823	31	48.4	421	2	F72213	hypothetical prote
824	31	48.4	428	2	T03891	hypothetical prote
825	31	48.4	429	2	F72784	probable dihydroor
826	31	48.4	430	2	A87541	major facilitator
827	31	48.4	435	2	H69607	alpha-ketoglutarat
828	31	48.4	442	2	T04815	hypothetical prote
829	31	48.4	447	2	T09414	pectinesterase hom
830	31	48.4	450	2	T16220	hypothetical prote
831	31	48.4	453	2	T05862	hypothetical prote
832	31	48.4	453	2	F90327	cytosine permease

833	31	48.4	455	2	T05861	hypothetical prote
834	31	48.4	457	2	S01839	nitrogenase molybd
835	31	48.4	458	2	E82340	probable gluconate
836	31	48.4	461	2	F81015	gluconate permease
837	31	48.4	461	2	H81957	probable gluconate
838	31	48.4	461	2	D85312	probable homeodoma
839	31	48.4	469	2	T09366	cytochrome P450 ho
840	31	48.4	469	2	T00429	probable pectinest
841	31	48.4	470	2	D84614	hypothetical prote
842	31	48.4	471	2	F95421	probable amidase [
843	31	48.4	473	2	A56377	rubber particle cy
844	31	48.4	474	2	S00880	nitrogenase molybd
845	31	48.4	474	2	B70597	hypothetical prote
846	31	48.4	475	2	F84140	amino acid transpo
847	31	48.4	477	2	D82179	probable multidrug
848	31	48.4	477	2	T05202	pectinesterase hom
849	31	48.4	484	2	T34251	hypothetical prote
850	31	48.4	485	2	F95238	PTS system, membra
851	31	48.4	496	2	T47884	pectinesterase-lik
852	31	48.4	498	2	T23525	hypothetical prote
853	31	48.4	500	2	H71075	hypothetical prote
854	31	48.4	508	2	G98102	hypothetical prote
855	31	48.4	508	2	AG2958	hypothetical prote
856	31	48.4	510	2	H84887	probable pectinest
857	31	48.4	512	2	T15669	hypothetical prote
858	31	48.4	516	2	T47075	hypothetical prote
859	31	48.4	517	2	E95959	probable membrane-
860	31	48.4	517	2	G98324	hypothetical prote
861	31	48.4	518	2	T01318	pectinesterase hom
862	31	48.4	518	2	D84861	probable pectinest
863	31	48.4	520	2	C87450	GMP synthase [impo
864	31	48.4	522	1	ACRYD1	nicotinic acetylch
865	31	48.4	523	2	B71985	hypothetical prote
866	31	48.4	525	2	T32481	hypothetical prote
867	31	48.4	526	2	T48497	hypothetical prote
868	31	48.4	527	2	T49241	pectinesterase-lik
869	31	48.4	529	2	T47783	pectinesterase-lik
870	31	48.4	529	2	H97402	apolipoprotein N-a
871	31	48.4	529	2	AH2620	apolipoprotein N-a
872	31	48.4	532	2	T01418	pectinesterase hom
873	31	48.4	534	2	A29776	glucan 1,4-alpha-g
874	31	48.4	537	2	F95993	probable arylsulfa
875	31	48.4	541	2	T37945	conserved hypothet
876	31	48.4	545	2	T47952	hypothetical prote
877	31	48.4	545	2	T02578	hypothetical prote
878	31	48.4	546	2	S46527	pectinesterase (EC
879	31	48.4	549	2	AF2678	choline dehydrogen
880	31	48.4	550	2	S46528	pectinesterase (EC
881	31	48.4	554	2	G84117	Na+/solute symport
882	31	48.4	554	2	T06374	probable pectinest
883	31	48.4	554	2	T06468	pectinesterase (EC
884	31	48.4	555	2	E75513	virulence factor-r
885	31	48.4	563	2	B70676	hypothetical prote
886	31	48.4	566	2	T45162	succinate dehydrog
887	31	48.4	568	2	T39897	hypothetical prote
888	31	48.4	572	2	T22547	hypothetical prote
889	31	48.4	573	2	T01317	probable pectinest
890	31	48.4	575	2	C86310	protein F1L3.2 [im
891	31	48.4	575	2	S12525	metalloproteinase
892	31	48.4	579	2	B86158	F22D16.20 protein
893	31	48.4	582	2	PC4168	pectinesterase (EC
894	31	48.4	583	2	C97460	choline dehydrogen
895	31	48.4	583	2	T07848	pectinesterase (EC
896	31	48.4	584	2	T10485	pectinesterase (EC
897	31	48.4	586	2	T51211	hypothetical prote
898	31	48.4	587	2	D96578	hypothetical prote
899	31	48.4	600	2	T34757	probable oligopept
900	31	48.4	604	2	E81905	probable sulfite r
901	31	48.4	604	2	C85069	hypothetical prote
902	31	48.4	612	2	JQ1346	glucan 1,4-alpha-g
903	31	48.4	613	2	A95292	hypothetical prote
904	31	48.4	622	2	S54585	hypothetical prote
905	31	48.4	626	2	T13444	trehalase homolog
906	31	48.4	628	2	AE1780	NADH dehydrogenase
907	31	48.4	628	2	AF1404	NADH dehydrogenase
908	31	48.4	639	2	JQ0607	glucan 1,4-alpha-g
909	31	48.4	639	2	JT0479	glucan 1,4-alpha-g
910	31	48.4	640	1	ALASGR	glucan 1,4-alpha-g
911	31	48.4	640	2	A29166	glucan 1,4-alpha-g
912	31	48.4	641	2	D87269	hypothetical prote
913	31	48.4	652	2	S52683	probable membrane
914	31	48.4	660	2	AD0661	invasin-like prote
915	31	48.4	671	2	E81040	cytochrome c-type
916	31	48.4	689	1	JN0585	prolyl oligopeptid
917	31	48.4	699	2	AC0504	probable chitinase
918	31	48.4	700	2	D75508	serine/threonine p
919	31	48.4	702	2	C86268	F13B4.2 protein -
920	31	48.4	704	2	I47228	carbonic anhydrase
921	31	48.4	706	2	S70991	DNA topoisomerase
922	31	48.4	735	2	F98228	1,4-alpha-glucan b
923	31	48.4	735	2	AH3057	glycogen branching
924	31	48.4	751	2	T30154	hypothetical prote
925	31	48.4	752	2	T20871	hypothetical prote
926	31	48.4	755	1	S20922	photosystem I prot
927	31	48.4	773	2	H70108	hypothetical prote
928	31	48.4	820	2	G86246	hypothetical prote
929	31	48.4	823	2	T02959	kaurene synthase A
930	31	48.4	844	2	I50159	anion transporter
931	31	48.4	848	2	A33810	band 3 anion trans
932	31	48.4	850	2	T14450	serine/threonine k
933	31	48.4	851	2	T31520	hypothetical prote
934	31	48.4	855	2	C82983	hypothetical prote
935	31	48.4	874	2	T19540	hypothetical prote
936	31	48.4	911	1	B3HU	band 3 anion trans
937	31	48.4	922	2	A30816	band 3 anion trans
938	31	48.4	929	2	A25314	band 3 protein - m
939	31	48.4	946	2	T31488	hypothetical prote
940	31	48.4	972	2	E97421	NADH dehydrogenase
941	31	48.4	994	2	AD2639	pH adaption potass
942	31	48.4	1006	2	A59384	oxytocinase/insuli
943	31	48.4	1025	2	A59383	oxytocinase/insuli
944	31	48.4	1030	2	I39987	lantibiotic subtil
945	31	48.4	1042	2	S43904	hyaluronidase - Cl
946	31	48.4	1153	2	T31080	nitric-oxide synth
947	31	48.4	1210	2	A83306	hypothetical prote
948	31	48.4	1252	2	S02004	phospholipase C (E
949	31	48.4	1265	2	A34163	1-phosphatidylinos
950	31	48.4	1307	2	T25106	hypothetical prote
951	31	48.4	1545	2	S48824	probable membrane
952	31	48.4	1644	2	F91286	hypothetical prote
953	31	48.4	1644	2	B86128	hypothetical prote
954	31	48.4	1735	1	S22812	DNA-directed RNA p
955	31	48.4	1865	2	G86152	T7I23.15 protein -
956	31	48.4	2692	2	T23768	hypothetical prote
957	31	48.4	3869	2	A48205	All-1 protein +GTE
958	31	48.4	3968	2	A44265	trithorax homolog
959	31	48.4	4199	2	S76412	hypothetical prote
960	30.5	47.7	115	2	S26470	Ig heavy chain V r
961	30.5	47.7	137	2	G69461	small multidrug ex
962	30.5	47.7	247	2	T17237	hypothetical prote
963	30.5	47.7	256	2	E72574	probable membrane
964	30.5	47.7	261	2	S76304	hypothetical prote
965	30.5	47.7	298	2	AD3224	hypothetical prote
966	30.5	47.7	308	2	I56573	synaptic glycoprot
967	30.5	47.7	308	2	T50639	synaptic glycoprot
968	30.5	47.7	308	2	T50638	synaptic glycoprot
969	30.5	47.7	345	2	E69725	potassium uptake t
970	30.5	47.7	350	2	E84109	potassium uptake p
971	30.5	47.7	356	2	S42388	torso-like protein
972	30.5	47.7	416	2	S77027	hypothetical prote
973	30.5	47.7	445	2	A97321	6-phospho-alpha-gl
974	30.5	47.7	461	2	T27229	hypothetical prote
975	30.5	47.7	495	2	G82371	FixG-related prote
976	30.5	47.7	508	2	T43154	nitrate transport
977	30.5	47.7	546	2	T48785	hypothetical prote
978	30	46.9	10	2	C39191	hypothetical prote

979	30	46.9	10	2	PQ0753	beta-fructofuranos
980	30	46.9	23	2	PH1361	Ig heavy chain DJ
981	30	46.9	40	2	F64009	hypothetical prote
982	30	46.9	43	2	S11111	Ig heavy chain V r
983	30	46.9	80	2	F96591	probable antifunga
984	30	46.9	81	2	S71962	trefoil factor pS2
985	30	46.9	81	2	AD2104	hypothetical prote
986	30	46.9	87	2	A40700	P-domain peptide p
987	30	46.9	89	2	B84312	hypothetical prote
988	30	46.9	100	1	G65105	hypothetical 11.3
989	30	46.9	100	2	G85978	hypothetical prote
990	30	46.9	100	2	D91133	hypothetical prote
991	30	46.9	100	2	S69323	probable membrane
992	30	46.9	101	2	S67034	probable membrane
993	30	46.9	102	2	E72482	hypothetical prote
994	30	46.9	114	2	PL0247	Ig heavy chain V r
995	30	46.9	117	2	T07281	NADH dehydrogenase
996	30	46.9	118	2	JV0006	NADH2 dehydrogenas
997	30	46.9	118	2	T15049	NADH2 dehydrogenas
998	30	46.9	118	2	T08055	NADH2 dehydrogenas
999	30	46.9	118	2	T08052	NADH2 dehydrogenas
1000	30	46.9	119	2	S69293	hypothetical prote

ALIGNMENTS

RESULT 1
A35944
Ig gamma-2a chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1990 #sequence_revision 30-Nov-1990 #text_change 16-Jul-1999
C;Accession: A35944
R;Igarashi, T.; Sato, M.; Katsube, Y.; Takio, K.; Tanaka, T.; Nakanishi, M.; Arata, Y.
Biochemistry 29, 5727-5733, 1990
A;Title: Structure of a mouse immunoglobulin G that lacks the entire C-H1 domain: protei
A;Reference number: A35944; MUID:90344795; PMID:2116900
A;Accession: A35944
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-170 <IGA>
A;Cross-references: UNIPARC:UPI0000176F39
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;56-120/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 48; DB 2; Length 170;
Best Local Similarity 60.0%; Pred. No. 0.93;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 LYFGFPWFAY 10
              :|: :|||||
Db         16 IYYHYPWFAY 25
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RESULT 2
RRXPLC
genome polyprotein - lymphocytic choriomeningitis virus (strain Armstrong 53b)
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: lymphocytic choriomeningitis virus
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 31-Dec-2004
C;Accession: A30181
R;Salvato, M.; Shimomaye, E.; Oldstone, M.B.A.
Virology 169, 377-384, 1989
A;Title: The primary structure of the lymphocytic choriomeningitis virus L gene encodes
A;Reference number: A30181; MUID:89204909; PMID:2705303
A;Accession: A30181
A;Molecule type: genomic RNA
A;Residues: 1-2210 <SAL>
A;Cross-references: UNIPROT:P14240; UNIPARC:UPI0000134B25; GB:J04331; NID:g331368; PIDN:
C;Genetics:
A;Map position: segment L
C;Superfamily: RNA-directed RNA polymerase, Arenaviridae type
C;Keywords: nucleotidyltransferase

Query Match 68.8%; Score 44; DB 1; Length 2210;
Best Local Similarity 70.0%; Pred. No. 48;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 LYFGFPWFAY 10
              | ||| ||:|
Db       1901 LQFGFGWFSY 1910
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RESULT 3
A40470
glucocorticoid-induced receptor precursor, short form RP39 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
C;Accession: A40470
R;Harrigan, M.T.; Campbell, N.F.; Bourgeois, S.
Mol. Endocrinol. 5, 1331-1338, 1991
A;Title: Identification of a gene induced by glucocorticoids in murine T-cells: a potent
A;Reference number: A40470; MUID:92123228; PMID:1663214
A;Accession: A40470
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-381 <HAR>
A;Cross-references: UNIPROT:P30731; UNIPARC:UPI0000004034; GB:M80610
C;Superfamily: neurokinin 1 receptor

Query Match 65.6%; Score 42; DB 2; Length 381;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 LYFGFPWFA 9
              ||| | |||
Db        284 LYFAFHWFA 292
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RESULT 4
B40470
glucocorticoid-induced receptor precursor, short form RP23 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
C;Accession: B40470
R;Harrigan, M.T.; Campbell, N.F.; Bourgeois, S.
Mol. Endocrinol. 5, 1331-1338, 1991
A;Title: Identification of a gene induced by glucocorticoids in murine T-cells: a potent
A;Reference number: A40470; MUID:92123228; PMID:1663214
A;Accession: B40470
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-423 <HAR>
A;Cross-references: UNIPROT:P30731; UNIPARC:UPI000000414E; GB:M80481; GB:M80610; NID:g191
C;Superfamily: neurokinin 1 receptor

Query Match 65.6%; Score 42; DB 2; Length 423;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 LYFGFPWFA 9
              ||| | |||
Db        326 LYFAFHWFA 334
```

RESULT 5
D40470
glucocorticoid-induced receptor, long form RP105 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
C;Accession: D40470
R;Harrigan, M.T.; Campbell, N.F.; Bourgeois, S.
Mol. Endocrinol. 5, 1331-1338, 1991
A;Title: Identification of a gene induced by glucocorticoids in murine T-cells: a potent
A;Reference number: A40470; MUID:92123228; PMID:1663214
A;Accession: D40470

```
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-443 <HAR>
A;Cross-references: UNIPROT:P30731; UNIPARC:UPI000002AAB4; GB:M80160
C;Superfamily: neurokinin 1 receptor

  Query Match             65.6%;  Score 42;  DB 2;  Length 443;
  Best Local Similarity   77.8%;  Pred. No. 22;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        346 LYFAFHWFA 354


RESULT 6
D69829
Na+/H+-exchanging protein yheL [similarity] - Bacillus subtilis
N;Alternate names: Na+/H+ antiporter homolog yheL
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 31-Dec-2004
C;Accession: D69829
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: D69829
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-453 <KUN>
A;Cross-references: UNIPROT:O07553; UNIPARC:UPI000006015D; GB:Z99109; GB:AL009126; NID:g
A;Experimental source: strain 168
C;Genetics:
A;Gene: yheL
C;Superfamily: Na(+)/H(+) antiporter, NhaC type
C;Keywords: ion transport; transmembrane protein

  Query Match             65.6%;  Score 42;  DB 2;  Length 453;
  Best Local Similarity   85.7%;  Pred. No. 22;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPW 7
              |:|||||
Db         50 LWFGFPW 56


RESULT 7
C40470
glucocorticoid-induced receptor, long form RP82 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
C;Accession: C40470
R;Harrigan, M.T.; Campbell, N.F.; Bourgeois, S.
Mol. Endocrinol. 5, 1331-1338, 1991
A;Title: Identification of a gene induced by glucocorticoids in murine T-cells: a potent
A;Reference number: A40470; MUID:92123228; PMID:1663214
A;Accession: C40470
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-491 <HAR>
A;Cross-references: UNIPROT:P30731; UNIPARC:UPI000002AAB3; GB:M80610
C;Superfamily: neurokinin 1 receptor

  Query Match             65.6%;  Score 42;  DB 2;  Length 491;
  Best Local Similarity   77.8%;  Pred. No. 24;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        394 LYFAFHWFA 402


RESULT 8
T24784
hypothetical protein T10B9.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24784
R;Gardner, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: Z19935
A;Accession: T24784
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-519 <WIL>
A;Cross-references: UNIPROT:Q27520; UNIPARC:UPI000013C029; EMBL:Z48717; PIDN:CAA88610.1;
A;Experimental source: clone T10B9
C;Genetics:
A;Gene: CESP:T10B9.8
A;Map position: 2
A;Introns: 18/2; 63/3; 143/2; 174/2; 207/3; 306/3; 392/2; 416/3; 440/2
C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
C;Keywords: heme; iron; metalloprotein
F;323-487/Domain: cytochrome P450 homology <P45>
F;465/Binding site: heme iron (Cys) (axial ligand) #status predicted

  Query Match             65.6%;  Score 42;  DB 2;  Length 519;
  Best Local Similarity   75.0%;  Pred. No. 25;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFA 9
              || |||| :
Db          3 YFWFPWFS 10


RESULT 9
G81391
amino-acid ABC transporter integral membrane protein Cj0468 [imported] - Campylobacter je
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: G81391
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: G81391
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-218 <PAR>
A;Cross-references: UNIPROT:Q9PI40; UNIPARC:UPI00000C2142; GB:AL139075; GB:AL111168; NID
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj0468
C;Superfamily: histidine permease protein M

  Query Match             64.8%;  Score 41.5;  DB 2;  Length 218;
  Best Local Similarity   63.6%;  Pred. No. 13;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 LYFGFP-WFAY 10
              :||||| || :
Db         72 VYFGFPRWFGW 82
```

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RESULT 10
H90730
hypothetical membrane protein [imported] - Escherichia coli (strain O157:H7, substrain R
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: H90730
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: H90730
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-222 <HAY>
A;Cross-references: UNIPROT:Q8X997; UNIPARC:UPI00001653D2; GB:BA000007; PIDN:BAB34239.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs0816

  Query Match             64.1%;  Score 41;  DB 2;  Length 222;
  Best Local Similarity   71.4%;  Pred. No. 16;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPWF 8
              |:||||:
Db         19 YYGFPWW 25


RESULT 11
D91066
hypothetical membrane protein [imported] - Escherichia coli (strain O157:H7, substrain R
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: D91066
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: D91066
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-247 <HAY>
A;Cross-references: UNIPROT:Q8X997; UNIPARC:UPI00001654CB; GB:BA000007; PIDN:BAB36923.1;
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs3500

  Query Match             64.1%;  Score 41;  DB 2;  Length 247;
  Best Local Similarity   71.4%;  Pred. No. 18;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPWF 8
              |:||||:
Db         44 YYGFPWW 50


RESULT 12
D85910
unknown protein encoded by prophage CP-933Y [imported] - Escherichia coli (strain O157:H
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D85910; E85581
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: D85910
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-252 <STO>
A;Cross-references: UNIPROT:Q8X997; UNIPARC:UPI00000D084F; GB:AE005174; NID:g12517061; PI
A;Experimental source: strain O157:H7, substrain EDL933
A;Accession: E85581
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-252 <ST2>
A;Cross-references: UNIPARC:UPI00000D084F; GB:AE005174; NID:g12513722; PIDN:AAG55113.1; C
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: Z3931; Z0957

  Query Match             64.1%;  Score 41;  DB 2;  Length 252;
  Best Local Similarity   71.4%;  Pred. No. 18;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPWF 8
              |:||||:
Db         49 YYGFPWW 55


RESULT 13
S14506
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S14506
R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in VH CI
A;Reference number: S14484
A;Accession: S14506
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <CHE>
A;Cross-references: UNIPARC:UPI0000115F38; EMBL:X58651; NID:g51291; PIDN:CAA41508.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

  Query Match             62.5%;  Score 40;  DB 2;  Length 107;
  Best Local Similarity   55.6%;  Pred. No. 12;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              |: : ||||
Db         99 YYAYDWFAY 107


RESULT 14
H88175
protein T24H7.1 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: H88175
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleg
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: H88175
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-286 <STO>
A;Cross-references: UNIPROT:P50093; UNIPARC:UPI000013C202; GB:chr_II; PID:g861323; GSPDB:
C;Genetics:
A;Gene: T24H7.1
A;Map position: 2
C;Superfamily: erythrocyte band 7 integral membrane protein

  Query Match             62.5%;  Score 40;  DB 2;  Length 286;
  Best Local Similarity   60.0%;  Pred. No. 30;
```

```
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              |:|  ||| |
Db         59 LHFRIPWFQY 68


RESULT 15
H85096
hypothetical protein AT4g09500 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85096
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: H85096
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-442 <STO>
A;Cross-references: UNIPROT:Q9M0P3; UNIPARC:UPI0000048919; GB:NC_001268; NID:g7267645; P
C;Genetics:
A;Gene: AT4g09500
A;Map position: 4
C;Superfamily: flavonol O3-glucosyltransferase

  Query Match             62.5%;  Score 40;  DB 2;  Length 442;
  Best Local Similarity   75.0%;  Pred. No. 46;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 FGFPWFAY 10
              | |||||:
Db          8 FMFPWFAF 15


RESULT 16
F84618
probable flavonol 3-O-glucosyltransferase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: F84618
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84618
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-442 <STO>
A;Cross-references: UNIPROT:O81010; UNIPARC:UPI0000048562; GB:AE002093; NID:g3445210; PI
C;Genetics:
A;Gene: At2g22930
A;Map position: 2
C;Superfamily: flavonol O3-glucosyltransferase

  Query Match             62.5%;  Score 40;  DB 2;  Length 442;
  Best Local Similarity   75.0%;  Pred. No. 46;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 FGFPWFAY 10
              | |||||:
Db          8 FMFPWFAF 15


RESULT 17
E96672
Similar to Flavonol 3-O-Glucosyltransferase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E96672
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: E96672
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-447 <STO>
A;Cross-references: UNIPROT:Q9XIQ5; UNIPARC:UPI00000483F4; GB:AE005173; NID:g5042426; PI
C;Genetics:
A;Gene: F13O11.21
A;Map position: 1
C;Superfamily: flavonol O3-glucosyltransferase

  Query Match             62.5%;  Score 40;  DB 2;  Length 447;
  Best Local Similarity   75.0%;  Pred. No. 46;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 FGFPWFAY 10
              | |||||:
Db          8 FMFPWFAF 15


RESULT 18
F96672
Similar to Flavonol 3-O-Glucosyltransferase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F96672
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F96672
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-452 <STO>
A;Cross-references: UNIPROT:Q9XIQ4; UNIPARC:UPI00000483F5; GB:AE005173; NID:g5042427; PI
C;Genetics:
A;Gene: F13O11.22
A;Map position: 1
C;Superfamily: flavonol O3-glucosyltransferase

  Query Match             62.5%;  Score 40;  DB 2;  Length 452;
  Best Local Similarity   75.0%;  Pred. No. 47;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 FGFPWFAY 10
              | |||||:
Db          8 FMFPWFAF 15


RESULT 19
S19444
hypothetical protein YCR032w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YCR591; hypothetical protein YCR601
C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: S19444; S15052; S19751; S17478; S40917; S40972
```

R;Pohl, F.; Richterich, P.; Wurst, H.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19437
A;Accession: S19444
A;Molecule type: DNA
A;Residues: 1-334 <POH>
A;Cross-references: UNIPROT:P25356; UNIPARC:UPI000017B2B1; EMBL:X59720; MIPS:YCR032w
R;Jia, Y.; Slonimski, P.P.; Herbert, C.J.
Yeast 7, 413-424, 1991
A;Title: The complete sequence of the unit YCR59, situated between CRY1 and MAT, reveals
A;Reference number: S15052; MUID:91335897; PMID:1872032
A;Accession: S15052
A;Molecule type: DNA
A;Residues: 335-2167 <JIA>
A;Cross-references: UNIPARC:UPI0000168F07; EMBL:X59075; NID:g4805; PIDN:CAA41798.1; PID:
R;Herbert, C.J.; Jia, Y.; Slonimski, P.P.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19445
A;Accession: S19751
A;Molecule type: DNA
A;Residues: 335-2167 <HER>
A;Cross-references: UNIPARC:UPI0000168F07; EMBL:X59720; MIPS:YCR032w
R;Rodriguez, F.; Martegani, E.; Mauri, I.; Alberghina, L.
Yeast 7, 631-641, 1991
A;Title: The sequence of 8.8 kb of yeast chromosome III cloned in lambda PM3270 contains
A;Reference number: S17478; MUID:92116648; PMID:1837415
A;Accession: S17478
A;Molecule type: DNA
A;Residues: 1-202,'G',204-260,'R',262-399,'T',401-648,'S',650-721,'I',723-970,'V',972-10
A;Cross-references: UNIPARC:UPI000006BC39; EMBL:X62452; NID:g4808; PIDN:CAA44309.1; PID:
R;Wicksteed, B.L.; Roberts, A.B.; Sagliocco, F.A.; Brown, A.J.P.
Yeast 7, 761-772, 1991
A;Title: The complete sequence of a 7.5 kb region of chromosome III from Saccharomyces c
A;Reference number: S40917; MUID:92133166; PMID:1776366
A;Accession: S40917
A;Molecule type: DNA
A;Residues: 1760-1784,'D',1786-1892,'N',1894-2105,'N',2107-2122,'K',2124-2167 <WIC>
A;Cross-references: UNIPARC:UPI000006A010; EMBL:S78624; NID:g244237; PIDN:AAB21258.1; PI
R;Carbone, M.L.A.; Panzeri, L.; Falconi, M.M.; Carcano, C.; Plevani, P.; Lucchini, G.
Yeast 8, 805-812, 1992
A;Title: Nucleotide sequence of 9.2 kb left of CRY1 on yeast chromosome III from strain
A;Reference number: S25336; MUID:93070619; PMID:1332309
A;Accession: S40972
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1298-1784,'D',1786-1943 <CAR>
A;Cross-references: UNIPARC:UPI000017B2B2; EMBL:S47818
C;Genetics:
A;Gene: SGD:BPH1
A;Cross-references: SGD:S0000628; MIPS:YCR032w
A;Map position: 3R

 Query Match 62.5%; Score 40; DB 2; Length 2167;
 Best Local Similarity 87.5%; Pred. No. 2.1e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FGFPWFAY 10
 |||| |||
Db 516 FGFPLFAY 523

RESULT 20
F70676
hypothetical protein Rv3541c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: F70676
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: F70676
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-129 <COL>
A;Cross-references: UNIPROT:P71860; UNIPARC:UPI00000D114D; GB:Z82098; GB:AL123456; NID:g
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv3541c
C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv3541c

 Query Match 60.9%; Score 39; DB 2; Length 129;
 Best Local Similarity 60.0%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
 | | ||:||
Db 78 LRLGVPWYAY 87

RESULT 21
C81803
CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5) NMA1779 [in
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: C81803
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: C81803
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-187 <PAR>
A;Cross-references: UNIPROT:Q9JTH1; UNIPARC:UPI00000C4C8E; GB:AL162757; GB:AL157959; NID
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: pgsA; NMA1779
C;Superfamily: CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
C;Keywords: transferase

 Query Match 60.9%; Score 39; DB 2; Length 187;
 Best Local Similarity 75.0%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YFGFPWFA 9
 | |||||
Db 25 YLPFPWFA 32

RESULT 22
F81065
CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase NMB1588 [imported] - N
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: F81065
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: F81065
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-187 <TET>
A;Cross-references: UNIPROT:Q9JYH2; UNIPARC:UPI00000C4744; GB:AE002509; GB:AE002098; NID
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1588
C;Superfamily: CDPdiacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase

```
  Query Match             60.9%;  Score 39;  DB 2;  Length 187;
  Best Local Similarity   75.0%;  Pred. No. 29;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFA 9
              |  |||||
Db         25 YLPFPWFA 32


RESULT 23
D90055
hypothetical protein SA2303 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D90055
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D90055
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-256 <KUR>
A;Cross-references: UNIPROT:Q99RC0; UNIPARC:UPI0000054897; GB:BA000018; PID:g13702465; P
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA2303

  Query Match             60.9%;  Score 39;  DB 2;  Length 256;
  Best Local Similarity   66.7%;  Pred. No. 39;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              | || |||:
Db         53 YNGFSWFAF 61


RESULT 24
S42926
hypothetical membrane spanning protein - Staphylococcus aureus
C;Species: Staphylococcus aureus
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S42926
R;Ross, J.I.; Eady, E.A.; Cove, J.H.; Bamberg, S.
submitted to the EMBL Data Library, March 1994
A;Description: A second ABC-transporter gene, located adjacent to the plasmid-encoded St
A;Reference number: S42925
A;Accession: S42926
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-256 <ROS>
A;Cross-references: UNIPROT:Q53764; UNIPARC:UPI00000B9381; EMBL:Z30588; NID:g459255; PID

  Query Match             60.9%;  Score 39;  DB 2;  Length 256;
  Best Local Similarity   66.7%;  Pred. No. 39;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              | || |||:
Db         53 YNGFSWFAF 61


RESULT 25
D82500
hypothetical protein VCA0121 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: D82500
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: D82500
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-421 <HEI>
A;Cross-references: UNIPROT:Q9KN44; UNIPARC:UPI00000C342C; GB:AE004353; GB:AE003853; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0121
A;Map position: 2

  Query Match             60.9%;  Score 39;  DB 2;  Length 421;
  Best Local Similarity   71.4%;  Pred. No. 63;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPWF 8
              |:|:|||
Db        221 YWGWPWF 227


RESULT 26
S77508
srrA protein - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein slr1897
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S77508
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S77508
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-433 <KAN>
A;Cross-references: UNIPROT:P73325; UNIPARC:UPI00000C0FD2; EMBL:D90905; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: srrA

  Query Match             60.9%;  Score 39;  DB 2;  Length 433;
  Best Local Similarity   83.3%;  Pred. No. 65;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 FGFPWF 8
              |||||:
Db        146 FGFPWY 151


RESULT 27
S54067
probable membrane protein YPR042c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YP3085.06c; hypothetical protein YP9499.01c
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: S54067; S61063
R;Badcock, K.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54059
A;Accession: S54067
A;Molecule type: DNA
A;Residues: 1-508 <BAD>
A;Cross-references: UNIPROT:Q12221; UNIPARC:UPI0000168AAA; EMBL:Z49219; NID:g805025; PID
A;Experimental source: strain AB972
R;Badcock, K.; Churcher, C.M.
submitted to the EMBL Data Library, November 1995
A;Reference number: S61058
```

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A;Accession: S61063
A;Molecule type: DNA
A;Residues: 465-1075 <BAW>
A;Cross-references: UNIPARC:UPI0000168A2B; EMBL:Z68111; MIPS:YPR042c
C;Genetics:
A;Gene: SGD:PUF2
A;Cross-references: SGD:S0006246
A;Map position: 16R
C;Keywords: transmembrane protein
F;711-727/Domain: transmembrane #status predicted <TMM>

  Query Match            60.9%;  Score 39;  DB 2;  Length 1075;
  Best Local Similarity  60.0%;  Pred. No. 1.6e+02;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              | ||||| ::
Db        671 LKFGFPWNSF 680


RESULT 28
S14492
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S14492
R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in VH C
A;Reference number: S14484
A;Accession: S14492
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <CHE>
A;Cross-references: UNIPARC:UPI0000176C06; EMBL:X58649; NID:g51287; PIDN:CAA41506.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

  Query Match            59.4%;  Score 38;  DB 2;  Length 107;
  Best Local Similarity  55.6%;  Pred. No. 24;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              |: : ||||
Db         99 YYRYDWFAY 107


RESULT 29
S14493
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S14493
R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in VH C
A;Reference number: S14484
A;Accession: S14493
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <CHE>
A;Cross-references: UNIPARC:UPI0000176C0B; EMBL:X58650; NID:g51289; PIDN:CAA41507.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

  Query Match            59.4%;  Score 38;  DB 2;  Length 107;
  Best Local Similarity  55.6%;  Pred. No. 24;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              |: : ||||
Db         99 YYRYDWFAY 107


RESULT 30
S14491
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S14491
R;Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A;Description: Natural polyreactive antibodies differ from Ag-induced antibodies in VH CI
A;Reference number: S14484
A;Accession: S14491
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-107 <CHE>
A;Cross-references: UNIPARC:UPI0000115F35; EMBL:X58648; NID:g51285; PIDN:CAA41505.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-97/Domain: immunoglobulin homology <IMM>

  Query Match            59.4%;  Score 38;  DB 2;  Length 107;
  Best Local Similarity  55.6%;  Pred. No. 24;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              |: : ||||
Db         99 YYRYDWFAY 107


RESULT 31
C34903
Ig heavy chain precursor V region (5-27) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 16-Aug-1996
C;Accession: C34903
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-reac
A;Reference number: A34903; MUID:90094387; PMID:2104617
A;Accession: C34903
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-142 <BED>
A;Cross-references: UNIPARC:UPI0000176C0F
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-119/Domain: immunoglobulin homology <IMM>

  Query Match            59.4%;  Score 38;  DB 2;  Length 142;
  Best Local Similarity  66.7%;  Pred. No. 32;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              |:|  ||||
Db        123 YYGGYWFAY 131


RESULT 32
C69760
amino acid ABC transporter (permease) homolog yckA - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: C69760
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.,
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
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y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Accession: C69760
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-226 <KUN>
A;Cross-references: UNIPROT:P42399; UNIPARC:UPI000005FEF7; GB:Z99105; GB:AL009126; NID:g
A;Experimental source: strain 168
C;Genetics:
A;Gene: yckA
C;Superfamily: histidine permease protein M

 Query Match 59.4%; Score 38; DB 2; Length 226;
 Best Local Similarity 85.7%; Pred. No. 50;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPW 7
|||||:
Db 82 LYFGFPY 88

RESULT 33
A82578
glycerol uptake facilitator protein XF2267 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C;Accession: A82578
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: A82578
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-275 <SIM>
A;Cross-references: UNIPROT:Q9PB77; UNIPARC:UPI00000C29B8; GB:AE004039; GB:AE003849; NID
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF2267
C;Superfamily: aquaporin

 Query Match 59.4%; Score 38; DB 2; Length 275;
 Best Local Similarity 85.7%; Pred. No. 61;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LYFGFPW 7
|| ||||
Db 78 LYRGFPW 84

RESULT 34
H70677
hypothetical protein Rv3551 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70677
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome s
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70677
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-292 <COL>
A;Cross-references: UNIPROT:P71850; UNIPARC:UPI000013C2CE; GB:Z82098; GB:AL123456; NID:g3
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv3551

 Query Match 59.4%; Score 38; DB 2; Length 292;
 Best Local Similarity 35.0%; Pred. No. 64;
 Matches 7; Conservative 3; Mismatches 0; Indels 10; Gaps 1;

Qy 1 LYFGF----------PWFAY 10
:|:|| ||||:
Db 69 VYYGFVSLDSPPFYDPWFAH 88

RESULT 35
B82447
conserved hypothetical protein VCA0546 [imported] - Vibrio cholerae (strain N16961 serogr
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82447
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82447
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-318 <HEI>
A;Cross-references: UNIPROT:Q9KM43; UNIPARC:UPI00000C3571; GB:AE004385; GB:AE003853; NID
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0546
A;Map position: 2

 Query Match 59.4%; Score 38; DB 2; Length 318;
 Best Local Similarity 55.6%; Pred. No. 70;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LYFGFPWFA 9
||:|: |:|
Db 52 LYYGWQWYA 60

RESULT 36
T16869
hypothetical protein T13C5.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16869
R;Wu, X.
submitted to the EMBL Data Library, October 1995
A;Description: The sequence of C. elegans cosmid T13C5.
A;Reference number: Z18592
A;Accession: T16869
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

```
A;Residues: 1-345 <WUX>
A;Cross-references: UNIPARC:UPI0000179F0D; EMBL:U39648; NID:g1049363; PID:g1049369; PIDN
C;Genetics:
A;Gene: CESP:T13C5.6
A;Introns: 4/1; 35/3; 71/1; 97/3; 123/2; 159/1; 179/3; 201/1; 243/3

  Query Match             59.4%;  Score 38;  DB 2;  Length 345;
  Best Local Similarity   75.0%;  Pred. No. 75;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWF 8
              |  |||||
Db         35 LIHGFPWF 42


RESULT 37
JC5891
omega 6 desaturase (EC 1.14.99.-) precursor, chloroplast - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 09-Jul-2004
C;Accession: JC5891
R;Sato, N.; Fujiwara, S.; Kawaguchi, A.; Tsuzuki, M.
J. Biochem. 122, 1224-1232, 1997
A;Title: Cloning of a gene for chloroplast omega 6 desaturase of a green alga, Chlamydom
A;Reference number: JC5891; MUID:98158334; PMID:9498569
A;Accession: JC5891
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-424 <SAT>
A;Cross-references: UNIPROT:O48663; UNIPARC:UPI000009EF4A; DDBJ:AB007640; NID:g2696716;
C;Comment: This enzyme catalyzes the desaturation of monoenoic to dienoic acids.
C;Genetics:
A;Gene: des6
C;Superfamily: fatty acid (acyl-CoA) desaturase
C;Keywords: chloroplast; oxidoreductase
F;1-40/Domain: transit peptide (chloroplast) #status predicted <TPS>

  Query Match             59.4%;  Score 38;  DB 2;  Length 424;
  Best Local Similarity   85.7%;  Pred. No. 92;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LYFGFPW 7
              |||| ||
Db        271 LYFGGPW 277


RESULT 38
F90447
amino acid transporter, probable SSO2726 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: F90447
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: F90447
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-529 <KUR>
A;Cross-references: UNIPROT:Q97VA8; UNIPARC:UPI0000064825; GB:AE006641; NID:g13816049; P
C;Genetics:
A;Gene: SSO2726

  Query Match             59.4%;  Score 38;  DB 2;  Length 529;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              | |  ||||
Db        117 YLGAQWFAY 125


RESULT 39
B32382
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) - Bradyrhizobium japonicum
N;Contains: ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b; ubiquinol-cytoch
C;Species: Bradyrhizobium japonicum
C;Date: 12-Oct-1989 #sequence_revision 20-Aug-1994 #text_change 05-Oct-2004
C;Accession: B32382; A39715
R;Thoeny-Meyer, L.; Stax, D.; Hennecke, H.
Cell 57, 683-697, 1989
A;Title: An unusual gene cluster for the cytochrome bc-1 complex in Bradyrhizobium japoni
A;Reference number: A32382; MUID:89249332; PMID:2541921
A;Accession: B32382
A;Molecule type: DNA
A;Residues: 1-687 <THO>
A;Cross-references: UNIPROT:P51131; UNIPARC:UPI000005E7B8; GB:J03176; NID:g152082; PIDN:
R;Thoeny-Meyer, L.; James, P.; Hennecke, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 5001-5005, 1991
A;Title: From one gene to two proteins: the biogenesis of cytochromes b and c-1 in Brady
A;Reference number: A39715; MUID:91271320; PMID:1647023
A;Accession: A39715
A;Status: preliminary
A;Molecule type: protein
A;Residues: 439-444 <TH2>
A;Cross-references: UNIPARC:UPI0000171D11
C;Genetics:
A;Gene: fcbH
C;Superfamily: bifunctional cytochrome b/c1; cytochrome b homology; cytochrome b6 homolog
C;Keywords: chromoprotein; electron transfer; heme; iron; membrane-associated complex; me
F;1-412/Product: ubiquinol-cytochrome-c reductase, cytochrome b #status predicted <CB1>
F;24-356/Domain: cytochrome b homology <CBH>
F;24-224/Domain: cytochrome b6 homology <CB6>
F;49-65/Domain: transmembrane #status predicted <TM1>
F;94-112/Domain: transmembrane #status predicted <TM2>
F;132-148/Domain: transmembrane #status predicted <TM3>
F;193-215/Domain: transmembrane #status predicted <TM4>
F;238-356/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>
F;244-260/Domain: transmembrane #status predicted <TM5>
F;303-319/Domain: transmembrane #status predicted <TM6>
F;338-358/Domain: transmembrane #status predicted <TM7>
F;368-383/Domain: transmembrane #status predicted <TM8>
F;413-687/Product: ubiquinol-cytochrome-c reductase, cytochrome c1 #status predicted <CC1
F;440-687/Domain: cytochrome c1 heme protein homology <C1H>
F;96,197/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F;110,211/Binding site: heme iron (His) (axial ligands) (high potential) #status predicte
F;471,474/Binding site: heme (Cys) (covalent) #status predicted
F;475,616/Binding site: heme iron (His, Met) (axial ligands) #status predicted

  Query Match             59.4%;  Score 38;  DB 1;  Length 687;
  Best Local Similarity   71.4%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GFPWFAY 10
              ||||| :
Db        562 GFPWFIF 568


RESULT 40
A87321
TonB-dependent receptor [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87321
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolona
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87321
A;Status: preliminary
A;Molecule type: DNA
```

```
A;Residues: 1-972 <STO>
A;Cross-references: UNIPROT:Q9AAL8; UNIPARC:UPI00000C70C4; GB:AE005673; NID:g13421777; P
C;Genetics:
A;Gene: CC0579

  Query Match             59.4%;  Score 38;  DB 2;  Length 972;
  Best Local Similarity   66.7%;  Pred. No. 2e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              |:||| ||:
Db        414 YYGFPIFAW 422


RESULT 41
S57112
JSN1 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein J1890; protein YJR091c
C;Species: Saccharomyces cerevisiae
C;Date: 23-Aug-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: S57112; S57110; S71710
R;Ramezani Rad, M.; Kirchrath, L.; Hollenberg, C.P.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S57111
A;Accession: S57112
A;Molecule type: DNA
A;Residues: 1-1091 <RAM>
A;Cross-references: UNIPROT:P47135; UNIPARC:UPI000012DAC9; EMBL:Z49591; NID:g2131101; PI
R;Manus, V.; Huang, M.E.; Galibert, F.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S57085
A;Accession: S57110
A;Molecule type: DNA
A;Residues: 206-1091 <MAN>
A;Cross-references: UNIPARC:UPI0000168D41; EMBL:Z49591; MIPS:YJR091c
R;Huang, M.E.; Manus, V.; Chuat, J.C.; Galibert, F.
Yeast 12, 869-875, 1996
A;Title: Analysis of a 62 kb DNA sequence of chromosome X reveals 36 open reading frames
A;Reference number: S71676; MUID:96437976; PMID:8840504
A;Accession: S71710
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 206-1091 <HUA>
A;Cross-references: UNIPARC:UPI0000168D41; EMBL:L47993; NID:g1019675; PIDN:AAB39314.1; P
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C;Genetics:
A;Gene: SGD:JSN1
A;Cross-references: SGD:S0003851; MIPS:YJR091c
A;Map position: 10R
C;Function:
A;Description: suppresses the high-temperature lethality of tub2-150

  Query Match             59.4%;  Score 38;  DB 2;  Length 1091;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LYFGFPW 7
              | |||||
Db        712 LKFGFPW 718


RESULT 42
T27007
hypothetical protein Y48B6A.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27007
R;Wall, M.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20297
A;Accession: T27007
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-894 <WIL>
A;Cross-references: UNIPROT:Q9U297; UNIPARC:UPI000007A207; EMBL:AL110490; NID:e1542263;
A;Experimental source: clone Y48B6A
C;Genetics:
A;Gene: CESP:Y48B6A.11
A;Introns: 71/2; 146/2; 510/1; 558/2

  Query Match             58.6%;  Score 37.5;  DB 2;  Length 894;
  Best Local Similarity   57.1%;  Pred. No. 2.3e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    5;  Gaps    1;

Qy          1 LYFG-----FPWFA 9
              ||||     ||| |
Db        253 LYFGMYKTTFPWHA 266


RESULT 43
S64949
probable membrane protein YLR112w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L2928
C;Species: Saccharomyces cerevisiae
C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: S64949; S69399
R;Verhasselt, P.; Voet, M.; Volckaert, G.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64943
A;Accession: S64949
A;Molecule type: DNA
A;Residues: 1-139 <VER>
A;Cross-references: UNIPROT:Q12130; UNIPARC:UPI000006B13E; EMBL:Z73284; NID:g1360505; PI
A;Experimental source: strain S288C
R;Verhasselt, P.; Volckaert, G.
submitted to the EMBL Data Library, September 1995
A;Reference number: S69393
A;Accession: S69399
A;Molecule type: DNA
A;Residues: 1-139 <VEW>
A;Cross-references: UNIPARC:UPI000006B13E; EMBL:X89514; NID:g1297019; PID:g1297026
C;Genetics:
A;Cross-references: SGD:S0004102
A;Map position: 12R
C;Superfamily: Saccharomyces probable membrane protein YLR112w
C;Keywords: transmembrane protein
F;66-82/Domain: transmembrane #status predicted <TMM>

  Query Match             57.8%;  Score 37;  DB 2;  Length 139;
  Best Local Similarity   71.4%;  Pred. No. 46;
  Matches    5;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWF 8
              ||  |||
Db         97 YFALPWF 103


RESULT 44
C44102
di-N-acetylchitobiase (EC 3.2.1.-) precursor - rat
N;Alternate names: chitobiase; lysosomal glycosidase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: C44102; S27882
R;Fisher, K.J.; Aronson Jr., N.N.
J. Biol. Chem. 267, 19607-19616, 1992
A;Title: Cloning and expression of the cDNA sequence encoding the lysosomal glycosidase
A;Reference number: A44102; MUID:92406917; PMID:1527079
A;Accession: C44102
A;Molecule type: mRNA
A;Residues: 1-367 <FIS>
A;Cross-references: UNIPROT:Q01460; UNIPARC:UPI00001293CC; GB:M95768; NID:g203452; PIDN:
A;Experimental source: placenta
R;Fisher, K.J.; Aronson Jr., N.N.
submitted to the EMBL Data Library, June 1992
A;Description: Cloning and expression of the cDNA sequence encoding the lysosomal glycos
```

```
A;Reference number: S27882
A;Accession: S27882
A;Molecule type: mRNA
A;Residues: 1-367 <FI2>
A;Cross-references: UNIPARC:UPI00001293CC; EMBL:M95768; NID:g203452; PIDN:AAA40924.1; PI
C;Keywords: glycoprotein; glycosidase; hydrolase
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-367/Product: di-N-acetylchitobiase #status predicted <MAT>
F;178,213,247,284/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             57.8%;  Score 37;  DB 2;  Length 367;
  Best Local Similarity   50.0%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              |  | ||: |
Db        232 LVMGIPWYGY 241


RESULT 45
S32879
lipA protein - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S32879; S28077
R;Frosch, M.; Mueller, A.
Mol. Microbiol. 8, 483-493, 1993
A;Title: Phospholipid substitution of capsular polysaccharides and mechanisms of capsule
A;Reference number: S32879; MUID:93316845; PMID:8326861
A;Accession: S32879
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-400 <FRO>
A;Cross-references: UNIPROT:Q05013; UNIPARC:UPI000017AA08; EMBL:Z13995
C;Genetics:
A;Gene: lipA

  Query Match             57.8%;  Score 37;  DB 2;  Length 400;
  Best Local Similarity   71.4%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 FGFPWFA 9
              || ||:|
Db         95 FGLPWYA 101


RESULT 46
C83544
probable MFS transporter PA0811 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: C83544
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: C83544
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-415 <STO>
A;Cross-references: UNIPROT:Q9I5C8; UNIPARC:UPI00000C5167; GB:AE004516; GB:AE004091; NID
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA0811
C;Superfamily: hypothetical protein c0103

  Query Match             57.8%;  Score 37;  DB 2;  Length 415;
  Best Local Similarity   53.8%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    4;  Gaps    1;

Qy          2 YFGF----PWFAY 10
                :|||    || ||
Db        328 FFGFGWYGPWVAY 340


RESULT 47
T02381
hypothetical protein At2g44250 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F4I1.6
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02381; C84876
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence.
A;Reference number: Z14667
A;Accession: T02381
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-427 <ROU>
A;Cross-references: UNIPROT:O64860; UNIPARC:UPI000009DF7E; EMBL:AC004521; NID:g3128166; I
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: C84876
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-427 <STO>
A;Cross-references: UNIPARC:UPI000009DF7E; GB:AE002093; NID:g3128171; PIDN:AAC16075.1; GS
C;Genetics:
A;Gene: At2g44250; F4I1.6
A;Map position: 2
A;Introns: 72/3; 101/3; 179/3; 233/3; 251/3; 300/3
C;Superfamily: Arabidopsis thaliana hypothetical protein F16G20.50

  Query Match             57.8%;  Score 37;  DB 2;  Length 427;
  Best Local Similarity   71.4%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 FGFPWFA 9
              | :||||
Db         60 FNYPWFA 66


RESULT 48
F71275
probable periplasmic serine proteinase DO (htrA-2) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: F71275
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinn
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDon
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: F71275
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-485 <COL>
A;Cross-references: UNIPROT:O83813; UNIPARC:UPI00000D32AC; GB:AE001254; GB:AE000520; NID
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0841
C;Superfamily: Helicobacter serine proteinase

  Query Match             57.8%;  Score 37;  DB 1;  Length 485;
  Best Local Similarity   71.4%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;
```

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Qy          4 GFPWFAY 10
              ||||| :
Db         73 GFPWFFF 79


RESULT 49
AD2349
hypothetical protein alr4347 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AD2349
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2349
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-515 <KUR>
A;Cross-references: UNIPROT:Q8YP53; UNIPARC:UPI00000CEAD0; GB:BA000019; PIDN:BAB76046.1;
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr4347

  Query Match             57.8%;  Score 37;  DB 2;  Length 515;
  Best Local Similarity   50.0%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              | :||||  :
Db        267 LKYGFPWLLF 276


RESULT 50
D81240
capsule polysaccharide modification protein LipA NMB0082 [imported] - Neisseria meningit
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: D81240
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: D81240
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-704 <TET>
A;Cross-references: UNIPROT:Q05013; UNIPARC:UPI000012E715; GB:AE002368; GB:AE002098; NID
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0082

  Query Match             57.8%;  Score 37;  DB 2;  Length 704;
  Best Local Similarity   71.4%;  Pred. No. 2.2e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 FGFPWFA 9
              || ||:|
Db        277 FGLPWYA 283


Search completed: March 23, 2006, 02:05:01
Job time : 21.8356 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:40:40 ; Search time 86.0274 Seconds
(without alignments)
82.012 Million cell updates/sec

Title: US-10-755-382-25
Perfect score: 64
Sequence: 1 LYFGFPWFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	47	73.4	1208	2	Q4RK84_TETNG	Q4rk84 tetraodon n
2	44	68.8	2209	2	Q9YZ25_9VIRU	Q9yz25 lymphocytic
3	44	68.8	2210	1	RRPO_LYCVA	P14240 lymphocytic
4	43.5	68.0	176	2	Q4SCE1_TETNG	Q4sce1 tetraodon n
5	43	67.2	302	2	Q9RK78_STRCO	Q9rk78 streptomyce
6	43	67.2	339	2	Q4KAB2_PSEF5	Q4kab2 pseudomonas
7	43	67.2	812	2	Q5ZYR8_LEGPH	Q5zyr8 legionella
8	43	67.2	812	2	Q5X882_LEGPA	Q5x882 legionella
9	43	67.2	812	2	Q5WZN5_LEGPL	Q5wzn5 legionella
10	42	65.6	110	2	P70629_RAT	P70629 rattus norv
11	42	65.6	381	2	Q544C4_MOUSE	Q544c4 mus musculu
12	42	65.6	396	2	Q88TD1_LACPL	Q88td1 lactobacill
13	42	65.6	422	1	GPR83_CANFA	Q9ttq9 canis famil
14	42	65.6	422	2	Q8VHD7_RAT	Q8vhd7 rattus norv
15	42	65.6	423	1	GPR83_HUMAN	Q9nym4 homo sapien
16	42	65.6	423	1	GPR83_MOUSE	P30731 mus musculu
17	42	65.6	423	2	Q6NWR3_HUMAN	Q6nwr3 homo sapien
18	42	65.6	423	2	Q6NWR4_HUMAN	Q6nwr4 homo sapien
19	42	65.6	423	2	Q542Q9_MOUSE	Q542q9 mus musculu
20	42	65.6	423	2	Q5PQ74_XENLA	Q5pq74 xenopus lae
21	42	65.6	431	2	Q7W591_BORPA	Q7w591 bordetella
22	42	65.6	444	2	Q7VZS0_BORPE	Q7vzs0 bordetella
23	42	65.6	444	2	Q7WCS1_BORBR	Q7wcs1 bordetella
24	42	65.6	453	1	NHAC_BACSU	O07553 bacillus su
25	42	65.6	463	2	Q9EPJ7_MOUSE	Q9epj7 mus musculu
26	42	65.6	519	1	C13A1_CAEEL	Q27520 caenorhabdi
27	41.5	64.8	218	2	Q5HVZ9_CAMJR	Q5hvz9 campylobact
28	41.5	64.8	218	2	Q9PI40_CAMJE	Q9pi40 campylobact
29	41	64.1	118	2	Q73FV1_WOLPM	Q73fv1 wolbachia p
30	41	64.1	120	2	Q57P30_SALCH	Q57p30 salmonella
31	41	64.1	120	2	Q8FIW0_ECOL6	Q8fiw0 escherichia
32	41	64.1	222	2	Q7AGG4_ECO57	Q7agg4 escherichia
33	41	64.1	238	2	Q8ZPA5_SALTY	Q8zpa5 salmonella
34	41	64.1	238	2	Q8VSF8_SHIFL	Q8vsf8 shigella fl
35	41	64.1	247	2	Q7ABG6_ECO57	Q7abg6 escherichia
36	41	64.1	252	2	Q8X997_ECO57	Q8x997 escherichia
37	41	64.1	258	2	Q99PZ3_SHIFL	Q99pz3 shigella fl
38	41	64.1	377	2	Q61XG3_CAEBR	Q61xg3 caenorhabdi
39	41	64.1	388	2	Q6AXX9_RAT	Q6axx9 rattus norv
40	41	64.1	407	2	Q9N476_CAEEL	Q9n476 caenorhabdi
41	41	64.1	465	2	Q5I0J0_RAT	Q5i0j0 rattus norv
42	41	64.1	695	2	Q4P0W0_USTMA	Q4p0w0 ustilago ma
43	41	64.1	720	2	Q5LIF7_BACFN	Q5lif7 bacteroides
44	41	64.1	720	2	Q64ZH9_BACFR	Q64zh9 bacteroides
45	40	62.5	74	2	Q4YFN0_PLABE	Q4yfn0 plasmodium
46	40	62.5	134	2	Q6SK73_ARTAU	Q6sk73 arthrobacte
47	40	62.5	137	2	Q6RK11_BURCE	Q6rk11 burkholderi
48	40	62.5	168	2	Q6HPK3_BACHK	Q6hpk3 bacillus th
49	40	62.5	227	2	Q5C3T7_SCHJA	Q5c3t7 schistosoma
50	40	62.5	239	2	Q4XWE8_PLACH	Q4xwe8 plasmodium
51	40	62.5	253	2	Q96XX9_SULTO	Q96xx9 sulfolobus
52	40	62.5	286	1	PHB2_CAEEL	P50093 caenorhabdi
53	40	62.5	287	2	Q6DII4_BRARE	Q6dii4 brachydanio
54	40	62.5	299	2	Q99623_HUMAN	Q99623 homo sapien
55	40	62.5	299	2	Q5RB19_PONPY	Q5rb19 pongo pygma
56	40	62.5	299	2	Q5XIH7_RAT	Q5xih7 rattus norv
57	40	62.5	299	2	O35129_MOUSE	O35129 mus musculu
58	40	62.5	301	2	Q5ZMN3_CHICK	Q5zmn3 gallus gall
59	40	62.5	302	2	Q6PC13_BRARE	Q6pc13 brachydanio
60	40	62.5	321	2	Q8LSK2_PHYPA	Q8lsk2 physcomitre
61	40	62.5	330	2	Q8GGL4_BACPU	Q8ggl4 bacillus pu
62	40	62.5	330	2	Q8GGL5_BACPU	Q8ggl5 bacillus pu
63	40	62.5	334	2	Q617R4_CAEBR	Q617r4 caenorhabdi
64	40	62.5	334	2	Q52445_PSEST	Q52445 pseudomonas
65	40	62.5	340	2	Q65VA0_MANSM	Q65va0 mannheimia
66	40	62.5	357	2	Q8EFX5_SHEON	Q8efx5 shewanella
67	40	62.5	374	2	Q4X4U2_PLACH	Q4x4u2 plasmodium
68	40	62.5	405	2	Q4KFP9_PSEF5	Q4kfp9 pseudomonas
69	40	62.5	417	2	Q84WC5_ARATH	Q84wc5 arabidopsis
70	40	62.5	420	2	Q4YUH3_PLABE	Q4yuh3 plasmodium
71	40	62.5	430	2	Q83BW4_COXBU	Q83bw4 coxiella bu
72	40	62.5	442	2	O81010_ARATH	O81010 arabidopsis
73	40	62.5	442	2	Q9M0P3_ARATH	Q9m0p3 arabidopsis
74	40	62.5	445	2	Q8NU37_CORGL	Q8nu37 corynebacte
75	40	62.5	447	2	Q9FN28_ARATH	Q9fn28 arabidopsis
76	40	62.5	447	2	Q9XIQ5_ARATH	Q9xiq5 arabidopsis
77	40	62.5	452	2	Q9XIQ4_ARATH	Q9xiq4 arabidopsis
78	40	62.5	475	2	Q7RK01_PLAYO	Q7rk01 plasmodium
79	40	62.5	477	2	Q5P0X2_AZOSE	Q5p0x2 azoarcus sp
80	40	62.5	501	2	Q7SHL0_NEUCR	Q7shl0 neurospora
81	40	62.5	513	2	Q7W920_BORPA	Q7w920 bordetella
82	40	62.5	513	2	Q7WKG5_BORBR	Q7wkg5 bordetella
83	40	62.5	716	2	Q8NIS0_NEUCR	Q8nis0 neurospora
84	40	62.5	728	2	P74829_9SPHN	P74829 sphingomona
85	40	62.5	730	2	Q7S7H5_NEUCR	Q7s7h5 neurospora
86	40	62.5	968	2	Q5P4I8_AZOSE	Q5p4i8 azoarcus sp
87	40	62.5	999	2	Q8XWU7_RALSO	Q8xwu7 ralstonia s
88	40	62.5	1246	2	Q7RBS8_PLAYO	Q7rbs8 plasmodium
89	40	62.5	1457	2	Q82XZ7_NITEU	Q82xz7 nitrosomona
90	40	62.5	2167	1	BPH1_YEAST	P25356 saccharomyc
91	39	60.9	129	2	Q7TW91_MYCBO	Q7tw91 mycobacteri
92	39	60.9	129	2	P71860_MYCTU	P71860 mycobacteri
93	39	60.9	133	2	Q743R5_MYCPA	Q743r5 mycobacteri
94	39	60.9	141	2	Q5YY18_NOCFA	Q5yy18 nocardia fa
95	39	60.9	184	2	Q6G4Q6_BARHE	Q6g4q6 bartonella
96	39	60.9	185	2	Q4IWH4_AZOVI	Q4iwh4 azotobacter
97	39	60.9	187	2	Q9JTH1_NEIMA	Q9jth1 neisseria m
98	39	60.9	187	2	Q9JYH2_NEIMB	Q9jyh2 neisseria m
99	39	60.9	213	2	Q5TPC0_ANOGA	Q5tpc0 anopheles g
100	39	60.9	243	2	Q7PMG2_ANOGA	Q7pmg2 anopheles g
101	39	60.9	256	2	Q53764_STAAU	Q53764 staphylococ
102	39	60.9	256	2	Q6G6G0_STAAS	Q6g6g0 staphylococ
103	39	60.9	256	2	Q6GDT0_STAAR	Q6gdt0 staphylococ
104	39	60.9	256	2	Q7A3I6_STAAN	Q7a3i6 staphylococ

105	39	60.9	256	2	Q8NUT8_STAAW	Q8nut8 staphylococ
106	39	60.9	256	2	Q99RC0_STAAM	Q99rc0 staphylococ
107	39	60.9	264	2	Q4X734_PLACH	Q4x734 plasmodium
108	39	60.9	294	2	Q620Y0_CAEBR	Q620y0 caenorhabdi
109	39	60.9	301	2	Q6DEB3_XENLA	Q6deb3 xenopus lae
110	39	60.9	301	2	Q6DKA8_XENLA	Q6dka8 xenopus lae
111	39	60.9	324	2	Q5TPC1_ANOGA	Q5tpc1 anopheles g
112	39	60.9	342	2	Q7V4A8_PROMM	Q7v4a8 prochloroco
113	39	60.9	345	2	Q6RWS5_9ZZZZ	Q6rws5 uncultured
114	39	60.9	358	2	Q535D9_BRARE	Q535d9 brachydanio
115	39	60.9	361	2	Q63LI4_BURPS	Q63li4 burkholderi
116	39	60.9	369	2	Q5HKY8_STAEQ	Q5hky8 staphylococ
117	39	60.9	369	2	Q8CQZ6_STAEP	Q8cqz6 staphylococ
118	39	60.9	371	2	Q8XYQ1_RALSO	Q8xyg1 ralstonia s
119	39	60.9	372	2	Q4L9F6_STAHJ	Q419f6 staphylococ
120	39	60.9	401	2	Q6BV71_DEBHA	Q6bv71 debaryomyce
121	39	60.9	416	2	Q67RF1_SYMTH	Q67rf1 symbiobacte
122	39	60.9	421	2	Q9KN44_VIBCH	Q9kn44 vibrio chol
123	39	60.9	433	2	P73325_SYNY3	P73325 synechocyst
124	39	60.9	476	1	NIFD_SYNP8	Q55029 synechococc
125	39	60.9	501	2	Q5P764_AZOSE	Q5p764 azoarcus sp
126	39	60.9	543	2	Q5M1B3_STRT1	Q5m1b3 streptococc
127	39	60.9	543	2	Q5M5U9_STRT2	Q5m5u9 streptococc
128	39	60.9	549	2	Q67JD5_SYMTH	Q67jd5 symbiobacte
129	39	60.9	559	2	Q969Y0_HUMAN	Q969y0 homo sapien
130	39	60.9	559	2	Q5RCA5_PONPY	Q5rca5 pongo pygma
131	39	60.9	595	2	Q7WTM6_HAEIN	Q7wtm6 haemophilus
132	39	60.9	611	2	Q7LH42_YEAST	Q7lh42 saccharomyc
133	39	60.9	680	2	Q714U6_HAEIN	Q714u6 haemophilus
134	39	60.9	680	2	Q7WTM7_HAEIN	Q7wtm7 haemophilus
135	39	60.9	680	2	Q7WTM9_HAEIN	Q7wtm9 haemophilus
136	39	60.9	680	2	Q7WTN3_HAEIN	Q7wtn3 haemophilus
137	39	60.9	696	2	Q9RP69_PASHA	Q9rp69 pasteurella
138	39	60.9	866	2	Q4MZV1_THEPA	Q4mzv1 theileria p
139	39	60.9	1065	2	Q6FRG4_CANGA	Q6frg4 candida gla
140	39	60.9	1075	2	Q12221_YEAST	Q12221 saccharomyc
141	38.5	60.2	315	2	Q6FVE5_CANGA	Q6fve5 candida gla
142	38.5	60.2	318	2	Q5Z6X3_ORYSA	Q5z6x3 oryza sativ
143	38.5	60.2	455	2	Q6Z0C5_ORYSA	Q6z0c5 oryza sativ
144	38.5	60.2	481	2	Q5VNI2_ORYSA	Q5vni2 oryza sativ
145	38.5	60.2	514	2	Q69TT8_ORYSA	Q69tt8 oryza sativ
146	38.5	60.2	603	2	Q6YTZ2_ORYSA	Q6ytz2 oryza sativ
147	38.5	60.2	650	2	Q53MN5_ORYSA	Q53mn5 oryza sativ
148	38.5	60.2	710	2	Q69Q67_ORYSA	Q69q67 oryza sativ
149	38.5	60.2	720	2	Q6EQM2_ORYSA	Q6eqm2 oryza sativ
150	38.5	60.2	778	2	Q6L2T9_PICTO	Q6l2t9 picrophilus
151	38	59.4	161	2	Q65Z26_CAEEL	Q65z26 caenorhabdi
152	38	59.4	161	2	Q6L8D2_9MAXI	Q6l8d2 tetraclita
153	38	59.4	161	2	Q6SL08_9MAXI	Q6sl08 pollicipes
154	38	59.4	162	2	Q65Z03_9MAXI	Q65z03 megabalanus
155	38	59.4	186	2	Q22461_CAEEL	Q22461 caenorhabdi
156	38	59.4	201	2	Q7R6Y4_PLAYO	Q7r6y4 plasmodium
157	38	59.4	217	2	Q8DTV7_STRMU	Q8dtv7 streptococc
158	38	59.4	226	1	YCKA_BACSU	P42399 bacillus su
159	38	59.4	227	2	Q65NM3_BACLD	Q65nm3 bacillus li
160	38	59.4	251	2	Q8SUY8_ENCCU	Q8suy8 encephalito
161	38	59.4	259	2	Q7YAK3_9VIRI	Q7yak3 chara vulga
162	38	59.4	275	2	Q87BZ3_XYLFT	Q87bz3 xylella fas
163	38	59.4	275	2	Q9PB77_XYLFA	Q9pb77 xylella fas
164	38	59.4	289	1	LGT_CHLTE	Q8kdg0 chlorobium
165	38	59.4	292	1	Y3551_MYCTU	P71850 mycobacteri
166	38	59.4	292	2	Q7TW82_MYCBO	Q7tw82 mycobacteri
167	38	59.4	306	2	Q5A372_CANAL	Q5a372 candida alb
168	38	59.4	310	2	Q8V9Q5_9VIRU	Q8v9q5 sulfolobus
169	38	59.4	318	2	Q9KM43_VIBCH	Q9km43 vibrio chol
170	38	59.4	335	2	Q568J3_BRARE	Q568j3 brachydanio
171	38	59.4	355	2	Q9MLG1_9CARA	Q9mlg1 carabus deh
172	38	59.4	376	2	Q8R9S3_THETN	Q8r9s3 thermoanaer
173	38	59.4	404	2	Q5HNF0_STAEQ	Q5hnf0 staphylococ
174	38	59.4	404	2	Q8CNU7_STAEP	Q8cnu7 staphylococ
175	38	59.4	407	2	Q7PR11_ANOGA	Q7pr11 anopheles g
176	38	59.4	423	2	Q89XA8_BRAJA	Q89xa8 bradyrhizob
177	38	59.4	424	2	O48663_CHLRE	O48663 chlamydomon
178	38	59.4	436	2	Q7RXP6_NEUCR	Q7rxp6 neurospora
179	38	59.4	459	1	DPOG2_MOUSE	Q9qzm2 mus musculu
180	38	59.4	459	2	Q98DN9_RHILO	Q98dn9 rhizobium l
181	38	59.4	465	2	Q75FL6_LEPIC	Q75fl6 leptospira
182	38	59.4	465	2	Q8EXJ8_LEPIN	Q8exj8 leptospira
183	38	59.4	485	1	DPOG2_HUMAN	Q9uhn1 homo sapien
184	38	59.4	485	2	Q96GW2_HUMAN	Q96gw2 homo sapien
185	38	59.4	485	2	Q8XZW9_RALSO	Q8xzw9 ralstonia s
186	38	59.4	497	2	Q6MYG5_ASPFU	Q6myg5 aspergillus
187	38	59.4	520	2	Q8TZ36_METKA	Q8tz36 methanopyru
188	38	59.4	529	2	Q97VA8_SULSO	Q97va8 sulfolobus
189	38	59.4	557	2	Q4WSC9_ASPFU	Q4wsc9 aspergillus
190	38	59.4	557	2	Q5TXJ2_ANOGA	Q5txj2 anopheles g
191	38	59.4	575	2	Q8H405_ORYSA	Q8h405 oryza sativ
192	38	59.4	596	2	Q8SSN6_DICDI	Q8ssn6 dictyosteli
193	38	59.4	621	2	Q7PTT8_ANOGA	Q7ptt8 anopheles g
194	38	59.4	622	2	Q4FQA1_9GAMM	Q4fqa1 psychrobact
195	38	59.4	687	1	CYBC_BRAJA	P51131 bradyrhizob
196	38	59.4	699	2	Q4PFZ3_USTMA	Q4pfz3 ustilago ma
197	38	59.4	740	2	Q5TTK8_ANOGA	Q5ttk8 anopheles g
198	38	59.4	801	2	Q7SEW1_NEUCR	Q7sew1 neurospora
199	38	59.4	850	2	Q52LL2_HUMAN	Q52ll2 homo sapien
200	38	59.4	886	2	Q7QBK1_ANOGA	Q7qbk1 anopheles g
201	38	59.4	936	1	PCDGA_HUMAN	Q9y5h3 homo sapien
202	38	59.4	936	1	PCDGA_PANTR	Q5drc1 pan troglod
203	38	59.4	972	2	Q9AAL8_CAUCR	Q9aal8 caulobacter
204	38	59.4	1057	2	Q751K6_ASHGO	Q751k6 ashbya goss
205	38	59.4	1091	1	JSN1_YEAST	P47135 saccharomyc
206	38	59.4	1094	2	Q6CPC1_KLULA	Q6cpc1 kluyveromyc
207	38	59.4	1163	2	Q7VJD7_HELHP	Q7vjd7 helicobacte
208	38	59.4	1721	2	Q9UAR3_PACLE	Q9uar3 pacifastacu
209	38	59.4	2535	2	Q755B8_ASHGO	Q755b8 ashbya goss
210	37.5	58.6	93	2	Q6LLY7_PHOPR	Q6lly7 photobacter
211	37.5	58.6	456	2	Q847V9_VIBPA	Q847v9 vibrio para
212	37.5	58.6	456	2	Q87I67_VIBPA	Q87i67 vibrio para
213	37.5	58.6	783	2	Q60T21_CAEBR	Q60t21 caenorhabdi
214	37.5	58.6	894	2	Q9U297_CAEEL	Q9u297 caenorhabdi
215	37	57.8	44	2	Q8WNF0_PAPHA	Q8wnf0 papio hamad
216	37	57.8	44	2	Q8WNF1_MACFA	Q8wnf1 macaca fasc
217	37	57.8	44	2	Q8WNF2_CERAE	Q8wnf2 cercopithec
218	37	57.8	78	2	Q9FPD3_9LAMI	Q9fpd3 orobanche c
219	37	57.8	79	2	Q6RT17_9LAMI	Q6rt17 orobanche r
220	37	57.8	97	2	Q4G0G2_HUMAN	Q4g0g2 homo sapien
221	37	57.8	98	2	Q8ZY78_PYRAE	Q8zy78 pyrobaculum
222	37	57.8	100	2	Q5N4F8_SYNP6	Q5n4f8 synechococc
223	37	57.8	105	2	Q89MX6_BRAJA	Q89mx6 bradyrhizob
224	37	57.8	118	2	Q9GLH3_BOVIN	Q9glh3 bos taurus
225	37	57.8	139	2	Q12130_YEAST	Q12130 saccharomyc
226	37	57.8	174	2	O97625_BOVIN	O97625 bos taurus
227	37	57.8	191	2	Q6CE95_YARLI	Q6ce95 yarrowia li
228	37	57.8	224	2	Q7UYU0_RHOBA	Q7uyu0 rhodopirell
229	37	57.8	232	2	Q6ITD5_9TOMB	Q6itd5 beet black
230	37	57.8	232	2	Q8B5R5_9TOMB	Q8b5r5 beet black
231	37	57.8	240	2	Q6QJL3_FAGES	Q6qjl3 fagopyrum e
232	37	57.8	246	2	Q9JRR1_ACTAC	Q9jrr1 actinobacil
233	37	57.8	254	2	Q6FUK2_CANGA	Q6fuk2 candida gla
234	37	57.8	259	2	Q9RL28_STRCO	Q9rl28 streptomyce
235	37	57.8	279	2	Q8ETT4_OCEIH	Q8ett4 oceanobacil
236	37	57.8	281	2	Q54B91_DICDI	Q54b91 dictyosteli
237	37	57.8	291	2	Q87U88_PSESM	Q87u88 pseudomonas
238	37	57.8	313	2	Q7RY71_NEUCR	Q7ry71 neurospora
239	37	57.8	351	2	Q50RC6_ENTHI	Q50rc6 entamoeba h
240	37	57.8	355	2	Q8HDN1_9CARA	Q8hdn1 carabus kim
241	37	57.8	358	2	Q4RU56_TETNG	Q4ru56 tetraodon n
242	37	57.8	367	1	DIAC_RAT	Q01460 rattus norv
243	37	57.8	373	2	Q7KWW8_DICDI	Q7kww8 dictyosteli
244	37	57.8	376	2	O33456_PSEPU	O33456 pseudomonas
245	37	57.8	385	2	Q8T293_DICDI	Q8t293 dictyosteli
246	37	57.8	403	2	Q59RP4_CANAL	Q59rp4 candida alb
247	37	57.8	405	2	Q6N3B2_RHOPA	Q6n3b2 rhodopseudo
248	37	57.8	415	2	Q9I5C8_PSEAE	Q9i5c8 pseudomonas
249	37	57.8	419	2	Q8LJD1_ORYSA	Q8ljd1 oryza sativ
250	37	57.8	420	2	Q5WBW2_BACSK	Q5wbw2 bacillus cl

251	37	57.8	422	2	Q9RCZ6_STRCO	Q9rcz6 streptomyce
252	37	57.8	425	2	Q4NZW7_9DELT	Q4nzw7 anaeromyxob
253	37	57.8	425	2	Q8ENC7_OCEIH	Q8enc7 oceanobacil
254	37	57.8	426	2	Q4V1F9_BACCZ	Q4v1f9 bacillus ce
255	37	57.8	426	2	Q81QB9_BACAN	Q81qb9 bacillus an
256	37	57.8	426	2	Q5NH71_FRATT	Q5nh71 francisella
257	37	57.8	426	2	Q6HIK6_BACHK	Q6hik6 bacillus th
258	37	57.8	426	2	Q63B77_BACCZ	Q63b77 bacillus ce
259	37	57.8	427	2	O64860_ARATH	O64860 arabidopsis
260	37	57.8	428	2	Q7N8J4_PHOLL	Q7n8j4 photorhabdu
261	37	57.8	444	2	Q89RQ3_BRAJA	Q89rq3 bradyrhizob
262	37	57.8	445	2	Q4TRJ9_9SPHN	Q4trj9 erythrobact
263	37	57.8	452	2	Q500J0_PSESY	Q500j0 pseudomonas
264	37	57.8	464	2	Q68YB0_RHOSR	Q68yb0 rhodococcus
265	37	57.8	464	2	Q6REL7_9NOCA	Q6rel7 rhodococcus
266	37	57.8	478	2	Q4KA20_PSEF5	Q4ka20 pseudomonas
267	37	57.8	479	2	Q88Q38_PSEPK	Q88q38 pseudomonas
268	37	57.8	485	2	O83813_TREPA	O83813 treponema p
269	37	57.8	492	2	Q93JT1_NEIME	Q93jt1 neisseria m
270	37	57.8	493	2	Q73KB9_TREDE	Q73kb9 treponema d
271	37	57.8	503	2	Q4I4S5_GIBZE	Q4i4s5 gibberella
272	37	57.8	515	2	Q8YP53_ANASP	Q8yp53 anabaena sp
273	37	57.8	520	1	LNT_PASMU	Q9cm14 pasteurella
274	37	57.8	530	2	Q7UMK7_RHOBA	Q7umk7 rhodopirell
275	37	57.8	544	1	LNT1_TREDE	P61037 treponema d
276	37	57.8	550	2	Q7RTL7_CIOSA	Q7rtl7 ciona savig
277	37	57.8	571	2	Q704A9_THETE	Q704a9 thermoprote
278	37	57.8	578	2	Q6KI68_MYCMO	Q6ki68 mycoplasma
279	37	57.8	585	2	Q7RTL6_CIOIN	Q7rtl6 ciona intes
280	37	57.8	602	2	Q8XMT5_CLOPE	Q8xmt5 clostridium
281	37	57.8	603	2	Q6TVT3_9POXV	Q6tvt3 orf virus.
282	37	57.8	603	2	Q6TW63_9POXV	Q6tw63 orf virus.
283	37	57.8	625	2	Q7W6F8_BORPA	Q7w6f8 bordetella
284	37	57.8	675	2	Q5LJ84_BACFN	Q5lj84 bacteroides
285	37	57.8	675	2	Q650R1_BACFR	Q650r1 bacteroides
286	37	57.8	684	2	Q5P5G5_AZOSE	Q5p5g5 azoarcus sp
287	37	57.8	685	2	Q7VXU8_BORPE	Q7vxu8 bordetella
288	37	57.8	685	2	Q7WIC8_BORBR	Q7wic8 bordetella
289	37	57.8	704	1	LIPM_NEIMA	P57037 neisseria m
290	37	57.8	704	1	LIPM_NEIMB	Q05013 neisseria m
291	37	57.8	712	2	Q66AF9_YERPS	Q66af9 yersinia ps
292	37	57.8	712	2	Q8ZEC6_YERPE	Q8zec6 yersinia pe
293	37	57.8	721	2	Q9L9L3_PASMU	Q9l9l3 pasteurella
294	37	57.8	727	2	Q6A0E8_MOUSE	Q6a0e8 mus musculu
295	37	57.8	731	2	Q6AVK7_ORYSA	Q6avk7 oryza sativ
296	37	57.8	733	2	Q22561_CAEEL	Q22561 caenorhabdi
297	37	57.8	744	2	Q8TJY7_METAC	Q8tjy7 methanosarc
298	37	57.8	748	2	Q7X9T5_LILLO	Q7x9t5 lilium long
299	37	57.8	764	2	P93567_SOLTU	P93567 solanum tub
300	37	57.8	780	2	Q40485_TOBAC	Q40485 nicotiana t
301	37	57.8	795	1	TLR1_MOUSE	Q9epq1 mus musculu
302	37	57.8	795	1	TLR6_MOUSE	Q9epw9 mus musculu
303	37	57.8	804	2	Q9RXW4_DEIRA	Q9rxw4 deinococcus
304	37	57.8	806	2	Q6P690_RAT	Q6p690 rattus norv
305	37	57.8	806	2	Q7TPC5_MOUSE	Q7tpc5 mus musculu
306	37	57.8	903	2	Q9YXD2_9POTY	Q9yxd2 wheat yello
307	37	57.8	904	2	O90734_9POTY	O90734 wheat yello
308	37	57.8	904	2	Q9IWA2_9POTY	Q9iwa2 wheat yello
309	37	57.8	904	2	Q9IWB9_9POTY	Q9iwb9 wheat yello
310	37	57.8	928	2	Q4HR60_CAMUP	Q4hr60 campylobact
311	37	57.8	963	2	Q7VY82_BORPE	Q7vy82 bordetella
312	37	57.8	989	2	Q7W940_BORPA	Q7w940 bordetella
313	37	57.8	989	2	Q7WKI5_BORBR	Q7wki5 bordetella
314	37	57.8	1064	2	Q53TV7_HUMAN	Q53tv7 homo sapien
315	37	57.8	1066	1	PUM2_HUMAN	Q8tb72 homo sapien
316	37	57.8	1066	1	PUM2_MOUSE	Q80u58 mus musculu
317	37	57.8	1182	2	Q4T9U8_TETNG	Q4t9u8 tetraodon n
318	37	57.8	1200	2	Q5TPW6_ANOGA	Q5tpw6 anopheles g
319	37	57.8	1393	2	Q4ID73_GIBZE	Q4id73 gibberella
320	37	57.8	1582	2	Q7KRP6_DROME	Q7krp6 drosophila
321	37	57.8	2101	2	Q4LTH7_9BURK	Q4lth7 burkholderi
322	37	57.8	2993	2	Q8NMS0_CORGL	Q8nms0 corynebacte
323	37	57.8	2996	2	Q6M2X6_CORGL	Q6m2x6 corynebacte
324	37	57.8	4780	2	Q5CRE3_CRYPV	Q5cre3 cryptospori
325	36.5	57.0	71	2	Q9X209_THEMA	Q9x209 thermotoga
326	36.5	57.0	92	2	Q4MKQ7_BACCE	Q4mkq7 bacillus ce
327	36.5	57.0	92	2	Q6HFP2_BACHK	Q6hfp2 bacillus th
328	36.5	57.0	92	2	Q733U0_BACC1	Q733u0 bacillus ce
329	36.5	57.0	92	2	Q637R9_BACCZ	Q637r9 bacillus ce
330	36.5	57.0	92	2	Q81YE1_BACAN	Q81ye1 bacillus an
331	36.5	57.0	309	2	Q600W2_MYCHY	Q600w2 mycoplasma
332	36	56.2	89	2	Q4X7K2_PLACH	Q4x7k2 plasmodium
333	36	56.2	89	2	Q72QX1_LEPIC	Q72qx1 leptospira
334	36	56.2	89	2	Q8F4X0_LEPIN	Q8f4x0 leptospira
335	36	56.2	126	2	P72643_SYNY3	P72643 synechocyst
336	36	56.2	139	2	Q8WYS2_HUMAN	Q8wys2 homo sapien
337	36	56.2	157	2	Q8TYN3_METKA	Q8tyn3 methanopyru
338	36	56.2	158	2	Q8RLY4_LACHE	Q8rly4 lactobacill
339	36	56.2	158	2	Q9KWF0_LACHE	Q9kwf0 lactobacill
340	36	56.2	159	2	Q5FMM8_LACAC	Q5fmm8 lactobacill
341	36	56.2	166	2	Q4FPB0_9RICK	Q4fpb0 candidatus
342	36	56.2	180	2	Q5ZD39_ORYSA	Q5zd39 oryza sativ
343	36	56.2	186	2	Q6MKP7_BDEBA	Q6mkp7 bdellovibri
344	36	56.2	190	2	O42940_SCHPO	O42940 schizosacch
345	36	56.2	190	2	Q9KZ84_STRCO	Q9kz84 streptomyce
346	36	56.2	197	2	Q50U70_ENTHI	Q50u70 entamoeba h
347	36	56.2	199	2	Q88BI5_PSESM	Q88bi5 pseudomonas
348	36	56.2	208	2	Q5LCH8_BACFN	Q5lch8 bacteroides
349	36	56.2	208	2	Q64TM5_BACFR	Q64tm5 bacteroides
350	36	56.2	208	2	Q8FGZ0_ECOL6	Q8fgz0 escherichia
351	36	56.2	212	2	Q91TR8_TUHV1	Q91tr8 tupaiid her
352	36	56.2	214	2	Q97PF2_STRPN	Q97pf2 streptococc
353	36	56.2	215	2	Q6FMZ2_CANGA	Q6fmz2 candida gla
354	36	56.2	220	2	Q5B6I1_EMENI	Q5b6i1 aspergillus
355	36	56.2	220	2	Q4WP34_ASPFU	Q4wp34 aspergillus
356	36	56.2	226	2	Q8WZY0_NEUCR	Q8wzy0 neurospora
357	36	56.2	230	2	Q5N8J1_ORYSA	Q5n8j1 oryza sativ
358	36	56.2	236	2	Q7RWI4_NEUCR	Q7rwi4 neurospora
359	36	56.2	236	2	Q527C5_MAGGR	Q527c5 magnaporthe
360	36	56.2	239	2	Q5XG75_HUMAN	Q5xg75 homo sapien
361	36	56.2	241	2	Q6TDF3_9RHIZ	Q6tdf3 roseomonas
362	36	56.2	241	2	Q6TDF4_9RHIZ	Q6tdf4 roseomonas
363	36	56.2	241	2	Q6TDF5_9RHIZ	Q6tdf5 roseomonas
364	36	56.2	241	2	Q6TDF6_9PROT	Q6tdf6 azospirillu
365	36	56.2	242	2	Q7PBR4_RICSI	Q7pbr4 rickettsia
366	36	56.2	242	2	Q92I68_RICCN	Q92i68 rickettsia
367	36	56.2	247	1	RHIR_RHILV	Q03316 rhizobium l
368	36	56.2	247	2	Q5YZ76_NOCFA	Q5yz76 nocardia fa
369	36	56.2	248	2	Q4ZM30_PSESY	Q4zm30 pseudomonas
370	36	56.2	248	2	Q88AH9_PSESM	Q88ah9 pseudomonas
371	36	56.2	249	2	Q8FQT7_COREF	Q8fqt7 corynebacte
372	36	56.2	253	2	Q5X2P9_LEGPA	Q5x2p9 legionella
373	36	56.2	253	2	Q5ZWP2_LEGPH	Q5zwp2 legionella
374	36	56.2	258	2	Q5I369_9RETR	Q5i369 equine infe
375	36	56.2	261	2	Q74EM0_GEOSL	Q74em0 geobacter s
376	36	56.2	267	2	Q4MLU4_BACCE	Q4mlu4 bacillus ce
377	36	56.2	267	2	Q81JM6_BACAN	Q81jm6 bacillus an
378	36	56.2	268	2	Q89GH1_BRAJA	Q89gh1 bradyrhizob
379	36	56.2	273	2	Q6HQ70_BACAN	Q6hq70 bacillus an
380	36	56.2	273	2	Q630H4_BACCZ	Q630h4 bacillus ce
381	36	56.2	274	2	Q42937_NICPL	Q42937 nicotiana p
382	36	56.2	275	2	Q4HS44_CAMUP	Q4hs44 campylobact
383	36	56.2	281	2	Q568X0_BRARE	Q568x0 brachydanio
384	36	56.2	282	2	Q4HIF5_CAMCO	Q4hif5 campylobact
385	36	56.2	282	2	Q5HUU0_CAMJR	Q5huu0 campylobact
386	36	56.2	282	2	Q9PP67_CAMJE	Q9pp67 campylobact
387	36	56.2	283	2	Q9BG86_RABIT	Q9bg86 oryctolagus
388	36	56.2	287	1	LEP4_LEGPN	O68433 legionella
389	36	56.2	287	2	Q5WWF1_LEGPL	Q5wwf1 legionella
390	36	56.2	287	2	Q5X539_LEGPA	Q5x539 legionella
391	36	56.2	288	2	Q4Y873_PLACH	Q4y873 plasmodium
392	36	56.2	289	2	Q4YVE5_PLABE	Q4yve5 plasmodium
393	36	56.2	289	2	Q5ZVB6_LEGPH	Q5zvb6 legionella
394	36	56.2	292	1	SFRP2_CHICK	Q9ia96 gallus gall
395	36	56.2	292	2	Q4J8R8_SULAC	Q4j8r8 sulfolobus
396	36	56.2	292	2	Q4ULU6_RICFE	Q4ulu6 rickettsia

397	36	56.2	292	2	Q97MV4_CLOAB	Q97mv4	clostridium
398	36	56.2	293	2	Q743S6_MYCPA	Q743s6	mycobacteri
399	36	56.2	294	1	SFRP2_CANFA	Q863h1	canis famil
400	36	56.2	294	2	Q5VX51_HUMAN	Q5vx51	homo sapien
401	36	56.2	294	2	Q6FFJ6_ACIAD	Q6ffj6	acinetobact
402	36	56.2	295	1	SFRP2_HUMAN	Q96hf1	homo sapien
403	36	56.2	295	1	SFRP2_MOUSE	P97299	mus musculu
404	36	56.2	295	2	Q4SS00_TETNG	Q4ss00	tetraodon n
405	36	56.2	295	2	Q6P8B8_XENTR	Q6p8b8	xenopus tro
406	36	56.2	296	2	Q7T2K9_BRARE	Q7t2k9	brachydanio
407	36	56.2	298	2	Q61336_MOUSE	Q61336	mus musculu
408	36	56.2	298	2	Q7ZXM6_XENLA	Q7zxm6	xenopus lae
409	36	56.2	299	2	Q4SPF4_TETNG	Q4spf4	tetraodon n
410	36	56.2	300	2	Q6N3A7_RHOPA	Q6n3a7	rhodopseudo
411	36	56.2	306	2	Q5TJB2_9VIRU	Q5tjb2	sulfolobus
412	36	56.2	306	2	Q8QL48_9VIRU	Q8ql48	sulfolobus
413	36	56.2	306	2	Q6GZK1_ORYLA	Q6gzk1	oryzias lat
414	36	56.2	309	2	O85832_SPHAR	O85832	sphingomona
415	36	56.2	312	2	Q8YLD4_ANASP	Q8yld4	anabaena sp
416	36	56.2	313	2	Q8VG26_MOUSE	Q8vg26	mus musculu
417	36	56.2	315	2	Q42935_NICPL	Q42935	nicotiana p
418	36	56.2	315	2	Q42936_NICPL	Q42936	nicotiana p
419	36	56.2	318	2	P95279_MYCTU	P95279	mycobacteri
420	36	56.2	318	2	Q83XB5_MYCBO	Q83xb5	mycobacteri
421	36	56.2	322	2	Q6C3E2_YARLI	Q6c3e2	yarrowia li
422	36	56.2	332	2	Q89GW1_BRAJA	Q89gw1	bradyrhizob
423	36	56.2	338	2	Q687Z4_ACIRA	Q687z4	acinetobact
424	36	56.2	339	2	Q5XY07_9CARA	Q5xy07	pamborus el
425	36	56.2	339	2	Q5XY08_9CARA	Q5xy08	pamborus el
426	36	56.2	339	2	Q5XY10_9CARA	Q5xy10	pamborus al
427	36	56.2	339	2	Q5XY23_9CARA	Q5xy23	pamborus al
428	36	56.2	339	2	Q5XY24_9CARA	Q5xy24	pamborus al
429	36	56.2	339	2	Q5XY35_9CARA	Q5xy35	pamborus al
430	36	56.2	339	2	Q5XY37_9CARA	Q5xy37	pamborus al
431	36	56.2	339	2	Q5XY41_9CARA	Q5xy41	pamborus al
432	36	56.2	339	2	Q5XY51_9CARA	Q5xy51	pamborus al
433	36	56.2	339	2	Q5XY52_9CARA	Q5xy52	pamborus vi
434	36	56.2	339	2	Q5XY55_9CARA	Q5xy55	pamborus vi
435	36	56.2	339	2	Q5XY57_9CARA	Q5xy57	pamborus tr
436	36	56.2	339	2	Q5XY67_9CARA	Q5xy67	pamborus tr
437	36	56.2	339	2	Q5XY70_9CARA	Q5xy70	pamborus op
438	36	56.2	339	2	Q5XY72_9CARA	Q5xy72	pamborus op
439	36	56.2	339	2	Q5XY76_9CARA	Q5xy76	pamborus op
440	36	56.2	339	2	Q5XY84_9CARA	Q5xy84	pamborus op
441	36	56.2	339	2	Q5XY92_9CARA	Q5xy92	pamborus su
442	36	56.2	339	2	Q5XY95_9CARA	Q5xy95	pamborus su
443	36	56.2	339	2	Q5XYA5_9CARA	Q5xya5	pamborus su
444	36	56.2	339	2	Q5XYB2_9CARA	Q5xyb2	pamborus br
445	36	56.2	339	2	Q5XYB7_9CARA	Q5xyb7	pamborus su
446	36	56.2	339	2	Q5XYB9_9CARA	Q5xyb9	pamborus pu
447	36	56.2	339	2	Q5XYC0_9CARA	Q5xyc0	pamborus gu
448	36	56.2	339	2	Q5XYC2_9CARA	Q5xyc2	pamborus pr
449	36	56.2	339	2	Q5XYC5_9CARA	Q5xyc5	pamborus pr
450	36	56.2	339	2	Q5XYC6_9CARA	Q5xyc6	pamborus pr
451	36	56.2	339	2	Q5XYC8_9CARA	Q5xyc8	pamborus pr
452	36	56.2	339	2	Q5XYC9_9CARA	Q5xyc9	pamborus pr
453	36	56.2	339	2	Q5XYD0_9CARA	Q5xyd0	pamborus ma
454	36	56.2	339	2	Q5XYD1_9CARA	Q5xyd1	pamborus ma
455	36	56.2	339	2	Q5XYD2_9CARA	Q5xyd2	pamborus ma
456	36	56.2	339	2	Q5XYD3_9CARA	Q5xyd3	pamborus ma
457	36	56.2	339	2	Q5XYD5_9CARA	Q5xyd5	pamborus tr
458	36	56.2	339	2	Q5XYD6_9CARA	Q5xyd6	pamborus tr
459	36	56.2	339	2	Q5XYD7_9CARA	Q5xyd7	pamborus tr
460	36	56.2	339	2	Q5XYD8_9CARA	Q5xyd8	pamborus vi
461	36	56.2	339	2	Q5XYE0_9CARA	Q5xye0	pamborus vi
462	36	56.2	339	2	Q5XYE2_9CARA	Q5xye2	pamborus vi
463	36	56.2	339	2	Q5XYE3_9CARA	Q5xye3	maoripambor
464	36	56.2	339	2	Q4LEV5_9CARA	Q4lev5	carabus arr
465	36	56.2	339	2	Q4LEV8_9CARA	Q4lev8	carabus arr
466	36	56.2	339	2	Q4LEV9_9CARA	Q4lev9	carabus arr
467	36	56.2	339	2	Q4LEW1_9CARA	Q4lew1	carabus ins
468	36	56.2	339	2	Q4LEW2_9CARA	Q4lew2	carabus ins
469	36	56.2	342	2	Q9ML22_9CARA	Q9ml22	carabus ins
470	36	56.2	342	2	Q7UZ77_RHOBA	Q7uz77	rhodopirell
471	36	56.2	347	2	Q5JFL9_PYRKO	Q5jfl9	pyrococcus
472	36	56.2	348	2	Q9ML24_9CARA	Q9ml24	carabus ins
473	36	56.2	349	2	Q9MDE3_9CARA	Q9mde3	carabus esa
474	36	56.2	349	2	Q9MKX8_9CARA	Q9mkx8	carabus esa
475	36	56.2	349	2	Q9MKX9_9CARA	Q9mkx9	carabus esa
476	36	56.2	349	2	Q9MKY1_9CARA	Q9mky1	carabus esa
477	36	56.2	349	2	Q9MKY3_9CARA	Q9mky3	carabus esa
478	36	56.2	349	2	Q9MKY5_9CARA	Q9mky5	carabus esa
479	36	56.2	349	2	Q9ML00_9CARA	Q9ml00	carabus arr
480	36	56.2	349	2	Q9ML01_9CARA	Q9ml01	carabus arr
481	36	56.2	349	2	Q9ML05_9CARA	Q9ml05	carabus ins
482	36	56.2	349	2	Q9ML18_9CARA	Q9ml18	carabus ins
483	36	56.2	349	2	Q9ML25_9CARA	Q9ml25	carabus ins
484	36	56.2	349	2	Q9ML26_9CARA	Q9ml26	carabus ins
485	36	56.2	349	2	Q9ML31_9CARA	Q9ml31	carabus ins
486	36	56.2	349	2	Q9ML33_9CARA	Q9ml33	carabus ins
487	36	56.2	349	2	Q9ML37_9CARA	Q9ml37	carabus ins
488	36	56.2	350	1	LASS1_HUMAN	P27544	homo sapien
489	36	56.2	350	2	Q8IDV3_PLAF7	Q8idv3	plasmodium
490	36	56.2	350	2	Q9ME84_9CARA	Q9me84	carabus ins
491	36	56.2	351	2	Q9ME82_9CARA	Q9me82	carabus ins
492	36	56.2	351	2	Q9MKY0_9CARA	Q9mky0	carabus esa
493	36	56.2	351	2	Q9ML35_9CARA	Q9ml35	carabus ins
494	36	56.2	351	2	Q9MLE3_9CARA	Q9mle3	carabus arr
495	36	56.2	352	1	YORM_TTV1	P19297	thermoprote
496	36	56.2	352	2	Q9ML04_9CARA	Q9ml04	carabus ins
497	36	56.2	353	2	Q9MEE2_9CARA	Q9mee2	carabus ins
498	36	56.2	353	2	Q9ML16_9CARA	Q9ml16	carabus ins
499	36	56.2	353	2	Q9ML32_9CARA	Q9ml32	carabus ins
500	36	56.2	353	2	Q9ML36_9CARA	Q9ml36	carabus ins
501	36	56.2	355	2	O47480_9CARA	O47480	cychropsis
502	36	56.2	355	2	O47481_9CARA	O47481	cychrus thi
503	36	56.2	355	2	O47482_9CARA	O47482	cychrus zho
504	36	56.2	355	2	O47483_9CARA	O47483	cychrus oka
505	36	56.2	355	2	O47484_9CARA	O47484	carabus vir
506	36	56.2	355	2	O47485_9CARA	O47485	carabus cra
507	36	56.2	355	2	O78724_9CARA	O78724	carabus bla
508	36	56.2	355	2	O79572_9CARA	O79572	carabus put
509	36	56.2	355	2	O79573_9CARA	O79573	carabus fai
510	36	56.2	355	2	O79574_9CARA	O79574	carabus put
511	36	56.2	355	2	O79575_9CARA	O79575	carabus put
512	36	56.2	355	2	O79576_9CARA	O79576	carabus put
513	36	56.2	355	2	O79577_9CARA	O79577	carabus con
514	36	56.2	355	2	O79578_CARSY	O79578	carabus syl
515	36	56.2	355	2	O79579_9CARA	O79579	carabus cri
516	36	56.2	355	2	O79580_9CARA	O79580	carabus cri
517	36	56.2	355	2	O79581_9CARA	O79581	carabus por
518	36	56.2	355	2	O79583_CARGL	O79583	carabus gla
519	36	56.2	355	2	O79584_9CARA	O79584	carabus lin
520	36	56.2	355	2	O79585_9CARA	O79585	carabus tit
521	36	56.2	355	2	O79586_9CARA	O79586	carabus sui
522	36	56.2	355	2	O79587_9CARA	O79587	carabus lat
523	36	56.2	355	2	O79588_9CARA	O79588	carabus pus
524	36	56.2	355	2	O79589_9CARA	O79589	carabus lat
525	36	56.2	355	2	O79978_9CARA	O79978	carabus fai
526	36	56.2	355	2	O80027_9CARA	O80027	carabus put
527	36	56.2	355	2	O99052_9CARA	O99052	carabus por
528	36	56.2	355	2	O99053_9CARA	O99053	carabus por
529	36	56.2	355	2	O99054_9CARA	O99054	carabus por
530	36	56.2	355	2	Q37388_9CARA	Q37388	carabus geh
531	36	56.2	355	2	Q37389_9CARA	Q37389	carabus geh
532	36	56.2	355	2	Q37391_9CARA	Q37391	carabus kur
533	36	56.2	355	2	Q37409_CAROP	Q37409	carabus opa
534	36	56.2	355	2	Q37421_CARAR	Q37421	carabus arv
535	36	56.2	355	2	Q37422_9CARA	Q37422	carabus aur
536	36	56.2	355	2	Q37423_9CARA	Q37423	carabus aur
537	36	56.2	355	2	Q37425_9CARA	Q37425	campalita c
538	36	56.2	355	2	Q37426_9CARA	Q37426	carabus con
539	36	56.2	355	2	Q37427_CARCI	Q37427	carabus cor
540	36	56.2	355	2	Q37428_9CARA	Q37428	carabus fru
541	36	56.2	355	2	Q37431_CALIN	Q37431	calosoma in
542	36	56.2	355	2	Q37432_9CARA	Q37432	carabus int

543	36	56.2	355	2	Q37433_9CARA	Q37433 cychrus mor
544	36	56.2	355	2	Q37436_CARNE	Q37436 carabus nem
545	36	56.2	355	2	Q37437_CARPR	Q37437 carabus pro
546	36	56.2	355	2	Q37441_9CARA	Q37441 carabus van
547	36	56.2	355	2	Q37442_9CARA	Q37442 carabus vio
548	36	56.2	355	2	Q37443_9CARA	Q37443 carabus bla
549	36	56.2	355	2	Q37444_9CARA	Q37444 carabus bla
550	36	56.2	355	2	Q37445_9CARA	Q37445 carabus bla
551	36	56.2	355	2	Q37446_9CARA	Q37446 carabus bla
552	36	56.2	355	2	Q37447_9CARA	Q37447 carabus bla
553	36	56.2	355	2	Q37448_9CARA	Q37448 carabus bla
554	36	56.2	355	2	Q37449_9CARA	Q37449 carabus bla
555	36	56.2	355	2	Q37453_9CARA	Q37453 carabus bla
556	36	56.2	355	2	Q37454_9CARA	Q37454 carabus bla
557	36	56.2	355	2	Q37457_9CARA	Q37457 carabus bla
558	36	56.2	355	2	Q37459_9CARA	Q37459 carabus bla
559	36	56.2	355	2	Q37465_9CARA	Q37465 carabus por
560	36	56.2	355	2	Q37518_9CARA	Q37518 carabus mae
561	36	56.2	355	2	Q37528_9CARA	Q37528 carabus tub
562	36	56.2	355	2	Q37536_9CARA	Q37536 carabus arb
563	36	56.2	355	2	Q37540_9CARA	Q37540 carabus kyu
564	36	56.2	355	2	Q37542_9CARA	Q37542 carabus maa
565	36	56.2	355	2	Q37543_9CARA	Q37543 carabus pro
566	36	56.2	355	2	Q37559_9CARA	Q37559 carabus arr
567	36	56.2	355	2	Q37560_9CARA	Q37560 carabus arr
568	36	56.2	355	2	Q37561_9CARA	Q37561 carabus arr
569	36	56.2	355	2	Q37562_9CARA	Q37562 carabus arr
570	36	56.2	355	2	Q37563_9CARA	Q37563 carabus arr
571	36	56.2	355	2	Q37564_9CARA	Q37564 carabus alb
572	36	56.2	355	2	Q37566_9CARA	Q37566 carabus deh
573	36	56.2	355	2	Q37567_9CARA	Q37567 carabus deh
574	36	56.2	355	2	Q37568_9CARA	Q37568 carabus deh
575	36	56.2	355	2	Q37569_9CARA	Q37569 carabus deh
576	36	56.2	355	2	Q37571_9CARA	Q37571 carabus deh
577	36	56.2	355	2	Q37572_9CARA	Q37572 carabus deh
578	36	56.2	355	2	Q37573_9CARA	Q37573 carabus deh
579	36	56.2	355	2	Q37574_9CARA	Q37574 carabus esa
580	36	56.2	355	2	Q37575_9CARA	Q37575 carabus iwa
581	36	56.2	355	2	Q37576_9CARA	Q37576 carabus ins
582	36	56.2	355	2	Q37577_9CARA	Q37577 carabus iwa
583	36	56.2	355	2	Q37578_9CARA	Q37578 carabus lew
584	36	56.2	355	2	Q37580_9CARA	Q37580 carabus mai
585	36	56.2	355	2	Q37581_9CARA	Q37581 carabus mai
586	36	56.2	355	2	Q37582_9CARA	Q37582 carabus shi
587	36	56.2	355	2	Q37583_9CARA	Q37583 carabus uen
588	36	56.2	355	2	Q37586_9CARA	Q37586 carabus yam
589	36	56.2	355	2	Q37587_9CARA	Q37587 carabus yac
590	36	56.2	355	2	Q37588_9CARA	Q37588 carabus yac
591	36	56.2	355	2	Q37589_9CARA	Q37589 carabus yac
592	36	56.2	355	2	Q37597_9CARA	Q37597 carabus har
593	36	56.2	355	2	Q37599_9CARA	Q37599 carabus kol
594	36	56.2	355	2	Q37767_9CARA	Q37767 carabus jap
595	36	56.2	355	2	Q6BBS4_9CARA	Q6bbs4 calosoma sy
596	36	56.2	355	2	Q6BBT3_9CARA	Q6bbt3 calosoma ma
597	36	56.2	355	2	Q6BBT5_9CARA	Q6bbt5 calosoma ma
598	36	56.2	355	2	Q6BBT9_9CARA	Q6bbt9 calosoma fr
599	36	56.2	355	2	Q6BBU1_9CARA	Q6bbu1 australodre
600	36	56.2	355	2	Q6BBU3_9CARA	Q6bbu3 australodre
601	36	56.2	355	2	Q6BBU5_9CARA	Q6bbu5 camedula le
602	36	56.2	355	2	Q6BBV8_9CARA	Q6bbv8 campalita c
603	36	56.2	355	2	Q6BBW2_9CARA	Q6bbw2 campalita c
604	36	56.2	355	2	Q6BBW4_9CARA	Q6bbw4 campalita d
605	36	56.2	355	2	Q6BBW7_9CARA	Q6bbw7 campalita a
606	36	56.2	355	2	Q6BBW9_9CARA	Q6bbw9 carabomorph
607	36	56.2	355	2	Q6BBX1_9CARA	Q6bbx1 charmosta l
608	36	56.2	355	2	Q6BBX3_9CARA	Q6bbx3 camedula an
609	36	56.2	355	2	Q6BBX5_9CARA	Q6bbx5 camedula an
610	36	56.2	355	2	Q6BBX7_9CARA	Q6bbx7 camedula pe
611	36	56.2	355	2	Q6BBY1_9CARA	Q6bby1 camedula ha
612	36	56.2	355	2	Q6BBY3_9CARA	Q6bby3 callisthene
613	36	56.2	355	2	Q6BBY6_9CARA	Q6bby6 callisthene
614	36	56.2	355	2	Q6BBY8_9CARA	Q6bby8 microcallis
615	36	56.2	355	2	Q6BBZ0_9CARA	Q6bbz0 callitropa
616	36	56.2	355	2	Q6BBZ2_9CARA	Q6bbz2 chrysostigm
617	36	56.2	355	2	Q6BBZ4_9CARA	Q6bbz4 carabomimus
618	36	56.2	355	2	Q6BBZ6_9CARA	Q6bbz6 carabomimus
619	36	56.2	355	2	Q6BBZ8_9CARA	Q6bbz8 carabomimus
620	36	56.2	355	2	Q6BC01_9CARA	Q6bc01 callitropa
621	36	56.2	355	2	Q6BC03_CALIN	Q6bc03 calosoma in
622	36	56.2	355	2	Q6BC07_CALIN	Q6bc07 calosoma in
623	36	56.2	355	2	Q6BC10_CALIN	Q6bc10 calosoma in
624	36	56.2	355	2	Q6BC12_CALIN	Q6bc12 calosoma in
625	36	56.2	355	2	Q6BC14_9CARA	Q6bc14 calodrepa s
626	36	56.2	355	2	Q6BC16_9CARA	Q6bc16 calodrepa s
627	36	56.2	355	2	Q6BC18_9CARA	Q6bc18 calodrepa s
628	36	56.2	355	2	Q6BC20_9CARA	Q6bc20 castrida sa
629	36	56.2	355	2	Q6BC23_9CARA	Q6bc23 castrida sa
630	36	56.2	355	2	Q6BC25_9CARA	Q6bc25 castrida al
631	36	56.2	355	2	Q6BC27_9CARA	Q6bc27 castrida fu
632	36	56.2	355	2	Q7GIL6_9CARA	Q7gil6 carabus jap
633	36	56.2	355	2	Q85AK9_9CARA	Q85ak9 carabus gal
634	36	56.2	355	2	Q85AL3_9CARA	Q85al3 carabus con
635	36	56.2	355	2	Q85AM0_9CARA	Q85am0 carabus sta
636	36	56.2	355	2	Q85AQ9_9CARA	Q85aq9 carabus sov
637	36	56.2	355	2	Q85AR5_9CARA	Q85ar5 carabus kas
638	36	56.2	355	2	Q85B37_CARCI	Q85b37 carabus cor
639	36	56.2	355	2	Q85B92_CARCI	Q85b92 carabus cor
640	36	56.2	355	2	Q85BA4_9CARA	Q85ba4 carabus cha
641	36	56.2	355	2	Q85BD7_9CARA	Q85bd7 carabus hey
642	36	56.2	355	2	Q85BJ8_9CARA	Q85bj8 carabus con
643	36	56.2	355	2	Q85BQ2_9CARA	Q85bq2 carabus cic
644	36	56.2	355	2	Q85BQ5_9CARA	Q85bq5 carabus bon
645	36	56.2	355	2	Q85C29_9CARA	Q85c29 carabus agn
646	36	56.2	355	2	Q85C81_9CARA	Q85c81 carabus vio
647	36	56.2	355	2	Q85GD7_9CARA	Q85gd7 pamborus op
648	36	56.2	355	2	Q85GD8_9CARA	Q85gd8 scaphinotus
649	36	56.2	355	2	Q85GL4_9CARA	Q85gl4 carabus sma
650	36	56.2	355	2	Q85GL5_9CARA	Q85gl5 carabus sma
651	36	56.2	355	2	Q85GL6_9CARA	Q85gl6 carabus kub
652	36	56.2	355	2	Q85GL7_9CARA	Q85gl7 carabus for
653	36	56.2	355	2	Q85GL8_9CARA	Q85gl8 carabus jan
654	36	56.2	355	2	Q85GL9_9CARA	Q85gl9 carabus osa
655	36	56.2	355	2	Q85GN0_9CARA	Q85gn0 carabus lam
656	36	56.2	355	2	Q85GN1_9CARA	Q85gn1 carabus cra
657	36	56.2	355	2	Q85GN2_9CARA	Q85gn2 carabus cra
658	36	56.2	355	2	Q85GN3_9CARA	Q85gn3 carabus vir
659	36	56.2	355	2	Q85GN4_9CARA	Q85gn4 carabus vir
660	36	56.2	355	2	Q85GN5_9CARA	Q85gn5 carabus sun
661	36	56.2	355	2	Q85GN8_9CARA	Q85gn8 carabus bur
662	36	56.2	355	2	Q85GN9_9CARA	Q85gn9 carabus tal
663	36	56.2	355	2	Q85GP0_9CARA	Q85gp0 carabus tur
664	36	56.2	355	2	Q85GP1_9CARA	Q85gp1 carabus tur
665	36	56.2	355	2	Q85GP2_9CARA	Q85gp2 carabus mer
666	36	56.2	355	2	Q85GP3_9CARA	Q85gp3 carabus kau
667	36	56.2	355	2	Q85GP4_9CARA	Q85gp4 carabus kau
668	36	56.2	355	2	Q85GP5_9CARA	Q85gp5 carabus pup
669	36	56.2	355	2	Q85GP6_9CARA	Q85gp6 carabus pup
670	36	56.2	355	2	Q85GP7_9CARA	Q85gp7 carabus pup
671	36	56.2	355	2	Q85GP8_9CARA	Q85gp8 carabus sol
672	36	56.2	355	2	Q85GP9_9CARA	Q85gp9 carabus sol
673	36	56.2	355	2	Q85GQ0_9CARA	Q85gq0 carabus bal
674	36	56.2	355	2	Q85GQ1_9CARA	Q85gq1 carabus pet
675	36	56.2	355	2	Q85GQ2_9CARA	Q85gq2 carabus sta
676	36	56.2	355	2	Q85GQ3_9CARA	Q85gq3 carabus eou
677	36	56.2	355	2	Q85GQ4_9CARA	Q85gq4 carabus eou
678	36	56.2	355	2	Q85GQ5_9CARA	Q85gq5 carabus eou
679	36	56.2	355	2	Q85GQ6_9CARA	Q85gq6 carabus val
680	36	56.2	355	2	Q85GQ7_9CARA	Q85gq7 carabus cic
681	36	56.2	355	2	Q85GQ8_9CARA	Q85gq8 carabus cic
682	36	56.2	355	2	Q85GQ9_9CARA	Q85gq9 carabus cic
683	36	56.2	355	2	Q85GR0_9CARA	Q85gr0 carabus aki
684	36	56.2	355	2	Q85GR1_9CARA	Q85gr1 carabus aki
685	36	56.2	355	2	Q85GR2_9CARA	Q85gr2 carabus aki
686	36	56.2	355	2	Q85GR3_9CARA	Q85gr3 carabus aki
687	36	56.2	355	2	Q85GR4_9CARA	Q85gr4 carabus aki
688	36	56.2	355	2	Q85GR5_9CARA	Q85gr5 carabus aki

689	36	56.2	355	2	Q85GR6_9CARA	Q85gr6 carabus jac
690	36	56.2	355	2	Q85GR7_9CARA	Q85gr7 carabus aki
691	36	56.2	355	2	Q85GR8_9CARA	Q85gr8 carabus jac
692	36	56.2	355	2	Q85GR9_9CARA	Q85gr9 carabus hie
693	36	56.2	355	2	Q85GS0_9CARA	Q85gs0 carabus bra
694	36	56.2	355	2	Q85GS1_9CARA	Q85gs1 carabus tur
695	36	56.2	355	2	Q85GS2_9CARA	Q85gs2 carabus bra
696	36	56.2	355	2	Q85GS3_9CARA	Q85gs3 carabus kau
697	36	56.2	355	2	Q85GS4_9CARA	Q85gs4 carabus pun
698	36	56.2	355	2	Q85GS5_9CARA	Q85gs5 carabus mul
699	36	56.2	355	2	Q85GS6_9CARA	Q85gs6 carabus imp
700	36	56.2	355	2	Q85GS7_9CARA	Q85gs7 carabus hem
701	36	56.2	355	2	Q85GS8_9CARA	Q85gs8 carabus mul
702	36	56.2	355	2	Q85GS9_9CARA	Q85gs9 carabus mul
703	36	56.2	355	2	Q85GT0_9CARA	Q85gt0 carabus syr
704	36	56.2	355	2	Q85GT1_9CARA	Q85gt1 carabus pio
705	36	56.2	355	2	Q85GT2_9CARA	Q85gt2 carabus pio
706	36	56.2	355	2	Q85GT3_9CARA	Q85gt3 carabus sap
707	36	56.2	355	2	Q85GT4_9CARA	Q85gt4 carabus sap
708	36	56.2	355	2	Q85GT5_9CARA	Q85gt5 carabus tor
709	36	56.2	355	2	Q85GT6_9CARA	Q85gt6 carabus ere
710	36	56.2	355	2	Q85GT7_9CARA	Q85gt7 carabus nor
711	36	56.2	355	2	Q85GT8_9CARA	Q85gt8 carabus nor
712	36	56.2	355	2	Q85GT9_9CARA	Q85gt9 carabus tor
713	36	56.2	355	2	Q85GU0_9CARA	Q85gu0 carabus tor
714	36	56.2	355	2	Q85GU1_9CARA	Q85gu1 carabus tor
715	36	56.2	355	2	Q85GU2_9CARA	Q85gu2 carabus cha
716	36	56.2	355	2	Q85GU3_9CARA	Q85gu3 carabus tor
717	36	56.2	355	2	Q85GU4_9CARA	Q85gu4 carabus pra
718	36	56.2	355	2	Q85GU5_9CARA	Q85gu5 carabus tal
719	36	56.2	355	2	Q85GU6_9CARA	Q85gu6 carabus tal
720	36	56.2	355	2	Q85GU7_CARCI	Q85gu7 carabus cor
721	36	56.2	355	2	Q85GU8_CARCI	Q85gu8 carabus cor
722	36	56.2	355	2	Q85GU9_9CARA	Q85gu9 carabus pun
723	36	56.2	355	2	Q85GV0_9CARA	Q85gv0 carabus pun
724	36	56.2	355	2	Q85GV1_9CARA	Q85gv1 carabus che
725	36	56.2	355	2	Q85GV2_9CARA	Q85gv2 carabus che
726	36	56.2	355	2	Q85GV3_9CARA	Q85gv3 carabus che
727	36	56.2	355	2	Q85GV4_9CARA	Q85gv4 carabus che
728	36	56.2	355	2	Q85GV5_9CARA	Q85gv5 carabus che
729	36	56.2	355	2	Q85GV6_9CARA	Q85gv6 carabus per
730	36	56.2	355	2	Q85GV7_9CARA	Q85gv7 carabus per
731	36	56.2	355	2	Q85GV8_9CARA	Q85gv8 carabus per
732	36	56.2	355	2	Q85GV9_9CARA	Q85gv9 carabus str
733	36	56.2	355	2	Q85GW0_9CARA	Q85gw0 carabus sca
734	36	56.2	355	2	Q85GW1_9CARA	Q85gw1 carabus sca
735	36	56.2	355	2	Q85GW2_9CARA	Q85gw2 carabus sca
736	36	56.2	355	2	Q85GW3_9CARA	Q85gw3 carabus sca
737	36	56.2	355	2	Q85GW4_9CARA	Q85gw4 carabus gig
738	36	56.2	355	2	Q85GW5_9CARA	Q85gw5 carabus ger
739	36	56.2	355	2	Q85GW6_9CARA	Q85gw6 carabus vio
740	36	56.2	355	2	Q85GW7_9CARA	Q85gw7 carabus vio
741	36	56.2	355	2	Q85GW8_9CARA	Q85gw8 carabus vio
742	36	56.2	355	2	Q85GW9_9CARA	Q85gw9 carabus vio
743	36	56.2	355	2	Q85GX0_9CARA	Q85gx0 carabus vio
744	36	56.2	355	2	Q85GX1_9CARA	Q85gx1 carabus erm
745	36	56.2	355	2	Q85GX2_9CARA	Q85gx2 carabus lea
746	36	56.2	355	2	Q85GX3_9CARA	Q85gx3 carabus vie
747	36	56.2	355	2	Q85GX4_9CARA	Q85gx4 carabus vie
748	36	56.2	355	2	Q85GX5_9CARA	Q85gx5 carabus sch
749	36	56.2	355	2	Q85GX6_9CARA	Q85gx6 carabus sch
750	36	56.2	355	2	Q85GX7_9CARA	Q85gx7 carabus sch
751	36	56.2	355	2	Q85GX8_9CARA	Q85gx8 carabus imp
752	36	56.2	355	2	Q85GX9_9CARA	Q85gx9 carabus sep
753	36	56.2	355	2	Q85GY0_9CARA	Q85gy0 carabus sep
754	36	56.2	355	2	Q85GY1_9CARA	Q85gy1 carabus exa
755	36	56.2	355	2	Q85GY2_9CARA	Q85gy2 carabus pus
756	36	56.2	355	2	Q85GY3_9CARA	Q85gy3 carabus pus
757	36	56.2	355	2	Q85GY4_9CARA	Q85gy4 carabus pus
758	36	56.2	355	2	Q85GY5_9CARA	Q85gy5 carabus pus
759	36	56.2	355	2	Q85GY6_9CARA	Q85gy6 carabus pus
760	36	56.2	355	2	Q85GY7_9CARA	Q85gy7 carabus cir
761	36	56.2	355	2	Q85GY8_9CARA	Q85gy8 carabus cir
762	36	56.2	355	2	Q85GY9_9CARA	Q85gy9 carabus tit
763	36	56.2	355	2	Q85GZ0_9CARA	Q85gz0 carabus sta
764	36	56.2	355	2	Q85GZ1_9CARA	Q85gz1 carabus sta
765	36	56.2	355	2	Q85GZ2_9CARA	Q85gz2 carabus sta
766	36	56.2	355	2	Q85GZ3_9CARA	Q85gz3 carabus oss
767	36	56.2	355	2	Q85GZ4_9CARA	Q85gz4 carabus rei
768	36	56.2	355	2	Q85GZ5_9CARA	Q85gz5 carabus rei
769	36	56.2	355	2	Q85GZ6_9CARA	Q85gz6 carabus sta
770	36	56.2	355	2	Q85GZ7_9CARA	Q85gz7 carabus con
771	36	56.2	355	2	Q85GZ8_9CARA	Q85gz8 carabus boe
772	36	56.2	355	2	Q85GZ9_9CARA	Q85gz9 carabus hey
773	36	56.2	355	2	Q85H00_9CARA	Q85h00 carabus hei
774	36	56.2	355	2	Q85H01_9CARA	Q85h01 carabus hei
775	36	56.2	355	2	Q85H02_9CARA	Q85h02 carabus ada
776	36	56.2	355	2	Q85H03_9CARA	Q85h03 carabus ada
777	36	56.2	355	2	Q85H04_9CARA	Q85h04 carabus rot
778	36	56.2	355	2	Q85H05_9CARA	Q85h05 carabus ada
779	36	56.2	355	2	Q85H06_9CARA	Q85h06 carabus arm
780	36	56.2	355	2	Q85H07_9CARA	Q85h07 carabus boh
781	36	56.2	355	2	Q85H08_9CARA	Q85h08 carabus mac
782	36	56.2	355	2	Q85H09_9CARA	Q85h09 carabus mac
783	36	56.2	355	2	Q85H10_9CARA	Q85h10 carabus mac
784	36	56.2	355	2	Q85H11_9CARA	Q85h11 carabus mac
785	36	56.2	355	2	Q85H12_9CARA	Q85h12 carabus oly
786	36	56.2	355	2	Q85H13_9CARA	Q85h13 carabus pac
787	36	56.2	355	2	Q85H14_9CARA	Q85h14 carabus bar
788	36	56.2	355	2	Q85H15_9CARA	Q85h15 carabus rut
789	36	56.2	355	2	Q85H16_9CARA	Q85h16 carabus his
790	36	56.2	355	2	Q85H17_9CARA	Q85h17 carabus aur
791	36	56.2	355	2	Q85H18_9CARA	Q85h18 carabus aur
792	36	56.2	355	2	Q85H19_9CARA	Q85h19 carabus mor
793	36	56.2	355	2	Q85H20_9CARA	Q85h20 carabus mor
794	36	56.2	355	2	Q85H21_9CARA	Q85h21 carabus asp
795	36	56.2	355	2	Q85H22_9CARA	Q85h22 carabus asp
796	36	56.2	355	2	Q85H23_9CARA	Q85h23 carabus mel
797	36	56.2	355	2	Q8HAX6_9CARA	Q8hax6 carabus tit
798	36	56.2	355	2	Q8HB21_9CARA	Q8hb21 carabus abb
799	36	56.2	355	2	Q8HBC7_9CARA	Q8hbc7 carabus por
800	36	56.2	355	2	Q8HBH6_9CARA	Q8hbh6 carabus con
801	36	56.2	355	2	Q8HBH8_9CARA	Q8hbh8 carabus ero
802	36	56.2	355	2	Q8HBJ8_9CARA	Q8hbj8 carabus reg
803	36	56.2	355	2	Q8HBN5_9CARA	Q8hbn5 carabus cat
804	36	56.2	355	2	Q8HBN9_9CARA	Q8hbn9 carabus reg
805	36	56.2	355	2	Q8HBQ2_9CARA	Q8hbq2 carabus ero
806	36	56.2	355	2	Q8HBZ7_9CARA	Q8hbz7 carabus lew
807	36	56.2	355	2	Q8HC31_9CARA	Q8hc31 carabus alb
808	36	56.2	355	2	Q8HC55_9CARA	Q8hc55 carabus nit
809	36	56.2	355	2	Q8HCE1_9CARA	Q8hce1 carabus alb
810	36	56.2	355	2	Q8HCF0_CARCC	Q8hcf0 carabus can
811	36	56.2	355	2	Q8HCF1_9CARA	Q8hcf1 carabus alb
812	36	56.2	355	2	Q8HCF2_9CARA	Q8hcf2 carabus alb
813	36	56.2	355	2	Q8HCF3_9CARA	Q8hcf3 carabus alb
814	36	56.2	355	2	Q8HCI2_9CARA	Q8hci2 carabus yam
815	36	56.2	355	2	Q8HDH2_9CARA	Q8hdh2 pamborus al
816	36	56.2	355	2	Q8HDH3_9CARA	Q8hdh3 pamborus gu
817	36	56.2	355	2	Q8HDH5_9CARA	Q8hdh5 sphaeroderu
818	36	56.2	355	2	Q8HDM2_9CARA	Q8hdm2 carabus jap
819	36	56.2	355	2	Q8HDM3_9CARA	Q8hdm3 carabus alb
820	36	56.2	355	2	Q8HDM4_9CARA	Q8hdm4 carabus alb
821	36	56.2	355	2	Q8HDM5_9CARA	Q8hdm5 carabus alb
822	36	56.2	355	2	Q8HDM6_9CARA	Q8hdm6 carabus alb
823	36	56.2	355	2	Q8HDM7_9CARA	Q8hdm7 carabus alb
824	36	56.2	355	2	Q8HDM8_9CARA	Q8hdm8 carabus alb
825	36	56.2	355	2	Q8HDM9_9CARA	Q8hdm9 carabus yam
826	36	56.2	355	2	Q8HDN0_9CARA	Q8hdn0 carabus alb
827	36	56.2	355	2	Q8HDN2_9CARA	Q8hdn2 carabus kim
828	36	56.2	355	2	Q8HDN3_9CARA	Q8hdn3 carabus lew
829	36	56.2	355	2	Q8HDN4_9CARA	Q8hdn4 carabus lew
830	36	56.2	355	2	Q8HDN5_9CARA	Q8hdn5 carabus alb
831	36	56.2	355	2	Q8HDN6_9CARA	Q8hdn6 carabus lew
832	36	56.2	355	2	Q8HDN7_9CARA	Q8hdn7 carabus lew
833	36	56.2	355	2	Q8HDN8_9CARA	Q8hdn8 carabus alb
834	36	56.2	355	2	Q8HDN9_9CARA	Q8hdn9 carabus alb

835	36	56.2	355	2	Q8HDP0_9CARA	Q8hdp0 carabus alb
836	36	56.2	355	2	Q8HDP1_9CARA	Q8hdp1 carabus alb
837	36	56.2	355	2	Q8HDP2_9CARA	Q8hdp2 carabus alb
838	36	56.2	355	2	Q8HDP3_9CARA	Q8hdp3 carabus alb
839	36	56.2	355	2	Q8HDP4_9CARA	Q8hdp4 carabus alb
840	36	56.2	355	2	Q8HDP5_9CARA	Q8hdp5 carabus alb
841	36	56.2	355	2	Q8HDP6_9CARA	Q8hdp6 carabus alb
842	36	56.2	355	2	Q8HDP7_9CARA	Q8hdp7 carabus alb
843	36	56.2	355	2	Q8HDP8_9CARA	Q8hdp8 carabus alb
844	36	56.2	355	2	Q8HDP9_9CARA	Q8hdp9 carabus alb
845	36	56.2	355	2	Q8HDQ0_9CARA	Q8hdq0 carabus alb
846	36	56.2	355	2	Q8HDQ1_9CARA	Q8hdq1 carabus alb
847	36	56.2	355	2	Q8HDQ2_9CARA	Q8hdq2 carabus alb
848	36	56.2	355	2	Q8HDQ3_9CARA	Q8hdq3 carabus alb
849	36	56.2	355	2	Q8HDQ4_9CARA	Q8hdq4 carabus alb
850	36	56.2	355	2	Q8HDQ5_9CARA	Q8hdq5 carabus alb
851	36	56.2	355	2	Q8HDS6_9CARA	Q8hds6 carabus ste
852	36	56.2	355	2	Q8HDS8_9CARA	Q8hds8 carabus nam
853	36	56.2	355	2	Q8HDS9_9CARA	Q8hds9 carabus nam
854	36	56.2	355	2	Q8HDT0_9CARA	Q8hdt0 carabus ste
855	36	56.2	355	2	Q8HDT1_9CARA	Q8hdt1 carabus ste
856	36	56.2	355	2	Q8HDT2_9CARA	Q8hdt2 carabus ste
857	36	56.2	355	2	Q8HDT3_9CARA	Q8hdt3 carabus car
858	36	56.2	355	2	Q8HDT4_9CARA	Q8hdt4 carabus car
859	36	56.2	355	2	Q8HDT5_9CARA	Q8hdt5 carabus ste
860	36	56.2	355	2	Q8HDT6_9CARA	Q8hdt6 carabus ste
861	36	56.2	355	2	Q8HDT7_9CARA	Q8hdt7 carabus man
862	36	56.2	355	2	Q8HDT8_9CARA	Q8hdt8 carabus man
863	36	56.2	355	2	Q8HDT9_9CARA	Q8hdt9 carabus man
864	36	56.2	355	2	Q8HDU0_9CARA	Q8hdu0 carabus man
865	36	56.2	355	2	Q8HDU1_9CARA	Q8hdu1 carabus bil
866	36	56.2	355	2	Q8HDU2_9CARA	Q8hdu2 carabus man
867	36	56.2	355	2	Q8HDU3_9CARA	Q8hdu3 carabus man
868	36	56.2	355	2	Q8HDU4_9CARA	Q8hdu4 carabus cum
869	36	56.2	355	2	Q8HDU5_9CARA	Q8hdu5 carabus cum
870	36	56.2	355	2	Q8HDV1_CARAR	Q8hdv1 carabus arv
871	36	56.2	355	2	Q8HDV2_9CARA	Q8hdv2 carabus dey
872	36	56.2	355	2	Q8HDV3_9CARA	Q8hdv3 carabus lim
873	36	56.2	355	2	Q8HDV4_9CARA	Q8hdv4 carabus lim
874	36	56.2	355	2	Q8HDW0_9CARA	Q8hdw0 carabus pse
875	36	56.2	355	2	Q8HDX1_9CARA	Q8hdx1 carabus mia
876	36	56.2	355	2	Q8HDX2_9CARA	Q8hdx2 carabus asc
877	36	56.2	355	2	Q8HDX3_9CARA	Q8hdx3 carabus mas
878	36	56.2	355	2	Q8HDX4_9CARA	Q8hdx4 carabus mas
879	36	56.2	355	2	Q8HDX5_9CARA	Q8hdx5 carabus inf
880	36	56.2	355	2	Q8HDX6_9CARA	Q8hdx6 carabus inf
881	36	56.2	355	2	Q8HDX7_9CARA	Q8hdx7 carabus pre
882	36	56.2	355	2	Q8HDX8_9CARA	Q8hdx8 carabus ero
883	36	56.2	355	2	Q8HDX9_9CARA	Q8hdx9 carabus ero
884	36	56.2	355	2	Q8HDY0_9CARA	Q8hdy0 carabus ero
885	36	56.2	355	2	Q8HDY1_9CARA	Q8hdy1 carabus ero
886	36	56.2	355	2	Q8HDY2_9CARA	Q8hdy2 carabus ero
887	36	56.2	355	2	Q8HDY3_9CARA	Q8hdy3 carabus ero
888	36	56.2	355	2	Q8HDY5_9CARA	Q8hdy5 carabus reg
889	36	56.2	355	2	Q8HDY6_9CARA	Q8hdy6 carabus reg
890	36	56.2	355	2	Q8HDY7_9CARA	Q8hdy7 carabus tra
891	36	56.2	355	2	Q8HDY8_9CARA	Q8hdy8 carabus min
892	36	56.2	355	2	Q8HDY9_9CARA	Q8hdy9 carabus sts
893	36	56.2	355	2	Q8HDZ0_9CARA	Q8hdz0 carabus bog
894	36	56.2	355	2	Q8HDZ1_9CARA	Q8hdz1 carabus for
895	36	56.2	355	2	Q8HDZ3_9CARA	Q8hdz3 carabus for
896	36	56.2	355	2	Q8HDZ4_9CARA	Q8hdz4 carabus syl
897	36	56.2	355	2	Q8HDZ5_9CARA	Q8hdz5 carabus kru
898	36	56.2	355	2	Q8HDZ6_9CARA	Q8hdz6 carabus sha
899	36	56.2	355	2	Q8HDZ7_CARCV	Q8hdz7 carabus con
900	36	56.2	355	2	Q8HDZ9_9CARA	Q8hdz9 carabus mal
901	36	56.2	355	2	Q8HE00_9CARA	Q8he00 carabus bud
902	36	56.2	355	2	Q8HE01_9CARA	Q8he01 carabus bud
903	36	56.2	355	2	Q8HE02_9CARA	Q8he02 carabus gig
904	36	56.2	355	2	Q8HE03_9CARA	Q8he03 carabus bud
905	36	56.2	355	2	Q8HE04_9CARA	Q8he04 carabus con
906	36	56.2	355	2	Q8HE05_9CARA	Q8he05 carabus con
907	36	56.2	355	2	Q8HE06_9CARA	Q8he06 carabus cat
908	36	56.2	355	2	Q8HE07_9CARA	Q8he07 carabus zhe
909	36	56.2	355	2	Q8HE08_9CARA	Q8he08 carabus lad
910	36	56.2	355	2	Q8HE09_9CARA	Q8he09 carabus itz
911	36	56.2	355	2	Q8HE10_9CARA	Q8he10 carabus itz
912	36	56.2	355	2	Q8HE11_9CARA	Q8he11 carabus itz
913	36	56.2	355	2	Q8HE12_9CARA	Q8he12 carabus han
914	36	56.2	355	2	Q8HE13_9CARA	Q8he13 carabus han
915	36	56.2	355	2	Q8HE23_9CARA	Q8he23 carabus vla
916	36	56.2	355	2	Q8HE24_9CARA	Q8he24 carabus vla
917	36	56.2	355	2	Q8HE25_9CARA	Q8he25 carabus tit
918	36	56.2	355	2	Q8HE26_9CARA	Q8he26 carabus sch
919	36	56.2	355	2	Q8HE27_9CARA	Q8he27 carabus swa
920	36	56.2	355	2	Q8HE28_9CARA	Q8he28 carabus tam
921	36	56.2	355	2	Q8HE29_9CARA	Q8he29 carabus tam
922	36	56.2	355	2	Q8HE31_9CARA	Q8he31 carabus ros
923	36	56.2	355	2	Q8HE32_9CARA	Q8he32 carabus sta
924	36	56.2	355	2	Q8HE33_9CARA	Q8he33 carabus koe
925	36	56.2	355	2	Q8HE34_9CARA	Q8he34 carabus gem
926	36	56.2	355	2	Q8HE35_9CARA	Q8he35 carabus por
927	36	56.2	355	2	Q8HE36_9CARA	Q8he36 carabus cri
928	36	56.2	355	2	Q8HE37_9CARA	Q8he37 carabus cri
929	36	56.2	355	2	Q8HE38_9CARA	Q8he38 carabus cri
930	36	56.2	355	2	Q8HE39_9CARA	Q8he39 carabus fam
931	36	56.2	355	2	Q8HE40_9CARA	Q8he40 carabus cri
932	36	56.2	355	2	Q8HE41_CARCC	Q8he41 carabus can
933	36	56.2	355	2	Q8HE42_CARCC	Q8he42 carabus can
934	36	56.2	355	2	Q8HE43_CARCC	Q8he43 carabus can
935	36	56.2	355	2	Q8HE44_CARCC	Q8he44 carabus can
936	36	56.2	355	2	Q96129_9CARA	Q96129 carabus alb
937	36	56.2	355	2	Q96130_9CARA	Q96130 carabus alb
938	36	56.2	355	2	Q96131_9CARA	Q96131 carabus alb
939	36	56.2	355	2	Q96132_9CARA	Q96132 carabus arr
940	36	56.2	355	2	Q96134_9CARA	Q96134 carabus dai
941	36	56.2	355	2	Q96135_9CARA	Q96135 carabus dai
942	36	56.2	355	2	Q96136_9CARA	Q96136 carabus deh
943	36	56.2	355	2	Q96137_9CARA	Q96137 carabus deh
944	36	56.2	355	2	Q96138_9CARA	Q96138 carabus deh
945	36	56.2	355	2	Q96139_9CARA	Q96139 carabus deh
946	36	56.2	355	2	Q96140_9CARA	Q96140 carabus deh
947	36	56.2	355	2	Q96141_9CARA	Q96141 carabus deh
948	36	56.2	355	2	Q96142_9CARA	Q96142 carabus deh
949	36	56.2	355	2	Q96143_9CARA	Q96143 carabus deh
950	36	56.2	355	2	Q96144_9CARA	Q96144 carabus deh
951	36	56.2	355	2	Q96146_9CARA	Q96146 carabus deh
952	36	56.2	355	2	Q96147_9CARA	Q96147 carabus ins
953	36	56.2	355	2	Q96148_9CARA	Q96148 carabus ins
954	36	56.2	355	2	Q96149_9CARA	Q96149 carabus ins
955	36	56.2	355	2	Q96150_9CARA	Q96150 carabus ins
956	36	56.2	355	2	Q96152_9CARA	Q96152 carabus ins
957	36	56.2	355	2	Q96153_9CARA	Q96153 carabus ins
958	36	56.2	355	2	Q96154_9CARA	Q96154 carabus ins
959	36	56.2	355	2	Q96155_9CARA	Q96155 carabus jap
960	36	56.2	355	2	Q96156_9CARA	Q96156 carabus jap
961	36	56.2	355	2	Q96157_9CARA	Q96157 carabus jap
962	36	56.2	355	2	Q96158_9CARA	Q96158 carabus jap
963	36	56.2	355	2	Q96159_9CARA	Q96159 carabus jap
964	36	56.2	355	2	Q96160_9CARA	Q96160 carabus jap
965	36	56.2	355	2	Q96161_9CARA	Q96161 carabus jap
966	36	56.2	355	2	Q96162_9CARA	Q96162 carabus jap
967	36	56.2	355	2	Q96163_9CARA	Q96163 carabus kim
968	36	56.2	355	2	Q96164_9CARA	Q96164 carabus mai
969	36	56.2	355	2	Q96165_9CARA	Q96165 carabus mai
970	36	56.2	355	2	Q96166_9CARA	Q96166 carabus tos
971	36	56.2	355	2	Q96167_9CARA	Q96167 carabus tos
972	36	56.2	355	2	Q96168_9CARA	Q96168 carabus yac
973	36	56.2	355	2	Q96169_9CARA	Q96169 carabus yac
974	36	56.2	355	2	Q96170_9CARA	Q96170 carabus yac
975	36	56.2	355	2	Q96171_9CARA	Q96171 carabus yac
976	36	56.2	355	2	Q96172_9CARA	Q96172 carabus yac
977	36	56.2	355	2	Q96173_9CARA	Q96173 carabus yac
978	36	56.2	355	2	Q96174_9CARA	Q96174 carabus yac
979	36	56.2	355	2	Q96192_9CARA	Q96192 carabus ins
980	36	56.2	355	2	Q96193_9CARA	Q96193 carabus alb

981	36	56.2	355	2	Q96194_9CARA	Q96194 carabus yac
982	36	56.2	355	2	Q96195_9CARA	Q96195 carabus mai
983	36	56.2	355	2	Q96196_9CARA	Q96196 carabus jap
984	36	56.2	355	2	Q9B0P2_9CARA	Q9b0p2 ceroglossus
985	36	56.2	355	2	Q9B0X6_9CARA	Q9b0x6 carabus ven
986	36	56.2	355	2	Q9B0Y8_9CARA	Q9b0y8 ceroglossus
987	36	56.2	355	2	Q9B119_9CARA	Q9b119 carabus sca
988	36	56.2	355	2	Q9B131_9CARA	Q9b131 ceroglossus
989	36	56.2	355	2	Q9B1A2_9CARA	Q9b1a2 carabus aer
990	36	56.2	355	2	Q9B1I6_9CARA	Q9b1i6 ceroglossus
991	36	56.2	355	2	Q9B1Q4_9CARA	Q9b1q4 ceroglossus
992	36	56.2	355	2	Q9B1Q5_9CARA	Q9b1q5 ceroglossus
993	36	56.2	355	2	Q9B1Q6_9CARA	Q9b1q6 ceroglossus
994	36	56.2	355	2	Q9B1W7_9CARA	Q9b1w7 ceroglossus
995	36	56.2	355	2	Q9B5W0_9CARA	Q9b5w0 ceroglossus
996	36	56.2	355	2	Q9B5W1_9CARA	Q9b5w1 ceroglossus
997	36	56.2	355	2	Q9B5W2_9CARA	Q9b5w2 ceroglossus
998	36	56.2	355	2	Q9B5W3_9CARA	Q9b5w3 ceroglossus
999	36	56.2	355	2	Q9B5W4_9CARA	Q9b5w4 ceroglossus
1000	36	56.2	355	2	Q9B5W5_9CARA	Q9b5w5 ceroglossus

ALIGNMENTS

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RESULT 1
Q4RK84_TETNG
ID   Q4RK84_TETNG PRELIMINARY;      PRT;  1208 AA.
AC   Q4RK84;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome 4 SCAF15031, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00033073001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
CC   -!- SIMILARITY: Contains 1 PH domain.
CC   -!- SIMILARITY: Contains 2 SH3 domains.
DR   EMBL; CAAE01015031; CAG11198.1; -; Genomic_DNA.
DR   InterPro; IPR002219; DAG_PE_bd.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR000219; RhoGEF.
DR   InterPro; IPR000980; SH2.
DR   InterPro; IPR001452; SH3.
DR   InterPro; IPR011511; SH3_2.
DR   Pfam; PF00130; C1_1; 1.
DR   Pfam; PF00169; PH; 1.
DR   Pfam; PF00621; RhoGEF; 1.
DR   Pfam; PF00017; SH2; 1.
DR   Pfam; PF00018; SH3_1; 1.
DR   Pfam; PF07653; SH3_2; 1.
DR   PRINTS; PR00008; DAGPEDOMAIN.
DR   PRINTS; PR00401; SH2DOMAIN.
DR   PRINTS; PR00452; SH3DOMAIN.
DR   ProDom; PD000093; SH2; 1.
DR   ProDom; PD000066; SH3; 1.
DR   SMART; SM00109; C1; 1.
DR   SMART; SM00233; PH; 1.
DR   SMART; SM00325; RhoGEF; 1.
DR   SMART; SM00252; SH2; 1.
DR   SMART; SM00326; SH3; 2.
DR   PROSITE; PS50010; DH_2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 1.
DR   PROSITE; PS50001; SH2; 1.
DR   PROSITE; PS50002; SH3; 2.
DR   PROSITE; PS00479; ZF_DAG_PE_1; 1.
DR   PROSITE; PS50081; ZF_DAG_PE_2; 1.
KW   Metal-binding; Phorbol-ester binding; SH2 domain; SH3 domain; Zinc;
KW   Zinc-finger.
FT   NON_TER       1       1
SQ   SEQUENCE   1208 AA;  138979 MW;  6A056254CCF12EE0 CRC64;

  Query Match             73.4%;  Score 47;  DB 2;  Length 1208;
  Best Local Similarity   75.0%;  Pred. No. 82;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFA 9
              |:|:||||
Db        538 YYGYPWFA 545


RESULT 2
Q9YZ25_9VIRU
ID   Q9YZ25_9VIRU PRELIMINARY;      PRT;  2209 AA.
AC   Q9YZ25;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   L protein.
OS   Lymphocytic choriomeningitis virus.
OC   Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus;
OC   Old world arenaviruses.
OX   NCBI_TaxID=11623;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=WE;
RX   MEDLINE=99073699; PubMed=9857988; DOI=10.1023/A:1008016724243;
RA   Djavani M., Lukashevich I.S., Salvato M.S.;
RT   "Sequence comparison of the large genomic RNA segments of two strains
RT   of lymphocytic choriomeningitis virus differing in pathogenic
RT   potential for guinea pigs.";
RL   Virus Genes 17:151-155(1998).
DR   EMBL; AF004519; AAD03396.1; -; Genomic_RNA.
DR   GO; GO:0003968; F:RNA-directed RNA polymerase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0019079; P:viral genome replication; IEA.
DR   InterPro; IPR010453; Arena_RNA_pol.
DR   InterPro; IPR007099; RNA_pol_NSvir.
DR   Pfam; PF06317; Arena_RNA_pol; 1.
SQ   SEQUENCE   2209 AA;  254432 MW;  40104EFA50EDCCCC CRC64;

  Query Match             68.8%;  Score 44;  DB 2;  Length 2209;
  Best Local Similarity   70.0%;  Pred. No. 4.2e+02;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              | ||| ||:|
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Db       1900 LQFGFPGWFSY 1909


RESULT 3
RRPO_LYCVA
ID   RRPO_LYCVA     STANDARD;      PRT;  2210 AA.
AC   P14240;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   RNA polymerase (EC 2.7.7.48).
GN   Name=L;
OS   Lymphocytic choriomeningitis virus (strain Armstrong).
OC   Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus;
OC   Old world arenaviruses.
OX   NCBI_TaxID=11624;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=89204909; PubMed=2705303;
RA   Salvato M.S., Shimomaye E.M., Oldstone M.B.A.;
RT   "The primary structure of the lymphocytic choriomeningitis virus L
RT   gene encodes a putative RNA polymerase.";
RL   Virology 169:377-384(1989).
RN   [2]
RP   NUCLEOTIDE SEQUENCE OF 161-387; 424-619 AND 1646-1906.
RX   MEDLINE=88072084; PubMed=3318094;
RA   Singh M.K., Fuller-Pace F.V., Buchmeier M.J., Southern P.J.;
RT   "Analysis of the genomic L RNA segment from lymphocytic
RT   choriomeningitis virus.";
RL   Virology 161:448-456(1987).
CC   -!- CATALYTIC ACTIVITY: Nucleoside triphosphate + RNA(n) = diphosphate
CC       + RNA(n+1).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; J04331; AAA66591.1; -; Genomic_RNA.
DR   EMBL; M18381; AAA46258.1; ALT_SEQ; Genomic_RNA.
DR   EMBL; M18382; AAA46259.1; -; Genomic_RNA.
DR   EMBL; M18383; AAA46260.1; ALT_SEQ; Genomic_RNA.
DR   PIR; A30181; RRXPLC.
DR   InterPro; IPR010453; Arena_RNA_pol.
DR   InterPro; IPR007099; RNA_pol_NSvir.
DR   Pfam; PF06317; Arena_RNA_pol; 1.
KW   Nucleotidyltransferase; RNA-directed RNA polymerase; Transferase.
FT   CONFLICT    164    164       L -> Y (in Ref. 2).
FT   CONFLICT    354    354       Q -> R (in Ref. 2).
FT   CONFLICT    361    361       K -> E (in Ref. 2).
FT   CONFLICT    382    382       H -> D (in Ref. 2).
FT   CONFLICT    552    552       C -> S (in Ref. 2).
FT   CONFLICT   1727   1727       R -> L (in Ref. 2).
SQ   SEQUENCE   2210 AA;  254532 MW;  470C8E623176AFD3 CRC64;

  Query Match             68.8%;  Score 44;  DB 1;  Length 2210;
  Best Local Similarity   70.0%;  Pred. No. 4.2e+02;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              | ||| ||:|
Db       1901 LQFGFPGWFSY 1910


RESULT 4
Q4SCE1_TETNG
ID   Q4SCE1_TETNG PRELIMINARY;      PRT;   176 AA.
AC   Q4SCE1;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Chromosome undetermined SCAF14656, whole genome shotgun sequence.
DE   (Fragment).
GN   ORFNames=GSTENG00020544001;
OS   Tetraodon nigroviridis (Green puffer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC   Tetradontoidea; Tetraodontidae; Tetraodon.
OX   NCBI_TaxID=99883;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA   Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA   Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA   Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA   Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA   Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA   Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA   Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA   Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J.,
RA   Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA   Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA   Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.;
RT   "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT   the early vertebrate proto-karyotype.";
RL   Nature 431:946-957(2004).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   Genoscope; Whitehead Institute Centre for Genome Research;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAE01014656; CAG01691.1; -; Genomic_DNA.
FT   NON_TER       1      1
SQ   SEQUENCE   176 AA;  20046 MW;  60BCCAF2E97F9849 CRC64;

  Query Match             68.0%;  Score 43.5;  DB 2;  Length 176;
  Best Local Similarity   72.7%;  Pred. No. 52;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 LYFGFPW-FAY 10
              |||| || | |
Db        123 LYFGLPWVFCY 133


RESULT 5
Q9RK78_STRCO
ID   Q9RK78_STRCO PRELIMINARY;      PRT;   302 AA.
AC   Q9RK78;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Putative sugar transporter membrane protein.
GN   OrderedLocusNames=SCO0532; ORFNames=SCF11.12;
OS   Streptomyces coelicolor.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=A3(2) / M145;
RX   MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA   Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA   Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA   Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA   Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA   Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neil S.,
RA   Rabbinowitsch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA   Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA   Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA   Hopwood D.A.;
RT   "Complete genome sequence of the model actinomycete Streptomyces
RT   coelicolor A3(2).";
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RL   Nature 417:141-147(2002).
CC   -!- FUNCTION: Part of a binding-protein-dependent transport system.
CC       Probably responsible for the translocation of the substrate across
CC       the membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC       system permease family.
DR   EMBL; AL939105; CAB59589.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005351; F:sugar porter activity; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR000515; BPD_transp.
DR   Pfam; PF00528; BPD_transp_1; 1.
DR   PROSITE; PS50928; ABC_TM1; 1.
KW   Complete proteome; Sugar transport; Transmembrane; Transport.
SQ   SEQUENCE   302 AA;  33279 MW;  79E18529A1212701 CRC64;

  Query Match             67.2%;  Score 43;  DB 2;  Length 302;
  Best Local Similarity   66.7%;  Pred. No. 1e+02;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              | |:||||:
Db        152 YEGYPWFAH 160


RESULT 6
Q4KAB2_PSEF5
ID   Q4KAB2_PSEF5 PRELIMINARY;      PRT;   339 AA.
AC   Q4KAB2;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Membrane protein, putative.
GN   ORFNames=PFL_3719;
OS   Pseudomonas fluorescens (strain Pf-5).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=220664;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Pf-5;
RX   PubMed=15980861; DOI=10.1038/nbt1110;
RA   Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
RA   Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA   Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA   Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
RA   Khouri H.M., Pierson E., Pierson L. III, Thomashow L., Loper J.;
RT   "Complete genome sequence of the plant commensal Pseudomonas
RT   fluorescens Pf-5.";
RL   Nat. Biotechnol. 23:873-878(2005).
DR   EMBL; CP000076; AAY92985.1; -; Genomic_DNA.
SQ   SEQUENCE   339 AA;  37164 MW;  8A6D664F9165A958 CRC64;

  Query Match             67.2%;  Score 43;  DB 2;  Length 339;
  Best Local Similarity   66.7%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              ||| ||  |
Db         85 YFGHPWLTY 93


RESULT 7
Q5ZYR8_LEGPH
ID   Q5ZYR8_LEGPH PRELIMINARY;      PRT;   812 AA.
AC   Q5ZYR8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Long chain acyl-CoA dehydrogenase (EC 1.3.99.-).
GN   OrderedLocusNames=lpg0293;
OS   Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 /
OS   ATCC 33152).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC   Legionellaceae; Legionella.
OX   NCBI_TaxID=272624;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15448271; DOI=10.1126/science.1099776;
RA   Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA   Asamani G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,
RA   Steshenko V., Park S.H., Zhao B., Teplitskaya E., Edwards J.R.,
RA   Pampou S., Georghiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
RA   Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
RA   Segal G., Qu X., Rzhetsky A., Zhang P., Cayanis E., De Jong P.J.,
RA   Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
RT   "The genomic sequence of the accidental pathogen Legionella
RT   pneumophila.";
RL   Science 305:1966-1968(2004).
DR   EMBL; AE017354; AAU26400.1; -; Genomic_DNA.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   Pfam; PF00441; Acyl-CoA_dh_1; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
KW   Complete proteome; FAD; Flavoprotein; Oxidoreductase.
SQ   SEQUENCE   812 AA;  91150 MW;  C4C2743CD23F317D CRC64;

  Query Match             67.2%;  Score 43;  DB 2;  Length 812;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPW 7
              ||||||
Db         40 YFGFPW 45


RESULT 8
Q5X882_LEGPA
ID   Q5X882_LEGPA PRELIMINARY;      PRT;   812 AA.
AC   Q5X882;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=lpp0371;
OS   Legionella pneumophila (strain Paris).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC   Legionellaceae; Legionella.
OX   NCBI_TaxID=297246;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15467720; DOI=10.1038/ng1447;
RA   Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA   Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA   Etienne J., Glaser P., Buchrieser C.;
RT   "Evidence in the Legionella pneumophila genome for exploitation of
RT   host cell functions and high genome plasticity.";
RL   Nat. Genet. 36:1165-1173(2004).
DR   EMBL; CR628336; CAH11519.1; -; Genomic_DNA.
DR   LegioList; lpp0371; -.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   Pfam; PF00441; Acyl-CoA_dh_1; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
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DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
KW   Complete proteome; FAD; Flavoprotein; Hypothetical protein;
KW   Oxidoreductase.
SQ   SEQUENCE   812 AA;  91169 MW;  1432CC1C297CADFF CRC64;

  Query Match            67.2%;  Score 43;  DB 2;  Length 812;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPW 7
              ||||||
Db         40 YFGFPW 45


RESULT 9
Q5WZN5_LEGPL
ID   Q5WZN5_LEGPL PRELIMINARY;      PRT;   812 AA.
AC   Q5WZN5;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=lpl0346;
OS   Legionella pneumophila (strain Lens).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC   Legionellaceae; Legionella.
OX   NCBI_TaxID=297245;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=15467720; DOI=10.1038/ng1447;
RA   Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA   Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA   Etienne J., Glaser P., Buchrieser C.;
RT   "Evidence in the Legionella pneumophila genome for exploitation of
RT   host cell functions and high genome plasticity.";
RL   Nat. Genet. 36:1165-1173(2004).
DR   EMBL; CR628337; CAH14577.1; -; Genomic_DNA.
DR   LegioList; lpl0346; -.
DR   GO; GO:0003995; F:acyl-CoA dehydrogenase activity; IEA.
DR   GO; GO:0016491; F:oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR006089; Acyl-CoA_dh.
DR   InterPro; IPR006090; Acyl-CoA_dh_C.
DR   InterPro; IPR006091; Acyl-CoA_dh_M.
DR   Pfam; PF00441; Acyl-CoA_dh_1; 1.
DR   Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR   PROSITE; PS00072; ACYL_COA_DH_1; 1.
KW   Complete proteome; FAD; Flavoprotein; Hypothetical protein;
KW   Oxidoreductase.
SQ   SEQUENCE   812 AA;  91192 MW;  9F6227DEDF909A3F CRC64;

  Query Match            67.2%;  Score 43;  DB 2;  Length 812;
  Best Local Similarity   100.0%;  Pred. No. 2.4e+02;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPW 7
              ||||||
Db         40 YFGFPW 45


RESULT 10
P70629_RAT
ID   P70629_RAT  PRELIMINARY;      PRT;   110 AA.
AC   P70629;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   B-cell receptor associated protein 37 (Fragment).
GN   Name=BAP-37;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Wistar-Kyoto;
RX   MEDLINE=20027749; PubMed=10559001;
RA   Adams L.D., Lemire J.M., Schwartz S.M.;
RT   "A systematic analysis of 40 random genes in cultured vascular smooth
RT   muscle subtypes reveals a heterogeneity of gene expression and
RT   identifies the tight junction gene zonula occludens 2 as a marker of
RT   epithelioid 'pup' smooth muscle cells and a participant in carotid
RT   neointimal formation.";
RL   Arterioscler. Thromb. Vasc. Biol. 19:2600-2608(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Wistar-Kyoto;
RA   Adams L.A., Werny I., Schwartz S.M.;
RL   Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U75391; AAB18746.1; -; mRNA.
DR   Ensembl; ENSRNOG00000012999; Rattus norvegicus.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0006259; P:DNA metabolism; IEA.
DR   InterPro; IPR001107; Band_7.
DR   InterPro; IPR000163; Prohibitin.
DR   Pfam; PF01145; Band_7; 1.
DR   PRINTS; PR00679; PROHIBITIN.
KW   Receptor.
FT   NON_TER     110    110
SQ   SEQUENCE   110 AA;  11988 MW;  8C34E72C638C4386 CRC64;

  Query Match            65.6%;  Score 42;  DB 2;  Length 110;
  Best Local Similarity   60.0%;  Pred. No. 58;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              |:|  ||| |
Db         68 LHFXIPWFXY 77


RESULT 11
Q544C4_MOUSE
ID   Q544C4_MOUSE PRELIMINARY;      PRT;   381 AA.
AC   Q544C4;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   3 days neonate thymus cDNA, RIKEN full-length enriched library,
DE   clone:A630019F13 product:PROBABLE G PROTEIN-COUPLED RECEPTOR GPR72
DE   (GLUCOCORTICOID- INDUCED RECEPTOR), full insert sequence.
GN   Name=Gpr83;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Thymus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
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RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AK041527; BAC30974.1; -; mRNA.
DR MGI; MGI:95712; Gpr83.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 381 AA; 43417 MW; 2EEDB8584184A0A3 CRC64;

Query Match 65.6%; Score 42; DB 2; Length 381;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LYFGFPWFA 9
||| | |||
Db 284 LYFAFHWFA 292

RESULT 12
Q88TD1_LACPL
ID Q88TD1_LACPL PRELIMINARY; PRT; 396 AA.
AC Q88TD1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE ABC transporter, permease protein (Putative).
GN OrderedLocusNames=lp_3038;
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566; DOI=10.1073/pnas.0337704100;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
DR EMBL; AL935260; CAD65216.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 396 AA; 44765 MW; E8F17A56A62E2500 CRC64;

Query Match 65.6%; Score 42; DB 2; Length 396;
Best Local Similarity 70.0%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
| ||| || |
Db 339 LNFGFRWFGY 348

RESULT 13
GPR83_CANFA
ID GPR83_CANFA STANDARD; PRT; 422 AA.
AC Q9TTQ9;
DT 16-OCT-2001 (Rel. 40, Created)

```
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Probable G-protein coupled receptor 83 precursor (Glucocorticoid-
DE   induced receptor).
GN   Name=GPR83; Synonyms=GIR, GPR72;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Thyroid;
RA   Perret J., Simons M., De Moerlooze L., Parmentier M.;
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Orphan receptor. Could be a neuropeptide y receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; Y19224; CAB57795.1; -; mRNA.
DR   Ensembl; ENSCAFG00000004171; Canis familiaris.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Signal;
KW   Transducer; Transmembrane.
FT   SIGNAL        1     16       Potential.
FT   CHAIN        17    422       Probable G-protein coupled receptor 83.
FT   TOPO_DOM     17     70       Extracellular (Potential).
FT   TRANSMEM     71     91       1 (Potential).
FT   TOPO_DOM     92    106       Cytoplasmic (Potential).
FT   TRANSMEM    107    128       2 (Potential).
FT   TOPO_DOM    129    144       Extracellular (Potential).
FT   TRANSMEM    145    166       3 (Potential).
FT   TOPO_DOM    167    185       Cytoplasmic (Potential).
FT   TRANSMEM    186    207       4 (Potential).
FT   TOPO_DOM    208    237       Extracellular (Potential).
FT   TRANSMEM    238    259       5 (Potential).
FT   TOPO_DOM    260    292       Cytoplasmic (Potential).
FT   TRANSMEM    293    314       6 (Potential).
FT   TOPO_DOM    315    326       Extracellular (Potential).
FT   TRANSMEM    327    347       7 (Potential).
FT   TOPO_DOM    348    422       Cytoplasmic (Potential).
FT   CARBOHYD     37     37       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     45     45       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    133    133       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   422 AA;  48043 MW;  C9C21DE85B9DFB67 CRC64;

  Query Match             65.6%;  Score 42;  DB 1;  Length 422;
  Best Local Similarity   77.8%;  Pred. No. 2e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        325 LYFAFHWFA 333


RESULT 14
Q8VHD7_RAT
ID   Q8VHD7_RAT  PRELIMINARY;      PRT;   422 AA.
AC   Q8VHD7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Glucocorticoid-induced receptor.
GN   Name=Gpr83;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=21555362; PubMed=11698613;
RA   Wang D., Herman J.P., Pritchard L.M., Spitzer R.H., Ahlbrand R.L.,
RA   Kramer G.L., Petty F., Sallee F.R., Richtand N.M.;
RT   "Cloning, expression, and regulation of a glucocorticoid-induced
RT   receptor in rat brain: effect of repetitive amphetamine.";
RL   J. Neurosci. 21:9027-9035(2001).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR   EMBL; AY029071; AAK29999.1; -; mRNA.
DR   Ensembl; ENSRNOG00000030318; Rattus norvegicus.
DR   RGD; 619891; Gpr83.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ   SEQUENCE   422 AA;  47957 MW;  4917CA9C33A8BFE9 CRC64;

  Query Match             65.6%;  Score 42;  DB 2;  Length 422;
  Best Local Similarity   77.8%;  Pred. No. 2e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        325 LYFAFHWFA 333


RESULT 15
GPR83_HUMAN
ID   GPR83_HUMAN    STANDARD;      PRT;   423 AA.
AC   Q9NYM4; Q9P1Y8;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Probable G-protein coupled receptor 83 precursor.
GN   Name=GPR83; Synonyms=GPR72, KIAA1540;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=20225484; PubMed=10760605; DOI=10.1016/S0167-4781(00)00023-3;
RA   Parker R., Liu M., Eyre H.J., Copeland N.G., Gilbert D.J.,
RA   Crawford J., Sutherland G.R., Jenkins N.A., Herzog H.;
RT   "Y-receptor-like genes GPR72 and GPR73: molecular cloning, genomic
RT   organisation and assignment to human chromosome 11q21.1 and 2p14 and
RT   mouse chromosome 9 and 6.";
RL   Biochim. Biophys. Acta 1491:369-375(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain;
RX   MEDLINE=20277482; PubMed=10819331;
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RA   Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XVII.
RT   The complete sequences of 100 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 7:143-150(2000).
CC   -!- FUNCTION: Orphan receptor. Could be a neuropeptide y receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Brain specific.
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF236081; AAF43705.1; -; mRNA.
DR   EMBL; AB040973; BAA96064.1; ALT_INIT; mRNA.
DR   Ensembl; ENSG00000123901; Homo sapiens.
DR   HGNC; HGNC:4523; GPR83.
DR   H-InvDB; HIX0010029; -.
DR   MIM; 605569; -.
DR   GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Glycoprotein; Receptor; Signal;
KW   Transducer; Transmembrane.
FT   SIGNAL        1    16       Potential.
FT   CHAIN        17   423       Probable G-protein coupled receptor 83.
FT   TOPO_DOM     18    71       Extracellular (Potential).
FT   TRANSMEM     72    92       1 (Potential).
FT   TOPO_DOM     93   107       Cytoplasmic (Potential).
FT   TRANSMEM    108   129       2 (Potential).
FT   TOPO_DOM    130   145       Extracellular (Potential).
FT   TRANSMEM    146   167       3 (Potential).
FT   TOPO_DOM    168   186       Cytoplasmic (Potential).
FT   TRANSMEM    187   208       4 (Potential).
FT   TOPO_DOM    209   238       Extracellular (Potential).
FT   TRANSMEM    239   260       5 (Potential).
FT   TOPO_DOM    261   293       Cytoplasmic (Potential).
FT   TRANSMEM    294   315       6 (Potential).
FT   TOPO_DOM    316   327       Extracellular (Potential).
FT   TRANSMEM    328   348       7 (Potential).
FT   TOPO_DOM    349   423       Cytoplasmic (Potential).
FT   CARBOHYD     37    37       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     46    46       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    134   134       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    144   224       By similarity.
FT   CONFLICT    373   373       G -> R (in Ref. 2).
SQ   SEQUENCE   423 AA;  48271 MW;  D9E30501B071F4AA CRC64;

  Query Match             65.6%;  Score 42;  DB 1;  Length 423;
  Best Local Similarity   77.8%;  Pred. No. 2e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        326 LYFAFHWFA 334


RESULT 16
GPR83_MOUSE
ID   GPR83_MOUSE    STANDARD;      PRT;   423 AA.
AC   P30731;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Probable G-protein coupled receptor 83 precursor (Glucocorticoid-
DE   induced receptor).
GN   Name=Gpr83; Synonyms=Gir, Gpr72;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE (ISOFORMS 1; 2; 3 AND 4).
RX   MEDLINE=92123228; PubMed=1663214;
RA   Harrigan M.T., Campbell N.F., Bourgeois S.;
RT   "Identification of a gene induced by glucocorticoids in murine T-
RT   cells: a potential G protein-coupled receptor.";
RL   Mol. Endocrinol. 5:1331-1338(1991).
CC   -!- FUNCTION: Orphan receptor. Could be a neuropeptide y receptor.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC         Comment=Experimental confirmation may be lacking for some
CC         isoforms;
CC       Name=1;
CC         IsoId=P30731-1; Sequence=Displayed;
CC       Name=2; Synonyms=RP39;
CC         IsoId=P30731-2; Sequence=VSP_001988;
CC       Name=3; Synonyms=RP82;
CC         IsoId=P30731-3; Sequence=VSP_001989;
CC       Name=4; Synonyms=RP105;
CC         IsoId=P30731-4; Sequence=VSP_001990;
CC   -!- TISSUE SPECIFICITY: Brain, thymus and spleen.
CC   -!- INDUCTION: By glucocorticoids and cAMP; in T-cells.
CC   -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M80481; AAA17882.1; -; mRNA.
DR   PIR; A40470; A40470.
DR   PIR; B40470; B40470.
DR   PIR; C40470; C40470.
DR   PIR; D40470; D40470.
DR   Ensembl; ENSMUSG00000031932; Mus musculus.
DR   MGI; MGI:95712; Gpr83.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW   Receptor; Signal; Transducer; Transmembrane.
FT   SIGNAL        1    17       Potential.
FT   CHAIN        18   423       Probable G-protein coupled receptor 83.
FT   TOPO_DOM     18    71       Extracellular (Potential).
FT   TRANSMEM     72    92       1 (Potential).
FT   TOPO_DOM     93   107       Cytoplasmic (Potential).
FT   TRANSMEM    108   129       2 (Potential).
FT   TOPO_DOM    130   145       Extracellular (Potential).
FT   TRANSMEM    146   167       3 (Potential).
FT   TOPO_DOM    168   186       Cytoplasmic (Potential).
FT   TRANSMEM    187   208       4 (Potential).
FT   TOPO_DOM    209   238       Extracellular (Potential).
FT   TRANSMEM    239   260       5 (Potential).
FT   TOPO_DOM    261   293       Cytoplasmic (Potential).
FT   TRANSMEM    294   315       6 (Potential).
FT   TOPO_DOM    316   327       Extracellular (Potential).
FT   TRANSMEM    328   348       7 (Potential).
FT   TOPO_DOM    349   423       Cytoplasmic (Potential).
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FT   CARBOHYD     38     38       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     46     46       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    134    134       N-linked (GlcNAc. . .) (Potential).
FT   DISULFID    144    224       By similarity.
FT   VARSPLIC    130    171       Missing (in isoform 2).
FT                                /FTId=VSP_001988.
FT   VARSPLIC    171    171       Q -> QGLTAIAVDRHQGLELQKMVRPRGDGGELRSPSVTF
FT                                VPSSLCPALFTCKRPWDFQESQSLHDTLFPPLE (in
FT                                isoform 3).
FT                                /FTId=VSP_001989.
FT   VARSPLIC    171    171       Q -> QRPWDFQESQSLHDTLFPPLE (in isoform
FT                                4).
FT                                /FTId=VSP_001990.
SQ   SEQUENCE   423 AA;  48137 MW;  3ACE43452BF15391 CRC64;

  Query Match             65.6%;  Score 42;  DB 1;  Length 423;
  Best Local Similarity   77.8%;  Pred. No. 2e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        326 LYFAFHWFA 334


RESULT 17
Q6NWR3_HUMAN
ID   Q6NWR3_HUMAN PRELIMINARY;      PRT;   423 AA.
AC   Q6NWR3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   G protein-coupled receptor 83.
GN   Name=GPR83;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RA   Strausberg R.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR   EMBL; BC067474; AAH67474.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ   SEQUENCE   423 AA;  48337 MW;  85580A552883620C CRC64;

  Query Match             65.6%;  Score 42;  DB 2;  Length 423;
  Best Local Similarity   77.8%;  Pred. No. 2e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        326 LYFAFHWFA 334


RESULT 18
Q6NWR4_HUMAN
ID   Q6NWR4_HUMAN PRELIMINARY;      PRT;   423 AA.
AC   Q6NWR4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   G protein-coupled receptor 83.
GN   Name=GPR83;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=PCR rescued clones;
RA   Strausberg R.;
RL   Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR   EMBL; BC067473; AAH67473.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
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DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ   SEQUENCE   423 AA;  48339 MW;  D9E2D96ADC1B44AA CRC64;

  Query Match             65.6%;  Score 42;  DB 2;  Length 423;
  Best Local Similarity   77.8%;  Pred. No. 2e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        326 LYFAFHWFA 334


RESULT 19
Q542Q9_MOUSE
ID   Q542Q9_MOUSE PRELIMINARY;      PRT;   423 AA.
AC   Q542Q9;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Adult male corpus striatum cDNA, RIKEN full-length enriched library,
DE   clone:C030041M14 product:PROBABLE G PROTEIN-COUPLED RECEPTOR GPR72
DE   (GLUCOCORTICOID- INDUCED RECEPTOR), full insert sequence.
GN   Name=Gpr83;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Corpus striatum;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Corpus striatum;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Corpus striatum;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Corpus striatum;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Corpus striatum;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Corpus striatum;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR   EMBL; AK081276; BAC38181.1; -; mRNA.
DR   MGI; MGI:95712; Gpr83.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
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DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ   SEQUENCE   423 AA;  48137 MW;  3ACE43452BF15391 CRC64;

  Query Match            65.6%;  Score 42;  DB 2;  Length 423;
  Best Local Similarity   77.8%;  Pred. No. 2e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        326 LYFAFHWFA 334


RESULT 20
Q5PQ74_XENLA
ID   Q5PQ74_XENLA PRELIMINARY;      PRT;   423 AA.
AC   Q5PQ74;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   LOC495959 protein.
GN   Name=LOC495959;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RX   MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RA   Klein S., Gerhard D.S.;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR   EMBL; BC087333; AAH87333.1; -; mRNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0004983; F:neuropeptide Y receptor activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ   SEQUENCE   423 AA;  48180 MW;  748C659CFA4D6705 CRC64;

  Query Match            65.6%;  Score 42;  DB 2;  Length 423;
  Best Local Similarity   77.8%;  Pred. No. 2e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        326 LYFAFHWFA 334


RESULT 21
Q7W591_BORPA
ID   Q7W591_BORPA PRELIMINARY;      PRT;   431 AA.
AC   Q7W591;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=BPP3410;
OS   Bordetella parapertussis.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Alcaligenaceae; Bordetella.
OX   NCBI_TaxID=519;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=12822 / ATCC BAA-587;
RX   MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA   Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA   Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA   Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA   Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA   Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA   Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA   Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA   Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA   Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA   Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT   "Comparative analysis of the genome sequences of Bordetella pertussis,
RT   Bordetella parapertussis and Bordetella bronchiseptica.";
RL   Nat. Genet. 35:32-40(2003).
CC   -!- COFACTOR: FAD (By similarity).
DR   EMBL; BX640433; CAE38695.1; -; Genomic_DNA.
DR   GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR006076; Fad_oxred.
DR   InterPro; IPR001327; FAD_pyr_redox.
DR   InterPro; IPR003042; Rng_hydrolase.
DR   Pfam; PF01266; DAO; 1.
DR   PRINTS; PR00368; FADPNR.
DR   PRINTS; PR00420; RNGMNOXGNASE.
KW   Complete proteome; FAD; Flavoprotein; Hypothetical protein;
KW   Oxidoreductase.
SQ   SEQUENCE   431 AA;  46529 MW;  6B806A6711706769 CRC64;

  Query Match            65.6%;  Score 42;  DB 2;  Length 431;
  Best Local Similarity   66.7%;  Pred. No. 2e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              ||| ||| :
Db        405 YFGNPWFLF 413
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RESULT 22
Q7VZS0_BORPE
ID   Q7VZS0_BORPE PRELIMINARY;      PRT;   444 AA.
AC   Q7VZS0;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=BP0820;
OS   Bordetella pertussis.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Alcaligenaceae; Bordetella.
OX   NCBI_TaxID=520;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX   MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA   Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA   Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA   Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA   Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA   Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA   Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA   Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA   Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA   Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA   Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT   "Comparative analysis of the genome sequences of Bordetella pertussis,
RT   Bordetella parapertussis and Bordetella bronchiseptica.";
RL   Nat. Genet. 35:32-40(2003).
CC   -!- COFACTOR: FAD (By similarity).
DR   EMBL; BX640413; CAE41123.1; -; Genomic_DNA.
DR   GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR006076; Fad_oxred.
DR   InterPro; IPR001327; FAD_pyr_redox.
DR   InterPro; IPR003042; Rng_hydrolase.
DR   Pfam; PF01266; DAO; 1.
DR   PRINTS; PR00368; FADPNR.
DR   PRINTS; PR00420; RNGMNOXGNASE.
KW   Complete proteome; FAD; Flavoprotein; Hypothetical protein;
KW   Oxidoreductase.
SQ   SEQUENCE   444 AA;  47990 MW;  C467343E047BFBB1 CRC64;

  Query Match             65.6%;  Score 42;  DB 2;  Length 444;
  Best Local Similarity   66.7%;  Pred. No. 2e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              ||| ||| :
Db        418 YFGNPWFLF 426


RESULT 23
Q7WCS1_BORBR
ID   Q7WCS1_BORBR PRELIMINARY;      PRT;   444 AA.
AC   Q7WCS1;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=BB3860;
OS   Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Alcaligenaceae; Bordetella.
OX   NCBI_TaxID=518;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=RB50 / ATCC BAA-588;
RX   MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA   Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA   Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA   Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA   Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA   Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA   Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA   Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA   Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA   Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA   Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT   "Comparative analysis of the genome sequences of Bordetella pertussis,
RT   Bordetella parapertussis and Bordetella bronchiseptica.";
RL   Nat. Genet. 35:32-40(2003).
CC   -!- COFACTOR: FAD (By similarity).
DR   EMBL; BX640448; CAE35834.1; -; Genomic_DNA.
DR   GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR006076; Fad_oxred.
DR   InterPro; IPR001327; FAD_pyr_redox.
DR   InterPro; IPR003042; Rng_hydrolase.
DR   Pfam; PF01266; DAO; 1.
DR   PRINTS; PR00368; FADPNR.
DR   PRINTS; PR00420; RNGMNOXGNASE.
KW   Complete proteome; FAD; Flavoprotein; Hypothetical protein;
KW   Oxidoreductase.
SQ   SEQUENCE   444 AA;  48002 MW;  E7CDA6E75C18C20D CRC64;

  Query Match             65.6%;  Score 42;  DB 2;  Length 444;
  Best Local Similarity   66.7%;  Pred. No. 2e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              ||| ||| :
Db        418 YFGNPWFLF 426


RESULT 24
NHAC_BACSU
ID   NHAC_BACSU     STANDARD;      PRT;   453 AA.
AC   O07553;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Na(+)/H(+) antiporter (Sodium/proton antiporter) (Sodium/hydrogen
DE   antiporter).
GN   Name=nhaC; OrderedLocusNames=BSU09680;
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=168;
RX   MEDLINE=98240224; PubMed=9579061;
RA   Noback M.A., Holsappel S., Kiewiet R., Terpstra P., Wambutt R.,
RA   Wedler H., Venema G., Bron S.;
RT   "The 172 kb prkA-addAB region from 83 degrees to 97 degrees of the
RT   Bacillus subtilis chromosome contains several dysfunctional genes, the
RT   glyB marker, many genes encoding transporter proteins, and the
RT   ubiquitous hit gene.";
RL   Microbiology 144:859-875(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=168;
RX   MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA   Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA   Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA   Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA   Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA   Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA   Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T.,
RA   Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA   Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA   Ghim S.-Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
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RA   Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA   Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,
RA   Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA   Klein C., Kobayashi Y., Koetter P., Koningstein G., Krogh S.,
RA   Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA   Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C.,
RA   Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA   Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA   Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
RA   Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
RA   Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA   Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
RA   Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P.,
RA   Shin B.-S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA   Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA   Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F.,
RA   Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA   Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA   Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E.,
RA   Yoshikawa H., Danchin A.;
RT   "The complete genome sequence of the Gram-positive bacterium Bacillus
RT   subtilis.";
RL   Nature 390:249-256(1997).
RN   [3]
RP   CHARACTERIZATION.
RX   MEDLINE=20459096; PubMed=10903309; DOI=10.1074/jbc.M001112200;
RA   Wei Y., Guffanti A.A., Ito M., Krulwich T.A.;
RT   "Bacillus subtilis YqkI is a novel malic/Na+-lactate antiporter that
RT   enhances growth on malate at low protonmotive force.";
RL   J. Biol. Chem. 275:30287-30292(2000).
RN   [4]
RP   CHARACTERIZATION.
RX   MEDLINE=21172867; PubMed=11274110;
RX   DOI=10.1128/JB.183.8.2505-2515.2001;
RA   Pragai Z., Eschevins C., Bron S., Harwood C.R.;
RT   "Bacillus subtilis NhaC, an Na+/H+ antiporter, influences expression
RT   of the phoPR operon and production of alkaline phosphatases.";
RL   J. Bacteriol. 183:2505-2515(2001).
CC   -!- FUNCTION: Is a secondary, electrogenic Na(+)/H(+) antiporter that
CC       catalyzes Na(+) uptake and proton efflux. Makes modest
CC       contributions to pH homeostasis in the alkaline range of pH but is
CC       not contributor to Na(+) resistance. Appears to have a repressive
CC       effect on growth and on alkaline phosphatases production in the
CC       presence of sodium, by affecting the transcription of the
CC       phoP/phoR two-component regulatory system.
CC   -!- ENZYME REGULATION: The antiport activity is markedly inhibited by
CC       both valinomycin and CCCP, and modestly by nigericin.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to the nhaC Na(+)/H(+) antiporter family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; Y14080; CAA74461.1; -; Genomic_DNA.
DR   EMBL; Z99109; CAB12807.1; -; Genomic_DNA.
DR   PIR; D69829; D69829.
DR   SubtiList; BG13044; nhaC.
DR   InterPro; IPR004770; Antiport_nhaC.
DR   Pfam; PF03553; Na_H_antiporter; 1.
DR   TIGRFAMs; TIGR00931; antiport_nhaC; 1.
KW   Antiport; Complete proteome; Ion transport; Sodium; Sodium transport;
KW   Transmembrane; Transport.
FT   TRANSMEM      9     29       Potential.
FT   TRANSMEM     36     56       Potential.
FT   TRANSMEM     71     91       Potential.
FT   TRANSMEM    109    129       Potential.
FT   TRANSMEM    137    157       Potential.
FT   TRANSMEM    193    215       Potential.
FT   TRANSMEM    257    277       Potential.
FT   TRANSMEM    320    340       Potential.
FT   TRANSMEM    353    375       Potential.
FT   TRANSMEM    429    451       Potential.
SQ   SEQUENCE   453 AA;  48053 MW;  1E1D8103F59235C8 CRC64;

  Query Match             65.6%;  Score 42;  DB 1;  Length 453;
  Best Local Similarity   85.7%;  Pred. No. 2.1e+02;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPW 7
              |:|||||
Db         50 LWFGFPW 56


RESULT 25
Q9EPJ7_MOUSE
ID   Q9EPJ7_MOUSE PRELIMINARY;      PRT;   463 AA.
AC   Q9EPJ7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Glucocorticoid induced receptor (Fragment).
GN   Name=Gpr83; Synonyms=GIR;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=129SV;
RX   MEDLINE=20515601; PubMed=11060465;
RA   De Moerlooze L., Williamson J., Liners F., Perret J., Parmentier M.;
RT   "Cloning and chromosomal mapping of the mouse and human genes encoding
RT   the orphan glucocorticoid-induced receptor (GPR83).";
RL   Cytogenet. Cell Genet. 90:146-150(2000).
DR   EMBL; Y19225; CAC19040.1; -; Genomic_DNA.
DR   EMBL; Y19226; CAC19040.1; JOINED; Genomic_DNA.
DR   EMBL; Y19227; CAC19040.1; JOINED; Genomic_DNA.
DR   MGI; MGI:95712; Gpr83.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   InterPro; IPR000611; NPY_receptor.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PRINTS; PR01012; NRPEPTIDEYR.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Receptor; Transducer; Transmembrane.
FT   NON_TER     463    463
SQ   SEQUENCE   463 AA;  52804 MW;  BBC7E96F8B717CE0 CRC64;

  Query Match             65.6%;  Score 42;  DB 2;  Length 463;
  Best Local Similarity   77.8%;  Pred. No. 2.1e+02;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        383 LYFAFHWFA 391


RESULT 26
C13A1_CAEEL
ID   C13A1_CAEEL    STANDARD;      PRT;   519 AA.
AC   Q27520;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Putative cytochrome P450 CYP13A1 (EC 1.14.-.-).
GN   Name=cyp-13A1; Synonyms=cyp13a1; ORFNames=T10B9.8;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
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OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   -!- FUNCTION: Cytochromes P450 are a group of heme-thiolate
CC       monooxygenases. They oxidize a variety of structurally unrelated
CC       compounds, including steroids, fatty acids, and xenobiotics.
CC   -!- SIMILARITY: Belongs to the cytochrome P450 family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; Z48717; CAA88610.1; -; Genomic_DNA.
DR   PIR; T24784; T24784.
DR   HSSP; P14779; 1JPZ.
DR   Ensembl; T10B9.8; Caenorhabditis elegans.
DR   WormBase; WBGene00011677; cyp-13A1.
DR   WormPep; T10B9.8; CE01660.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   InterPro; IPR002401; EP450I.
DR   PANTHER; PTHR19383; Cytochrome_P450; 1.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00463; EP450I.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
KW   Complete proteome; Heme; Hypothetical protein; Iron; Metal-binding;
KW   Monooxygenase; Oxidoreductase.
FT   METAL       465    465       Iron (heme axial ligand) (By similarity).
SQ   SEQUENCE   519 AA;  60044 MW;  3AF37EDC43539D7A CRC64;

  Query Match             65.6%;  Score 42;  DB 1;  Length 519;
  Best Local Similarity   75.0%;  Pred. No. 2.4e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFA 9
              || |||| :
Db          3 YFWFPWFS 10


RESULT 27
Q5HVZ9_CAMJR
ID   Q5HVZ9_CAMJR PRELIMINARY;      PRT;   218 AA.
AC   Q5HVZ9;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Amino acid ABC transporter, permease protein, His/Glu/Gln/Arg/opine
DE   family.
GN   OrderedLocusNames=CJE0518;
OS   Campylobacter jejuni (strain RM1221).
OC   Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC   Campylobacteraceae; Campylobacter.
OX   NCBI_TaxID=195099;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15660156; DOI=10.1371/journal.pbio.0030015;
RA   Fouts D.E., Mongodin E.F., Mandrell R.E., Miller W.G., Rasko D.A.,
RA   Ravel J., Brinkac L.M., DeBoy R.T., Parker C.T., Daugherty S.C.,
RA   Dodson R.J., Durkin A.S., Madupu R., Sullivan S.A., Shetty J.U.,
RA   Ayodeji M.A., Shvartsbeyn A., Schatz M.C., Badger J.H., Fraser C.M.,
RA   Nelson K.E.;
RT   "Major structural differences and novel potential virulence mechanisms
RT   from the genomes of multiple Campylobacter species.";
RL   PLoS Biol. 3:72-85(2005).
CC   -!- FUNCTION: Part of a binding-protein-dependent transport system.
CC       Probably responsible for the translocation of the substrate across
CC       the membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC       system permease family.
DR   EMBL; CP000025; AAW35105.1; -; Genomic_DNA.
DR   TIGR; CJE0518; -.
DR   GO; GO:0019866; C:inner membrane; IEA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR000515; BPD_transp.
DR   InterPro; IPR010065; HEQRo_ABC_3TM.
DR   Pfam; PF00528; BPD_transp_1; 1.
DR   TIGRFAMs; TIGR01726; HEQRo_perm_3TM; 1.
DR   PROSITE; PS50928; ABC_TM1; 1.
KW   Complete proteome; Transmembrane; Transport.
SQ   SEQUENCE   218 AA;  25274 MW;  5C38F06389FB0227 CRC64;

  Query Match             64.8%;  Score 41.5;  DB 2;  Length 218;
  Best Local Similarity   63.6%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 LYFGFP-WFAY 10
              :||||| || :
Db         72 VYFGFPRWFGW 82


RESULT 28
Q9PI40_CAMJE
ID   Q9PI40_CAMJE PRELIMINARY;      PRT;   218 AA.
AC   Q9PI40;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Amino-acid ABC transporter integral membrane protein.
GN   OrderedLocusNames=Cj0468;
OS   Campylobacter jejuni.
OC   Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC   Campylobacteraceae; Campylobacter.
OX   NCBI_TaxID=197;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=NCTC 11168;
RX   MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
RA   Parkhill J., Wren B.W., Mungall K.L., Ketley J.M., Churcher C.M.,
RA   Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
RA   Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
RA   Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
RA   Whitehead S., Barrell B.G.;
RT   "The genome sequence of the food-borne pathogen Campylobacter jejuni
RT   reveals hypervariable sequences.";
RL   Nature 403:665-668(2000).
CC   -!- FUNCTION: Part of a binding-protein-dependent transport system.
CC       Probably responsible for the translocation of the substrate across
CC       the membrane (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the binding-protein-dependent transport
CC       system permease family.
DR   EMBL; AL139075; CAB75106.1; -; Genomic_DNA.
DR   PIR; G81391; G81391.
DR   GO; GO:0019866; C:inner membrane; IEA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR000515; BPD_transp.
DR   InterPro; IPR010065; HEQRo_ABC_3TM.
DR   Pfam; PF00528; BPD_transp_1; 1.
DR   TIGRFAMs; TIGR01726; HEQRo_perm_3TM; 1.
DR   PROSITE; PS50928; ABC_TM1; 1.
KW   Complete proteome; Transmembrane; Transport.
SQ   SEQUENCE   218 AA;  25274 MW;  5C38F06389FB0227 CRC64;
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  Query Match             64.8%;  Score 41.5;  DB 2;  Length 218;
  Best Local Similarity   63.6%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    2;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 LYFGFP-WFAY 10
              :|||||  || :
Db         72 VYFGFPRWFGW 82


RESULT 29
Q73FV1_WOLPM
ID   Q73FV1_WOLPM PRELIMINARY;      PRT;   118 AA.
AC   Q73FV1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Succinate dehydrogenase, hydrophobic membrane anchor protein,
DE   putative.
GN   OrderedLocusNames=WD1222;
OS   Wolbachia pipientis wMel.
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC   Rickettsiaceae; Wolbachieae; Wolbachia.
OX   NCBI_TaxID=66077;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15024419; DOI=10.1371/journal.pbio.0020069;
RA   Wu M., Sun L.V., Vamathevan J.J., Riegler M., DeBoy R.T.,
RA   Brownlie J.C., McGraw E.A., Martin W., Esser C., Ahmadinejad N.,
RA   Wiegand C., Madupu R., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA   Durkin A.S., Kolonay J.F., Nelson W.C., Mohamoud Y., Lee P.,
RA   Berry K.J., Young M.B., Utterback T.R., Weidman J.F., Nierman W.C.,
RA   Paulsen I.T., Nelson K.E., Tettelin H., O'Neill S.L., Eisen J.A.;
RT   "Phylogenomics of the reproductive parasite Wolbachia pipientis wMel:
RT   a streamlined genome overrun by mobile genetic elements.";
RL   PLoS Biol. 2:327-341(2004).
DR   EMBL; AE017260; AAS14868.1; -; Genomic_DNA.
DR   TIGR; WD1222; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0000104; F:succinate dehydrogenase activity; IEA.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   GO; GO:0006099; P:tricarboxylic acid cycle; IEA.
DR   InterPro; IPR000701; Sdh_cyt.
DR   Pfam; PF01127; Sdh_cyt; 1.
KW   Complete proteome.
SQ   SEQUENCE   118 AA;  14054 MW;  84608B9092968909 CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 118;
  Best Local Similarity   70.0%;  Pred. No. 89;
  Matches    7;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              | |  |||| |
Db         21 LLFLFPWFIY 30


RESULT 30
Q57P30_SALCH
ID   Q57P30_SALCH PRELIMINARY;      PRT;   120 AA.
AC   Q57P30;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Putative inner membrane protein.
GN   Name=tfpB; OrderedLocusNames=SC1625;
OS   Salmonella cholerae-suis (Salmonella enterica).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=591;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=SC-B67;
RX   PubMed=15781495;
RA   Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
RA   Wang H.-S., Lee Y.-S.;
RT   "The genome sequence of Salmonella enterica serovar Choleraesuis, a
RT   highly invasive and resistant zoonotic pathogen.";
RL   Nucleic Acids Res. 33:1690-1698(2005).
DR   EMBL; AE017220; AAX65531.1; -; Genomic_DNA.
KW   Complete proteome.
SQ   SEQUENCE   120 AA;  14167 MW;  3B7C2DA69F6A4EB6 CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 120;
  Best Local Similarity   71.4%;  Pred. No. 91;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPWF 8
              |:||||:
Db         16 YYGFPWW 22


RESULT 31
Q8FIW0_ECOL6
ID   Q8FIW0_ECOL6 PRELIMINARY;      PRT;   120 AA.
AC   Q8FIW0;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein c1258.
GN   OrderedLocusNames=c1258;
OS   Escherichia coli O6.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=217992;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX   MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA   Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA   Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA   Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA   Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT   "Extensive mosaic structure revealed by the complete genome sequence
RT   of uropathogenic Escherichia coli.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR   EMBL; AE016759; AAN79732.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   120 AA;  13734 MW;  B47AD624F3C5BE1F CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 120;
  Best Local Similarity   71.4%;  Pred. No. 91;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPWF 8
              |:||||:
Db         14 YYGFPWW 20


RESULT 32
Q7AGG4_ECO57
ID   Q7AGG4_ECO57 PRELIMINARY;      PRT;   222 AA.
AC   Q7AGG4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical membrane protein.
GN   OrderedLocusNames=ECs0816;
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=83334;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX   MEDLINE=21156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
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RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
DR   EMBL; BA000007; BAB34239.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   222 AA;  25823 MW;  7050677A8D981CD1 CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 222;
  Best Local Similarity   71.4%;  Pred. No. 1.6e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPWF 8
              |:||||:
Db         19 YYGFPWW 25


RESULT 33
Q8ZPA5_SALTY
ID   Q8ZPA5_SALTY PRELIMINARY;      PRT;   238 AA.
AC   Q8ZPA5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Putative inner membrane protein.
GN   OrderedLocusNames=STM1630;
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=LT2;
RX   MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
DR   EMBL; AE008772; AAL20548.1; -; Genomic_DNA.
KW   Complete proteome.
SQ   SEQUENCE   238 AA;  27866 MW;  D8863AD8C3985880 CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 238;
  Best Local Similarity   71.4%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPWF 8
              |:||||:
Db         35 YYGFPWW 41


RESULT 34
Q8VSF8_SHIFL
ID   Q8VSF8_SHIFL PRELIMINARY;      PRT;   238 AA.
AC   Q8VSF8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=CP0168;
OS   Shigella flexneri.
OG   Plasmid pCP301.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Shigella.
OX   NCBI_TaxID=623;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=301;
RX   MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
RA   Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA   Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA   Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA   Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA   Yu J.;
RT   "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT   through comparison with genomes of Escherichia coli K12 and O157.";
RL   Nucleic Acids Res. 30:4432-4441(2002).
DR   EMBL; AF386526; AAL72434.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein; Plasmid.
SQ   SEQUENCE   238 AA;  28050 MW;  E166795F10AA199D CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 238;
  Best Local Similarity   71.4%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPWF 8
              |:||||:
Db         35 YYGFPWW 41


RESULT 35
Q7ABG6_ECO57
ID   Q7ABG6_ECO57 PRELIMINARY;      PRT;   247 AA.
AC   Q7ABG6;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical membrane protein.
GN   OrderedLocusNames=ECs3500;
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=83334;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX   MEDLINE=21156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
DR   EMBL; BA000007; BAB36923.1; -; Genomic_DNA.
KW   Hypothetical protein.
SQ   SEQUENCE   247 AA;  28467 MW;  55CB2048EE3E7A61 CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 247;
  Best Local Similarity   71.4%;  Pred. No. 1.7e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPWF 8
              |:||||:
Db         44 YYGFPWW 50


RESULT 36
Q8X997_ECO57
ID   Q8X997_ECO57 PRELIMINARY;      PRT;   252 AA.
AC   Q8X997;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=z0957, z3931;
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=83334;
RN   [1]
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RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX   MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL   Nature 409:529-533(2001).
DR   EMBL; AE005174; AAG57744.1; -; Genomic_DNA.
DR   EMBL; AE005174; AAG55113.1; -; Genomic_DNA.
DR   PIR; D85910; D85910.
DR   PIR; D91066; D91066.
DR   PIR; H90730; H90730.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   252 AA;  29014 MW;  2F7DBAA2FF438C80 CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 252;
  Best Local Similarity   71.4%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPWF 8
              |:||||:
Db         49 YYGFPWW 55


RESULT 37
Q99PZ3_SHIFL
ID   Q99PZ3_SHIFL PRELIMINARY;      PRT;   258 AA.
AC   Q99PZ3;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   ORF137 (Orf, hypothetical).
GN   Name=S0177;
OS   Shigella flexneri.
OG   Plasmid virulence plasmid pWR501.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Shigella.
OX   NCBI_TaxID=623;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=M90T;
RX   MEDLINE=20566792; PubMed=11115111;
RA   Buchrieser C., Glaser P., Rusniok C., Nedjari H., d'Hauteville H.,
RA   Kunst F., Sansonetti P., Parsot C.;
RT   "The virulence plasmid pWR100 and the repertoire of proteins secreted
RT   by the type III secretion apparatus of Shigella flexneri.";
RL   Mol. Microbiol. 38:760-771(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   PLASMID=virulence plasmid pWR501;
RX   MEDLINE=21189246; PubMed=11292750;
RX   DOI=10.1128/IAI.69.5.3271-3285.2001;
RA   Venkatesan M.M., Goldberg M.B., Rose D.J., Grotbeck E.J., Burland V.,
RA   Blattner F.R.;
RT   "Complete DNA sequence and analysis of the large virulence plasmid of
RT   Shigella flexneri.";
RL   Infect. Immun. 69:3271-3285(2001).
DR   EMBL; AL391753; CAC05835.1; -; Genomic_DNA.
DR   EMBL; AF348706; AAK18487.1; -; Genomic_DNA.
KW   Hypothetical protein; Plasmid.
SQ   SEQUENCE   258 AA;  30506 MW;  EA75C2A846242AF5 CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 258;
  Best Local Similarity   71.4%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPWF 8
              |:||||:
Db         55 YYGFPWW 61


RESULT 38
Q61XG3_CAEBR
ID   Q61XG3_CAEBR PRELIMINARY;      PRT;   377 AA.
AC   Q61XG3;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein CBG03995 (Fragment).
GN   Name=CBG03995;
OS   Caenorhabditis briggsae.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6238;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RG   The C.briggsae Sequencing Consortium;
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAC01000016; CAE60393.1; -; Genomic_DNA.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   377 AA;  42466 MW;  38D480709D8D80D1 CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 377;
  Best Local Similarity   66.7%;  Pred. No. 2.5e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              || |||  |
Db         66 YFSFPWAIY 74


RESULT 39
Q6AXX9_RAT
ID   Q6AXX9_RAT  PRELIMINARY;      PRT;   388 AA.
AC   Q6AXX9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein LOC498251.
GN   Name=LOC498251;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Testis;
RG   NIH MGC Project;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC079272; AAH79272.1; -; mRNA.
KW   Hypothetical protein.
SQ   SEQUENCE   388 AA;  44519 MW;  BCA0DA5452C94F1E CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 388;
  Best Local Similarity   75.0%;  Pred. No. 2.6e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 FGFPWFAY 10
              |||||  |
Db         52 FGFPWSTY 59


RESULT 40
Q9N476_CAEEL
ID   Q9N476_CAEEL PRELIMINARY;      PRT;   407 AA.
AC   Q9N476;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein Y23H5B.4.
GN   ORFNames=Y23H5B.4;
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RG   The C. elegans sequencing consortium;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR   EMBL; AC024753; AAF60458.2; -; Genomic_DNA.
DR   Ensembl; Y23H5B.4; Caenorhabditis elegans.
DR   WormBase; WBGene00021275; Y23H5B.4.
DR   WormPep; Y23H5B.4; CE31098.
DR   GO; GO:0016021; C:integral to membrane; IEA.
DR   GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR   GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   407 AA;  46021 MW;  F64670D074BCD680 CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 407;
  Best Local Similarity   66.7%;  Pred. No. 2.7e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              || |||  |
Db         96 YFSFPWAIY 104


RESULT 41
Q5I0J0_RAT
ID   Q5I0J0_RAT  PRELIMINARY;      PRT;   465 AA.
AC   Q5I0J0;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical LOC299354.
GN   Name=LOC299354;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Thymus;
RG   NIH MGC Project;
RL   Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Beta-2-microglobulin is the beta-chain of major
CC       histocompatibility complex class I molecules (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
DR   EMBL; BC088271; AAH88271.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 3.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 4.
KW   Hypothetical protein; Immunoglobulin domain; Repeat.
SQ   SEQUENCE   465 AA;  51699 MW;  97C4533A213A424F CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 465;
  Best Local Similarity   55.6%;  Pred. No. 3.1e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              |:|: || |
Db        120 YYGYNWFTY 128


RESULT 42
Q4P0W0_USTMA
ID   Q4P0W0_USTMA PRELIMINARY;      PRT;   695 AA.
AC   Q4P0W0;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein.
GN   ORFNames=UM06253.1;
```

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OS   Ustilago maydis 521.
OC   Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC   Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX   NCBI_TaxID=237631;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=521;
RA   Birren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,
RA   Ait-zahra M., Allen N., Allen T., An P., Anderson M., Anderson S.,
RA   Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
RA   Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavskiy L.,
RA   Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
RA   Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
RA   Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
RA   David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
RA   Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
RA   Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
RA   Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
RA   Gnirke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
RA   Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
RA   Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
RA   Jaffe D., Jones C., Kamal M., Kamat A., Kamvysselis M., Karlsson E.,
RA   Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
RA   Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
RA   Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,
RA   Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,
RA   Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,
RA   Mccarthy M., Mcdonough S., Mcghee T., Meldrim J., Meneus L.,
RA   Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
RA   Mozes J., Mulrain L., Munson G., Naylor J., Newes C., Nguyen C.,
RA   Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
RA   Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
RA   O'neill K., Osman S., Parker S., Perrin D., Phunkhang P., Piqani B.,
RA   Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
RA   Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,
RA   Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
RA   Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
RA   Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
RA   Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,
RA   Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
RA   Towey S., Tsamla T., Tsomo N., Vallee D., Vassiliev H.,
RA   Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
RA   Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
RA   Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
RA   Zimmer A., Zody M., Lander E.;
RT   "The genome sequence of Ustilago maydis.";
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AACP01000237; EAK87133.1; -; Genomic_DNA.
DR   InterPro; IPR001734; Na/solut_symport.
DR   Pfam; PF00474; SSF; 1.
DR   TIGRFAMs; TIGR00813; sss; 1.
DR   PROSITE; PS50283; NA_SOLUT_SYMP_3; 1.
KW   Hypothetical protein; Transmembrane; Transport.
SQ   SEQUENCE   695 AA;  74541 MW;  7602189A7397F812 CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 695;
  Best Local Similarity   85.7%;  Pred. No. 4.4e+02;
  Matches    6;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LYFGFPW 7
              |||| ||
Db        299 LYFGLPW 305


RESULT 43
Q5LIF7_BACFN
ID   Q5LIF7_BACFN PRELIMINARY;      PRT;   720 AA.
AC   Q5LIF7;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   Putative exported protein.
GN   OrderedLocusNames=BF0296;
OS   Bacteroides fragilis (strain ATCC 25285 / NCTC 9343).
OC   Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales;
OC   Bacteroidaceae; Bacteroides.
OX   NCBI_TaxID=272559;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15746427; DOI=10.1126/science.1107008;
RA   Cerdeno-Tarraga A.-M., Patrick S., Crossman L.C., Blakely G.,
RA   Abratt V., Lennard N., Poxton I., Duerden B., Harris B., Quail M.A.,
RA   Barron A., Clark L., Corton C., Doggett J., Holden M.T.G., Larke N.,
RA   Line A., Lord A., Norbertczak H., Ormond D., Price C.,
RA   Rabbinowitsch E., Woodward J., Barrell B.G., Parkhill J.;
RT   "Extensive DNA inversions in the B. fragilis genome control variable
RT   gene expression.";
RL   Science 307:1463-1465(2005).
DR   EMBL; CR626927; CAH06069.1; -; Genomic_DNA.
KW   Complete proteome.
SQ   SEQUENCE   720 AA;  82598 MW;  8A1CE9065EDE5598 CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 720;
  Best Local Similarity   75.0%;  Pred. No. 4.5e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFA 9
              |:|||| |
Db        171 YYGFPWRA 178


RESULT 44
Q64ZH9_BACFR
ID   Q64ZH9_BACFR PRELIMINARY;      PRT;   720 AA.
AC   Q64ZH9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=BF0348;
OS   Bacteroides fragilis.
OC   Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC   Bacteroidaceae; Bacteroides.
OX   NCBI_TaxID=817;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=YCH46;
RX   PubMed=15466707; DOI=10.1073/pnas.0404172101;
RA   Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA   Kuhara S., Hattori M., Hayashi T., Ohnishi Y.;
RT   "Genomic analysis of Bacteroides fragilis reveals extensive DNA
RT   inversions regulating cell surface adaptation.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:14919-14924(2004).
DR   EMBL; AP006841; BAD47097.1; -; Genomic_DNA.
KW   Complete proteome; Hypothetical protein.
SQ   SEQUENCE   720 AA;  82669 MW;  058689AB62FE67FC CRC64;

  Query Match             64.1%;  Score 41;  DB 2;  Length 720;
  Best Local Similarity   75.0%;  Pred. No. 4.5e+02;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFA 9
              |:|||| |
Db        171 YYGFPWRA 178


RESULT 45
Q4YFN0_PLABE
ID   Q4YFN0_PLABE PRELIMINARY;      PRT;    74 AA.
AC   Q4YFN0;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
```

```
DE   Hypothetical protein (Fragment).
GN   ORFNames=PB301084.00.0;
OS   Plasmodium berghei.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5821;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA   Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA   James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA   Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA   Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C.,
RA   Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT   "A comprehensive survey of the Plasmodium life cycle by genomic,
RT   transcriptomic, and proteomic analyses.";
RL   Science 307:82-86(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAI01005588; CAI03188.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER       1      1
FT   NON_TER      74     74
SQ   SEQUENCE   74 AA;  9038 MW;  E96830D12269C2DF CRC64;

  Query Match             62.5%;  Score 40;  DB 2;  Length 74;
  Best Local Similarity   60.0%;  Pred. No. 84;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||  || :
Db          5 LYFGLAWFIH 14


RESULT 46
Q6SK73_ARTAU
ID   Q6SK73_ARTAU PRELIMINARY;      PRT;   134 AA.
AC   Q6SK73;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Arthrobacter aurescens.
OG   Plasmid pAA1.
OC   Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC   Micrococcineae; Micrococcaceae; Arthrobacter.
OX   NCBI_TaxID=43663;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=TC1;
RX   PubMed=15240330; DOI=10.1128/AEM.70.7.4402-4407.2004;
RA   Sajjaphan K., Shapir N., Wackett L.P., Palmer M., Blackmon B.,
RA   Tomkins J., Sadowsky M.J.;
RT   "Arthrobacter aurescens TC1 Atrazine Catabolism Genes trzN, atzB, and
RT   atzC Are Linked on a 160-Kilobase Region and Are Functional in
RT   Escherichia coli.";
RL   Appl. Environ. Microbiol. 70:4402-4407(2004).
DR   EMBL; AY456696; AAS20099.1; -; Genomic_DNA.
DR   InterPro; IPR000238; Rib_bind_factA.
DR   PROSITE; PS01319; RBFA; UNKNOWN_1.
KW   Hypothetical protein; Plasmid.
SQ   SEQUENCE   134 AA;  14458 MW;  FF4377607D3934FF CRC64;

  Query Match             62.5%;  Score 40;  DB 2;  Length 134;
  Best Local Similarity   75.0%;  Pred. No. 1.4e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 FGFPWFAY 10
              | |||| |
Db         34 FRFPWFIY 41


RESULT 47
Q6RK11_BURCE
ID   Q6RK11_BURCE PRELIMINARY;      PRT;   137 AA.
AC   Q6RK11;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   CyaB (Fragment).
GN   Name=cyaB;
OS   Burkholderia cepacia (Pseudomonas cepacia).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
OX   NCBI_TaxID=292;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Klein W., Keusgen M.;
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY496070; AAR88792.1; -; Genomic_DNA.
DR   GO; GO:0016810; F:hydrolase activity, acting on carbon-nitrog. . .; IEA.
DR   GO; GO:0006807; P:nitrogen compound metabolism; IEA.
DR   InterPro; IPR000132; N/CN_hydratase.
DR   InterPro; IPR003010; Ntlse/CNhydtse.
DR   Pfam; PF00795; CN_hydrolase; 1.
DR   PROSITE; PS50263; CN_HYDROLASE; 1.
DR   PROSITE; PS00920; NITRIL_CHT_1; 1.
FT   NON_TER       1      1
FT   NON_TER     137    137
SQ   SEQUENCE   137 AA;  15424 MW;  F2A9F4A064F4985D CRC64;

  Query Match             62.5%;  Score 40;  DB 2;  Length 137;
  Best Local Similarity   71.4%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GFPWFAY 10
              |:||||:
Db         55 GYPWFAF 61


RESULT 48
Q6HPK3_BACHK
ID   Q6HPK3_BACHK PRELIMINARY;      PRT;   168 AA.
AC   Q6HPK3;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
GN   OrderedLocusNames=BT9727_0162;
OS   Bacillus thuringiensis (subsp. konkukian).
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC   Bacillus cereus group.
OX   NCBI_TaxID=180856;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=97-27;
RA   Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA   Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA   Richardson P., Rubin E., Tice H.;
RT   "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE017355; AAT62128.1; -; Genomic_DNA.
DR   InterPro; IPR011637; DoxX.
DR   Pfam; PF07681; DoxX; 1.
KW   Complete proteome.
SQ   SEQUENCE   168 AA;  18367 MW;  755F2BCD8EA2F760 CRC64;

  Query Match             62.5%;  Score 40;  DB 2;  Length 168;
  Best Local Similarity   66.7%;  Pred. No. 1.8e+02;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              || |: |||
Db         21 LYIGYTWFA 29
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RESULT 49
Q5C3T7_SCHJA
ID   Q5C3T7_SCHJA PRELIMINARY;      PRT;   227 AA.
AC   Q5C3T7;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein.
OS   Schistosoma japonicum (Blood fluke).
OC   Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC   Schistosomatoidea; Schistosomatidae; Schistosoma.
OX   NCBI_TaxID=6182;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Han Z.;
RL   Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY809799; AAX25688.1; -; mRNA.
DR   InterPro; IPR001107; Band_7.
DR   InterPro; IPR012282; Cytochrome_c_R.
DR   InterPro; IPR011992; EF-Hand_type.
DR   InterPro; IPR012292; Globin_related.
DR   InterPro; IPR011993; PH_type.
DR   InterPro; IPR000163; Prohibitin.
DR   Pfam; PF01145; Band_7; 1.
DR   PRINTS; PR00679; PROHIBITIN.
DR   SMART; SM00244; PHB; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   227 AA;  25237 MW;  A9BA78C4472EE37A CRC64;

  Query Match             62.5%;  Score 40;  DB 2;  Length 227;
  Best Local Similarity   60.0%;  Pred. No. 2.3e+02;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              |:|  ||| |
Db         59 LHFRIPWFQY 68


RESULT 50
Q4XWE8_PLACH
ID   Q4XWE8_PLACH PRELIMINARY;      PRT;   239 AA.
AC   Q4XWE8;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Hypothetical protein (Fragment).
GN   ORFNames=PC001286.02.0;
OS   Plasmodium chabaudi.
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=5825;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA   Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA   James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA   Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA   Bidwell S.L., Rajandream M.A., Carucci D.J, Yates J.R., Kafatos F.C.,
RA   Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT   "A comprehensive survey of the Plasmodium life cycle by genomic,
RT   transcriptomic, and proteomic analyses.";
RL   Science 307:82-86(2005).
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; CAAJ01002654; CAH78763.1; -; Genomic_DNA.
KW   Hypothetical protein.
FT   NON_TER       1      1
FT   NON_TER     239    239
SQ   SEQUENCE   239 AA;  28015 MW;  CCAA3C5A567F3BAE CRC64;

  Query Match             62.5%;  Score 40;  DB 2;  Length 239;
  Best Local Similarity   66.7%;  Pred. No. 2.4e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              |  |||| |
Db        183 YSTFPWFGY 191


Search completed: March 23, 2006, 02:04:54
Job time : 102.17 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:05:22 ; Search time 21.6438 Seconds
(without alignments)
38.198 Million cell updates/sec

Title: US-10-755-382-25
Perfect score: 64
Sequence: 1 LYFGFPWFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	64	100.0	10	1	US-08-318-157B-25	Sequence 25, Appl
2	64	100.0	10	2	US-09-253-794-25	Sequence 25, Appl
3	64	100.0	119	1	US-08-318-157B-2	Sequence 2, Appli
4	64	100.0	119	1	US-08-318-157B-8	Sequence 8, Appli
5	64	100.0	119	1	US-08-318-157B-9	Sequence 9, Appli
6	64	100.0	119	1	US-08-318-157B-10	Sequence 10, Appl
7	64	100.0	119	1	US-08-318-157B-11	Sequence 11, Appl
8	64	100.0	119	1	US-08-318-157B-12	Sequence 12, Appl
9	64	100.0	119	1	US-08-318-157B-13	Sequence 13, Appl
10	64	100.0	119	1	US-08-318-157B-14	Sequence 14, Appl
11	64	100.0	119	1	US-08-318-157B-15	Sequence 15, Appl
12	64	100.0	119	1	US-08-318-157B-17	Sequence 17, Appl
13	64	100.0	119	1	US-08-318-157B-57	Sequence 57, Appl
14	64	100.0	119	1	US-08-318-157B-58	Sequence 58, Appl
15	64	100.0	119	2	US-09-253-794-2	Sequence 2, Appli
16	64	100.0	119	2	US-09-253-794-8	Sequence 8, Appli
17	64	100.0	119	2	US-09-253-794-9	Sequence 9, Appli
18	64	100.0	119	2	US-09-253-794-10	Sequence 10, Appl
19	64	100.0	119	2	US-09-253-794-11	Sequence 11, Appl
20	64	100.0	119	2	US-09-253-794-12	Sequence 12, Appl
21	64	100.0	119	2	US-09-253-794-13	Sequence 13, Appl
22	64	100.0	119	2	US-09-253-794-14	Sequence 14, Appl
23	64	100.0	119	2	US-09-253-794-15	Sequence 15, Appl
24	64	100.0	119	2	US-09-253-794-17	Sequence 17, Appl
25	64	100.0	119	2	US-09-253-794-57	Sequence 57, Appl
26	64	100.0	119	2	US-09-253-794-58	Sequence 58, Appl
27	44	68.8	2210	2	US-09-309-572-7	Sequence 7, Appli
28	44	68.8	2210	2	US-09-718-096-7	Sequence 7, Appli
29	43	67.2	116	2	US-08-881-037-19	Sequence 19, Appl
30	42	65.6	119	2	US-08-767-128-20	Sequence 20, Appl
31	42	65.6	349	1	US-08-118-270-71	Sequence 71, Appl
32	42	65.6	349	4	PCT-US93-08528-71	Sequence 71, Appl
33	40	62.5	299	2	US-08-851-971-3	Sequence 3, Appli
34	40	62.5	299	2	US-08-851-971-5	Sequence 5, Appli
35	40	62.5	445	2	US-09-605-703B-72	Sequence 72, Appl
36	39	60.9	66	2	US-09-248-796A-23660	Sequence 23660, A
37	39	60.9	120	2	US-09-065-059-1	Sequence 1, Appli
38	39	60.9	120	2	US-08-913-555-1	Sequence 1, Appli
39	39	60.9	121	2	US-08-913-555-19	Sequence 19, Appl
40	39	60.9	363	2	US-09-710-279-302	Sequence 302, App
41	39	60.9	370	2	US-09-134-001C-4393	Sequence 4393, Ap
42	39	60.9	479	2	US-09-902-540-16455	Sequence 16455, A
43	38	59.4	110	2	US-09-270-767-48123	Sequence 48123, A
44	38	59.4	120	2	US-10-092-246-9	Sequence 9, Appli
45	38	59.4	120	2	US-10-096-246A-9	Sequence 9, Appli
46	38	59.4	275	2	US-09-902-540-15009	Sequence 15009, A
47	38	59.4	357	2	US-09-710-279-2558	Sequence 2558, Ap
48	38	59.4	357	2	US-09-902-540-9903	Sequence 9903, Ap
49	38	59.4	415	2	US-09-134-001C-5101	Sequence 5101, Ap
50	38	59.4	489	2	US-09-949-016-9590	Sequence 9590, Ap
51	38	59.4	567	2	US-09-252-991A-27014	Sequence 27014, A
52	38	59.4	1091	2	US-09-538-092-469	Sequence 469, App
53	37	57.8	296	2	US-09-543-681A-4672	Sequence 4672, Ap
54	37	57.8	349	2	US-09-252-991A-18987	Sequence 18987, A
55	37	57.8	483	2	US-09-252-991A-29267	Sequence 29267, A
56	37	57.8	695	2	US-09-602-787A-52	Sequence 52, Appl
57	37	57.8	850	2	US-09-129-603-2	Sequence 2, Appli
58	37	57.8	1064	2	US-10-104-047-3830	Sequence 3830, Ap
59	37	57.8	2012	2	US-09-602-787A-50	Sequence 50, Appl
60	36	56.2	113	2	US-09-087-031E-24	Sequence 24, Appl
61	36	56.2	123	1	US-08-356-272-3	Sequence 3, Appli
62	36	56.2	134	2	US-09-270-767-37945	Sequence 37945, A
63	36	56.2	134	2	US-09-270-767-53162	Sequence 53162, A
64	36	56.2	141	2	US-09-902-540-15488	Sequence 15488, A
65	36	56.2	201	2	US-09-902-540-13764	Sequence 13764, A
66	36	56.2	212	2	US-08-937-067-4	Sequence 4, Appli
67	36	56.2	214	2	US-09-583-110-3186	Sequence 3186, Ap
68	36	56.2	295	2	US-08-937-067-2	Sequence 2, Appli
69	36	56.2	295	2	US-09-148-545-179	Sequence 179, App
70	36	56.2	295	2	US-09-621-011-179	Sequence 179, App
71	36	56.2	295	2	US-09-999-833A-415	Sequence 415, App
72	36	56.2	295	2	US-10-020-445A-415	Sequence 415, App
73	36	56.2	296	2	US-09-148-545-237	Sequence 237, App
74	36	56.2	296	2	US-09-621-011-237	Sequence 237, App
75	36	56.2	298	2	US-08-851-971-8	Sequence 8, Appli
76	36	56.2	348	2	US-09-328-352-6843	Sequence 6843, Ap
77	36	56.2	373	2	US-09-107-532A-4519	Sequence 4519, Ap
78	36	56.2	410	2	US-09-328-352-4860	Sequence 4860, Ap
79	36	56.2	424	2	US-09-826-509-455	Sequence 455, App
80	36	56.2	613	2	US-09-252-991A-23154	Sequence 23154, A
81	36	56.2	630	2	US-09-252-991A-19702	Sequence 19702, A
82	36	56.2	800	2	US-10-101-464A-912	Sequence 912, App
83	36	56.2	1211	2	US-09-328-352-7967	Sequence 7967, Ap
84	35.5	55.5	116	1	US-08-888-366-12	Sequence 12, Appl
85	35	54.7	9	2	US-07-987-264-3	Sequence 3, Appli
86	35	54.7	75	2	US-09-605-703B-2082	Sequence 2082, Ap
87	35	54.7	96	2	US-09-248-796A-16797	Sequence 16797, A
88	35	54.7	118	1	US-08-428-257A-74	Sequence 74, Appl
89	35	54.7	118	1	US-08-428-257A-78	Sequence 78, Appl
90	35	54.7	118	2	US-07-987-264-14	Sequence 14, Appl
91	35	54.7	118	2	US-07-987-264-60	Sequence 60, Appl
92	35	54.7	267	2	US-09-270-767-37278	Sequence 37278, A
93	35	54.7	267	2	US-09-270-767-52495	Sequence 52495, A
94	35	54.7	290	2	US-09-328-352-4323	Sequence 4323, Ap
95	35	54.7	296	2	US-10-101-464A-633	Sequence 633, App
96	35	54.7	342	2	US-09-107-532A-6412	Sequence 6412, Ap
97	35	54.7	405	2	US-09-107-532A-6766	Sequence 6766, Ap
98	35	54.7	455	2	US-09-999-833A-430	Sequence 430, App
99	35	54.7	455	2	US-10-020-445A-430	Sequence 430, App
100	35	54.7	458	2	US-09-583-110-5167	Sequence 5167, Ap

101	35	54.7	463	2	US-09-107-433-3506	Sequence 3506, Ap
102	35	54.7	501	2	US-09-248-796A-15119	Sequence 15119, A
103	35	54.7	514	2	US-09-489-039A-10028	Sequence 10028, A
104	35	54.7	626	2	US-09-489-039A-9106	Sequence 9106, Ap
105	35	54.7	835	2	US-09-949-016-7379	Sequence 7379, Ap
106	35	54.7	944	2	US-09-437-568A-39	Sequence 39, Appl
107	35	54.7	1698	2	US-09-902-540-12813	Sequence 12813, A
108	34.5	53.9	116	1	US-08-888-366-10	Sequence 10, Appl
109	34.5	53.9	346	2	US-09-248-796A-16397	Sequence 16397, A
110	34	53.1	59	2	US-09-227-357-645	Sequence 645, App
111	34	53.1	59	2	US-09-973-278-430	Sequence 430, App
112	34	53.1	69	2	US-09-270-767-38277	Sequence 38277, A
113	34	53.1	69	2	US-09-270-767-53494	Sequence 53494, A
114	34	53.1	80	2	US-09-621-976-5613	Sequence 5613, Ap
115	34	53.1	81	2	US-09-904-615-115	Sequence 115, App
116	34	53.1	81	2	US-09-904-615-122	Sequence 122, App
117	34	53.1	81	2	US-10-054-988-115	Sequence 115, App
118	34	53.1	81	2	US-10-054-988-122	Sequence 122, App
119	34	53.1	97	2	US-09-904-615-170	Sequence 170, App
120	34	53.1	97	2	US-10-054-988-170	Sequence 170, App
121	34	53.1	127	2	US-09-902-540-10040	Sequence 10040, A
122	34	53.1	150	1	US-07-668-517-11	Sequence 11, Appl
123	34	53.1	151	1	US-07-668-517-25	Sequence 25, Appl
124	34	53.1	159	2	US-09-134-000C-3971	Sequence 3971, Ap
125	34	53.1	228	2	US-09-248-796A-14223	Sequence 14223, A
126	34	53.1	262	2	US-09-198-452A-646	Sequence 646, App
127	34	53.1	262	2	US-09-438-185A-608	Sequence 608, App
128	34	53.1	267	2	US-09-540-236-3025	Sequence 3025, Ap
129	34	53.1	289	2	US-09-134-000C-5932	Sequence 5932, Ap
130	34	53.1	300	2	US-09-248-796A-20855	Sequence 20855, A
131	34	53.1	308	2	US-09-252-991A-16800	Sequence 16800, A
132	34	53.1	312	1	US-09-014-969-17	Sequence 17, Appl
133	34	53.1	322	2	US-09-248-796A-17951	Sequence 17951, A
134	34	53.1	325	2	US-09-902-540-14385	Sequence 14385, A
135	34	53.1	326	2	US-09-371-307-65	Sequence 65, Appl
136	34	53.1	327	2	US-09-614-912-14	Sequence 14, Appl
137	34	53.1	328	2	US-09-438-185A-1025	Sequence 1025, Ap
138	34	53.1	341	2	US-09-252-991A-28938	Sequence 28938, A
139	34	53.1	344	1	US-08-690-493-1	Sequence 1, Appli
140	34	53.1	355	2	US-09-489-039A-9302	Sequence 9302, Ap
141	34	53.1	358	2	US-09-107-532A-5676	Sequence 5676, Ap
142	34	53.1	382	2	US-09-614-912-6	Sequence 6, Appli
143	34	53.1	387	2	US-09-457-302-1	Sequence 1, Appli
144	34	53.1	393	2	US-09-252-991A-27132	Sequence 27132, A
145	34	53.1	397	2	US-09-270-767-62336	Sequence 62336, A
146	34	53.1	405	2	US-09-252-991A-17862	Sequence 17862, A
147	34	53.1	419	1	US-08-385-186-2	Sequence 2, Appli
148	34	53.1	419	1	US-08-385-186-4	Sequence 4, Appli
149	34	53.1	419	2	US-09-949-016-6002	Sequence 6002, Ap
150	34	53.1	420	2	US-09-769-787-35	Sequence 35, Appl
151	34	53.1	440	2	US-09-949-016-10558	Sequence 10558, A
152	34	53.1	462	2	US-09-198-452A-668	Sequence 668, App
153	34	53.1	465	2	US-09-438-185A-631	Sequence 631, App
154	34	53.1	482	2	US-09-538-092-905	Sequence 905, App
155	34	53.1	495	2	US-09-543-681A-8121	Sequence 8121, Ap
156	34	53.1	515	2	US-09-252-991A-32251	Sequence 32251, A
157	34	53.1	529	2	US-09-252-991A-29757	Sequence 29757, A
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160	34	53.1	620	2	US-09-000-145-5	Sequence 5, Appli
161	34	53.1	639	2	US-09-252-991A-25089	Sequence 25089, A
162	34	53.1	748	2	US-09-543-681A-6676	Sequence 6676, Ap
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164	34	53.1	1668	2	US-09-949-016-11611	Sequence 11611, A
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167	34	53.1	1873	1	US-08-336-257A-7	Sequence 7, Appli
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169	34	53.1	3106	2	US-09-562-702A-10	Sequence 10, Appl
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171	33.5	52.3	11	1	US-08-129-930B-42	Sequence 42, Appl
172	33.5	52.3	11	2	US-08-976-288A-42	Sequence 42, Appl
173	33.5	52.3	11	2	US-09-947-839B-42	Sequence 42, Appl
174	33.5	52.3	139	1	US-08-129-930B-96	Sequence 96, Appl
175	33.5	52.3	139	2	US-08-134-346A-51	Sequence 51, Appl
176	33.5	52.3	139	2	US-08-976-288A-96	Sequence 96, Appl
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179	33	51.6	10	1	US-08-382-013A-74	Sequence 74, Appl
180	33	51.6	20	1	US-08-382-013A-72	Sequence 72, Appl
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182	33	51.6	68	2	US-09-107-532A-4449	Sequence 4449, Ap
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262	32.5	50.8	299	2	US-09-904-462-119	Sequence 119, App
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277	32	50.0	141	1	US-08-253-877C-4	Sequence 4, Appli
278	32	50.0	141	1	US-08-452-164A-4	Sequence 4, Appli
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295	32	50.0	303	2	US-09-225-024-9	Sequence 9, Appli
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313	32	50.0	386	2	US-09-605-703B-756	Sequence 756, App
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331	32	50.0	502	2	US-10-054-988-69	Sequence 69, Appl
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341	32	50.0	717	2	US-08-872-855-9	Sequence 9, Appli
342	32	50.0	722	2	US-10-048-621-1	Sequence 1, Appli
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346	32	50.0	783	2	US-09-012-871-2	Sequence 2, Appli
347	32	50.0	785	2	US-09-487-558B-122	Sequence 122, App
348	32	50.0	787	2	US-09-712-363-178	Sequence 178, App
349	32	50.0	800	2	US-09-583-110-2916	Sequence 2916, Ap
350	32	50.0	801	2	US-09-107-433-4536	Sequence 4536, Ap
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352	32	50.0	811	2	US-09-990-444-57	Sequence 57, Appl
353	32	50.0	811	2	US-09-997-333-57	Sequence 57, Appl
354	32	50.0	811	2	US-09-992-598-57	Sequence 57, Appl
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360	32	50.0	969	2	US-09-438-185A-469	Sequence 469, App
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364	32	50.0	1114	2	US-08-811-583-2	Sequence 2, Appli
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373	31.5	49.2	221	2	US-09-205-426-156	Sequence 156, App
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376	31.5	49.2	300	2	US-09-953-499-10	Sequence 10, Appl
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378	31.5	49.2	336	1	US-08-997-362-156	Sequence 156, App
379	31.5	49.2	336	2	US-09-095-855-156	Sequence 156, App
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385	31	48.4	13	2	US-09-030-619-36	Sequence 36, Appl
386	31	48.4	13	2	US-09-667-486-35	Sequence 35, Appl
387	31	48.4	13	2	US-10-225-087-13	Sequence 13, Appl
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389	31	48.4	38	2	US-09-413-068-18	Sequence 18, Appl
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534	30.5	47.7	101	2	US-08-424-550B-45	Sequence 45, Appl
535	30.5	47.7	106	2	US-08-469-260A-253	Sequence 253, App
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537	30.5	47.7	106	2	US-08-467-344A-253	Sequence 253, App
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556	30	46.9	18	2	US-08-439-157-54	Sequence 54, Appl
557	30	46.9	18	2	US-09-437-895-54	Sequence 54, Appl
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559	30	46.9	18	2	US-10-158-825-135	Sequence 135, App
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566	30	46.9	23	1	US-08-471-052A-119	Sequence 119, App
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568	30	46.9	23	1	US-08-471-939-119	Sequence 119, App
569	30	46.9	23	1	US-08-471-800-119	Sequence 119, App
570	30	46.9	23	1	US-08-471-068-119	Sequence 119, App
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576	30	46.9	38	1	US-08-471-068-181	Sequence 181, App
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596	30	46.9	80	2	US-08-817-795-69	Sequence 69, Appl
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643	30	46.9	142	2	US-09-303-518D-760	Sequence 760, App
644	30	46.9	142	2	US-09-303-518D-762	Sequence 762, App
645	30	46.9	142	2	US-09-303-518D-764	Sequence 764, App
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679	30	46.9	212	2	US-09-293-724-3	Sequence 3, Appli
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687	30	46.9	218	2	US-09-949-016-8217	Sequence 8217, Ap
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698	30	46.9	247	2	US-09-252-991A-24999	Sequence 24999, A
699	30	46.9	247	2	US-09-107-433-3896	Sequence 3896, Ap
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703	30	46.9	252	2	US-09-134-000C-4645	Sequence 4645, Ap
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707	30	46.9	257	2	US-09-270-767-48359	Sequence 48359, A
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716	30	46.9	287	2	US-09-252-991A-21670	Sequence 21670, A
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962	30	46.9	2332	2	US-09-324-867-3	Sequence 3, Appli
963	30	46.9	2332	2	US-09-315-179-2	Sequence 2, Appli
964	30	46.9	2332	2	US-09-523-656-2	Sequence 2, Appli
965	30	46.9	2332	2	US-09-957-641A-2	Sequence 2, Appli
966	30	46.9	2332	2	US-10-360-101-229	Sequence 229, App
967	30	46.9	2332	4	PCT-US93-03275-4	Sequence 4, Appli
968	30	46.9	2332	4	PCT-US94-13200-2	Sequence 2, Appli
969	30	46.9	2351	1	US-08-121-202-2	Sequence 2, Appli
970	30	46.9	2351	1	US-08-366-851A-2	Sequence 2, Appli
971	30	46.9	2351	2	US-10-133-907-4	Sequence 4, Appli
972	30	46.9	2351	2	US-09-001-039B-45	Sequence 45, Appl
973	30	46.9	2351	6	5171844-2	Patent No. 5171844
974	30	46.9	2351	6	5422260-1	Patent No. 5422260
975	29.5	46.1	76	2	US-09-543-681A-5417	Sequence 5417, Ap
976	29.5	46.1	87	2	US-09-270-767-38674	Sequence 38674, A

977	29.5	46.1	87	2	US-09-270-767-53891	Sequence 53891, A
978	29.5	46.1	114	2	US-09-450-520A-9	Sequence 9, Appli
979	29.5	46.1	114	2	US-09-450-520A-10	Sequence 10, Appl
980	29.5	46.1	114	2	US-09-450-520A-11	Sequence 11, Appl
981	29.5	46.1	117	1	US-07-634-278-105	Sequence 105, App
982	29.5	46.1	117	1	US-08-477-728-105	Sequence 105, App
983	29.5	46.1	117	1	US-08-474-040-105	Sequence 105, App
984	29.5	46.1	117	1	US-08-487-200-105	Sequence 105, App
985	29.5	46.1	117	2	US-08-484-537-105	Sequence 105, App
986	29.5	46.1	136	2	US-09-450-520A-4	Sequence 4, Appli
987	29.5	46.1	136	2	US-09-450-520A-8	Sequence 8, Appli
988	29.5	46.1	152	1	US-07-634-278-101	Sequence 101, App
989	29.5	46.1	152	1	US-08-477-728-101	Sequence 101, App
990	29.5	46.1	152	1	US-08-474-040-101	Sequence 101, App
991	29.5	46.1	152	1	US-08-487-200-101	Sequence 101, App
992	29.5	46.1	152	2	US-08-484-537-101	Sequence 101, App
993	29.5	46.1	195	2	US-09-328-352-4743	Sequence 4743, Ap
994	29.5	46.1	210	2	US-09-248-796A-20133	Sequence 20133, A
995	29.5	46.1	266	2	US-09-328-352-6525	Sequence 6525, Ap
996	29.5	46.1	267	2	US-09-902-540-15787	Sequence 15787, A
997	29.5	46.1	367	2	US-09-543-681A-4184	Sequence 4184, Ap
998	29.5	46.1	394	2	US-09-134-000C-6314	Sequence 6314, Ap
999	29.5	46.1	480	2	US-09-252-991A-32853	Sequence 32853, A
1000	29	45.3	8	2	US-08-444-818-279	Sequence 279, App

ALIGNMENTS

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RESULT 1
US-08-318-157B-25
; Sequence 25, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-25

  Query Match           100.0%;  Score 64;  DB 1;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.00034;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db          1 LYFGFPWFAY 10


RESULT 2
US-09-253-794-25
; Sequence 25, Application US/09253794
; Patent No. 6676924
;  GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;  INFORMATION FOR SEQ ID NO: 25:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 10 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-253-794-25

  Query Match           100.0%;  Score 64;  DB 2;  Length 10;
  Best Local Similarity  100.0%;  Pred. No. 0.00034;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db          1 LYFGFPWFAY 10


RESULT 3
US-08-318-157B-2
; Sequence 2, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
```

```
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-2

  Query Match             100.0%;  Score 64;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 4
US-08-318-157B-8
; Sequence 8, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-8

  Query Match             100.0%;  Score 64;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 5
US-08-318-157B-9
; Sequence 9, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-9

  Query Match             100.0%;  Score 64;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108
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```
RESULT 6
US-08-318-157B-10
; Sequence 10, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-10

  Query Match             100.0%;  Score 64;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 7
US-08-318-157B-11
; Sequence 11, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-11

  Query Match             100.0%;  Score 64;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 8
US-08-318-157B-12
; Sequence 12, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-12
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  Query Match             100.0%;  Score 64;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 9
US-08-318-157B-13
; Sequence 13, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-13

  Query Match             100.0%;  Score 64;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 10
US-08-318-157B-14
; Sequence 14, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-14

  Query Match             100.0%;  Score 64;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 11
US-08-318-157B-15
; Sequence 15, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
```

```
;       TELEFAX:  (202)672-5399
;       TELEX:  904136
;   INFORMATION FOR SEQ ID NO:  15:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  119 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-15

  Query Match             100.0%;  Score 64;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 12
US-08-318-157B-17
; Sequence 17, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-17

  Query Match             100.0%;  Score 64;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 13
US-08-318-157B-57
; Sequence 57, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-318-157B-57

  Query Match             100.0%;  Score 64;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 14
US-08-318-157B-58
; Sequence 58, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
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;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-318-157B-58

  Query Match             100.0%;  Score 64;  DB 1;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 15
US-09-253-794-2
; Sequence 2, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-253-794-2

  Query Match             100.0%;  Score 64;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 16
US-09-253-794-8
; Sequence 8, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-253-794-8

  Query Match             100.0%;  Score 64;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 17
US-09-253-794-9
; Sequence 9, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
```

```
;                          MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-253-794-9

  Query Match             100.0%;  Score 64;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 18
US-09-253-794-10
; Sequence 10, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 10:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-253-794-10

  Query Match             100.0%;  Score 64;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 19
US-09-253-794-11
; Sequence 11, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 11:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
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;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-253-794-11

  Query Match           100.0%;  Score 64;  DB 2;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 20
US-09-253-794-12
; Sequence 12, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-253-794-12

  Query Match           100.0%;  Score 64;  DB 2;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 21
US-09-253-794-13
; Sequence 13, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-253-794-13

  Query Match           100.0%;  Score 64;  DB 2;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 22
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
```

```
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

  Query Match             100.0%;  Score 64;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 23
US-09-253-794-15
; Sequence 15, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-253-794-15

  Query Match             100.0%;  Score 64;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 24
US-09-253-794-17
; Sequence 17, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-253-794-17

  Query Match             100.0%;  Score 64;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108
```

```
RESULT 25
US-09-253-794-57
; Sequence 57, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 57:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-253-794-57

  Query Match             100.0%;  Score 64;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 26
US-09-253-794-58
; Sequence 58, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 58:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-253-794-58

  Query Match             100.0%;  Score 64;  DB 2;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.0043;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 27
US-09-309-572-7
; Sequence 7, Application US/09309572
; Patent No. 6440730
; GENERAL INFORMATION:
;  APPLICANT: Heinrich-Pette-Institut
;  TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV
;  FILE REFERENCE: P50489
;  CURRENT APPLICATION NUMBER: US/09/309,572
;  CURRENT FILING DATE: 1999-05-11
;  EARLIER APPLICATION NUMBER: DE 198 56 463
;  EARLIER FILING DATE: 1998-11-26
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 2210
;   TYPE: PRT
;   ORGANISM: Lymphocytic choriomeningitis virus
;   FEATURE:
;   OTHER INFORMATION: L protein
US-09-309-572-7

  Query Match             68.8%;  Score 44;  DB 2;  Length 2210;
  Best Local Similarity   70.0%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              | ||| ||:|
Db       1901 LQFGFGWFSY 1910


RESULT 28
US-09-718-096-7
; Sequence 7, Application US/09718096
; Patent No. 6589763
```

```
; GENERAL INFORMATION:
;  APPLICANT:  Von Laer, Meike-Dorothee
;  TITLE OF INVENTION:  RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV
;  FILE REFERENCE:  35-195
;  CURRENT APPLICATION NUMBER: US/09/718,096
;  CURRENT FILING DATE:  2000-11-22
;  PRIOR APPLICATION NUMBER:  DE 19856463.5
;  PRIOR FILING DATE:  1998-11-26
;  PRIOR APPLICATION NUMBER:  EP 99250415.9
;  PRIOR FILING DATE:  1999-11-25
;  PRIOR APPLICATION NUMBER:  US 09/309,572
;  PRIOR FILING DATE:  1999-05-11
;  NUMBER OF SEQ ID NOS:  26
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 2210
;   TYPE: PRT
;   ORGANISM: Lymphocytic choriomeningitis virus
;   FEATURE:
;   OTHER INFORMATION: L protein
US-09-718-096-7

  Query Match             68.8%;  Score 44;  DB 2;  Length 2210;
  Best Local Similarity   70.0%;  Pred. No. 1.3e+02;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              | ||| ||:|
Db       1901 LQFGFGWFSY 1910


RESULT 29
US-08-881-037-19
; Sequence 19, Application US/08881037
; Patent No. 6080588
;  GENERAL INFORMATION:
;    APPLICANT:  Glick, Gary D.
;    APPLICANT:  Swanson, Patrick C.
;    TITLE OF INVENTION:  DNA BINDING ANTIBODIES
;    NUMBER OF SEQUENCES:  113
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/881,037
;      FILING DATE:  23-JUN-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/443,540
;      FILING DATE:  18-MAY-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Konski, Antoinette F.
;      REGISTRATION NUMBER:  34,202
;      REFERENCE/DOCKET NUMBER:  203442110710
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 813-5600
;      TELEFAX:  (650) 494-0792
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  116 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-881-037-19

  Query Match             67.2%;  Score 43;  DB 2;  Length 116;
  Best Local Similarity   66.7%;  Pred. No. 9;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              |  :|||||
Db         97 YSNYPWFAY 105


RESULT 30
US-08-767-128-20
; Sequence 20, Application US/08767128
; Patent No. 6111079
;  GENERAL INFORMATION:
;    APPLICANT:  WYLIE, DWANE E.
;    APPLICANT:  LOPEZ, OSVALDO
;    APPLICANT:  MURRAY, PETER JOSEPH
;    APPLICANT:  GOEBEL, PETER
;    TITLE OF INVENTION:  LEAD BINDING POLYPEPTIDES AND
;    TITLE OF INVENTION:  NUCLEOTIDES CODING THEREFORE
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Merchant, Gould, Smith, Edell, Welter & Schmidt
;      STREET:  3100 No. 6111079west Center, 90 South Seventh St
;      CITY:  Minneapolis
;      STATE:  MN
;      COUNTRY:  USA
;      ZIP:  55402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/767,128
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:  04-DEC-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/09258
;      FILING DATE:  05-JUN-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/541,373
;      FILING DATE:  10-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/462,798
;      FILING DATE:  05-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carter, Charles G.
;      REGISTRATION NUMBER:  35,093
;      REFERENCE/DOCKET NUMBER:  8648.49USF1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  612/371-5278
;      TELEFAX:  612/332-9081
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  119 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
US-08-767-128-20
```

```
  Query Match             65.6%;  Score 42;  DB 2;  Length 119;
  Best Local Similarity   60.0%;  Pred. No. 13;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              :|:|  ||||
Db         99 IYYGHLWFAY 108


RESULT 31
US-08-118-270-71
; Sequence 71, Application US/08118270
; Patent No. 5508384
;  GENERAL INFORMATION:
;    APPLICANT:  Murphy, Randall B.
;    APPLICANT:  Schuster, David I.
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/118,270
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  349 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-118-270-71

  Query Match             65.6%;  Score 42;  DB 1;  Length 349;
  Best Local Similarity   77.8%;  Pred. No. 40;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        254 LYFAFHWFA 262


RESULT 32
PCT-US93-08528-71
; Sequence 71, Application PC/TUS9308528
;  GENERAL INFORMATION:
;    APPLICANT:  New York University
;    TITLE OF INVENTION:  POLYPEPTIDES OF G-COUPLED PROTEIN
;    TITLE OF INVENTION:  RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
;    NUMBER OF SEQUENCES:  348
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BROWDY AND NEIMARK
;      STREET:  419 Seventh Street, N.W., Suite 300
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08528
;      FILING DATE:  09-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,236
;      FILING DATE:  10-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Townsend, Kevin G.
;      REGISTRATION NUMBER:  34,033
;      REFERENCE/DOCKET NUMBER:  MURPHY=2 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-628-5197
;      TELEFAX:  202-737-3528
;      TELEX:  248633
;  INFORMATION FOR SEQ ID NO:  71:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  349 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US93-08528-71

  Query Match             65.6%;  Score 42;  DB 4;  Length 349;
  Best Local Similarity   77.8%;  Pred. No. 40;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||| | |||
Db        254 LYFAFHWFA 262


RESULT 33
US-08-851-971-3
; Sequence 3, Application US/08851971E
; Patent No. 6485933
; GENERAL INFORMATION:
;  APPLICANT: Bandman, Olga
;  APPLICANT: Hillman, Jennifer L.
;  APPLICANT: Goli, Surya K.
;  APPLICANT: Capitant, Sherry A.
;  TITLE OF INVENTION: B-CELL RECEPTOR ASSOCIATED PROTEINS
;  FILE REFERENCE: PF-0188 US
;  CURRENT APPLICATION NUMBER: US/08/851,971E
;  CURRENT FILING DATE: 1997-05-07
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 105, 111, 114, 118, 137, 138, 139, 261
;   OTHER INFORMATION: unknown or other
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte Clone No. 6485933 484722
US-08-851-971-3

  Query Match             62.5%;  Score 40;  DB 2;  Length 299;
  Best Local Similarity   60.0%;  Pred. No. 71;
```

```
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              |:|  ||| |
Db         68 LHFRIPWFQY 77


RESULT 34
US-08-851-971-5
; Sequence 5, Application US/08851971E
; Patent No. 6485933
; GENERAL INFORMATION:
;  APPLICANT: Bandman, Olga
;  APPLICANT: Hillman, Jennifer L.
;  APPLICANT: Goli, Surya K.
;  APPLICANT: Capitant, Sherry A.
;  TITLE OF INVENTION: B-CELL RECEPTOR ASSOCIATED PROTEINS
;  FILE REFERENCE: PF-0188 US
;  CURRENT APPLICATION NUMBER: US/08/851,971E
;  CURRENT FILING DATE: 1997-05-07
;  NUMBER OF SEQ ID NOS: 10
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 155
;   OTHER INFORMATION: unknown or other
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte Clone No. 6485933 454790
US-08-851-971-5

  Query Match             62.5%;  Score 40;  DB 2;  Length 299;
  Best Local Similarity   60.0%;  Pred. No. 71;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              |:|  ||| |
Db         68 LHFRIPWFQY 77


RESULT 35
US-09-605-703B-72
; Sequence 72, Application US/09605703B
; Patent No. 6962989
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Markus
;  APPLICANT:  Kroger, Burkhard
;  APPLICANT:  Schroder, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
;  TITLE OF INVENTION:  PROTEINS
;  FILE REFERENCE: BGI-129CP
;  CURRENT APPLICATION NUMBER: US/09/605,703B
;  CURRENT FILING DATE:  2000-06-27
;  PRIOR APPLICATION NUMBER: 60/142,764
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: 60/152,318
;  PRIOR FILING DATE: 1999-09-03
;  NUMBER OF SEQ ID NOS: 2934
; SEQ ID NO 72
;   LENGTH: 445
;   TYPE: PRT
;   ORGANISM: Corynebacterium glutamicum
US-09-605-703B-72

  Query Match             62.5%;  Score 40;  DB 2;  Length 445;
  Best Local Similarity   75.0%;  Pred. No. 1.1e+02;
  Matches    6;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 FGFPWFAY 10
              ||:|:|||
Db        121 FGYPFFAY 128


RESULT 36
US-09-248-796A-23660
; Sequence 23660, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
;  APPLICANT: Keith Weinstock et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
;  TITLE OF INVENTION:  FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: 107196.132
;  CURRENT APPLICATION NUMBER: US/09/248,796A
;  CURRENT FILING DATE:  1999-02-12
;  PRIOR APPLICATION NUMBER: US 60/074,725
;  PRIOR FILING DATE: 1998-02-13
;  PRIOR APPLICATION NUMBER: US 60/096,409
;  PRIOR FILING DATE: 1998-08-13
;  NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 23660
;   LENGTH: 66
;   TYPE: PRT
;   ORGANISM: Candida albicans
US-09-248-796A-23660

  Query Match             60.9%;  Score 39;  DB 2;  Length 66;
  Best Local Similarity   71.4%;  Pred. No. 22;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YFGFPWF 8
              :| ||||
Db         21 FFSFPWF 27


RESULT 37
US-09-065-059-1
; Sequence 1, Application US/09065059
; Patent No. 6068841
;  GENERAL INFORMATION:
;    APPLICANT:  SEINO, Ken-ichiro
;    APPLICANT:  KAYAGAKI, No. 6068841uhiko
;    APPLICANT:  YAGITA, Hideo
;    APPLICANT:  OKUMURA, Ko
;    APPLICANT:  NAKATA, Motomi
;    TITLE OF INVENTION:  THERAPEUTIC AGENT FOR HEPATITIS
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDermott, Will & Emery
;      STREET:  99 Canal Center Plaza
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/065,059
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bucca Ph.D., Daniel
;      REGISTRATION NUMBER:  P-42,368
;      REFERENCE/DOCKET NUMBER:  50356-151
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-518-5100
;      TELEFAX:  703-684-1124
;  INFORMATION FOR SEQ ID NO:  1:
```

```
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-065-059-1

  Query Match             60.9%;  Score 39;  DB 2;  Length 120;
  Best Local Similarity   66.7%;  Pred. No. 40;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              | | ||| |
Db        101 YDGSPWFTY 109


RESULT 38
US-08-913-555-1
; Sequence 1, Application US/08913555
; Patent No. 6946255
;  GENERAL INFORMATION:
;    APPLICANT:  KAYAGAKI, No. 6946255uhiko
;    APPLICANT:  YAGITA, Kideo
;    APPLICANT:  OKUMURA, Ko
;    APPLICANT:  NAKATA, Motomi
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY SPECIFICALLY
;    TITLE OF INVENTION:  REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDermott, Will & Emery
;      STREET:  99 Canal Center Plaza, Suite 300
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/913,555
;      FILING DATE:  19-SEP-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bucca Ph.D., Daniel
;      REGISTRATION NUMBER:  42,368
;      REFERENCE/DOCKET NUMBER:  50356-150
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-756-8600
;      TELEFAX:  202-756-8699
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  120 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-913-555-1

  Query Match             60.9%;  Score 39;  DB 2;  Length 120;
  Best Local Similarity   66.7%;  Pred. No. 40;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              | | ||| |
Db        101 YDGSPWFTY 109


RESULT 39
US-08-913-555-19
; Sequence 19, Application US/08913555
; Patent No. 6946255
;  GENERAL INFORMATION:
;    APPLICANT:  KAYAGAKI, No. 6946255uhiko
;    APPLICANT:  YAGITA, Kideo
;    APPLICANT:  OKUMURA, Ko
;    APPLICANT:  NAKATA, Motomi
;    TITLE OF INVENTION:  MONOCLONAL ANTIBODY SPECIFICALLY
;    TITLE OF INVENTION:  REACTING WITH Fas LIGAND AND PRODUCTION PROCESS THEREOF
;    NUMBER OF SEQUENCES:  31
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McDermott, Will & Emery
;      STREET:  99 Canal Center Plaza, Suite 300
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/913,555
;      FILING DATE:  19-SEP-1997
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bucca Ph.D., Daniel
;      REGISTRATION NUMBER:  42,368
;      REFERENCE/DOCKET NUMBER:  50356-150
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-756-8600
;      TELEFAX:  202-756-8699
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  121 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-913-555-19

  Query Match             60.9%;  Score 39;  DB 2;  Length 121;
  Best Local Similarity   66.7%;  Pred. No. 41;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              | | ||| |
Db        102 YDGSPWFTY 110


RESULT 40
US-09-710-279-302
; Sequence 302, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/09/710,279
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 302
;   LENGTH: 363
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-09-710-279-302
```

```
  Query Match             60.9%;  Score 39;  DB 2;  Length 363;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||   ||||
Db        317 LYLSIPWFA 325


RESULT 41
US-09-134-001C-4393
; Sequence 4393, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4393
;   LENGTH: 370
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4393

  Query Match             60.9%;  Score 39;  DB 2;  Length 370;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||   ||||
Db        324 LYLSIPWFA 332


RESULT 42
US-09-902-540-16455
; Sequence 16455, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16455
;   LENGTH: 479
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-16455

  Query Match             60.9%;  Score 39;  DB 2;  Length 479;
  Best Local Similarity   75.0%;  Pred. No. 1.7e+02;
  Matches    6;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWF 8
              ||| | ||
Db        209 LYFNFAWF 216


RESULT 43
US-09-270-767-48123
; Sequence 48123, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
;  APPLICANT: Homburger et al.
;  TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
;  FILE REFERENCE: File Reference: 7326-094
;  CURRENT APPLICATION NUMBER: US/09/270,767
;  CURRENT FILING DATE: 1999-03-17
;  NUMBER OF SEQ ID NOS: 62517
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 48123
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Drosophila melanogaster
US-09-270-767-48123

  Query Match             59.4%;  Score 38;  DB 2;  Length 110;
  Best Local Similarity   83.3%;  Pred. No. 53;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 YFGFPW 7
              :|||||
Db         27 HFGFPW 32


RESULT 44
US-10-092-246-9
; Sequence 9, Application US/10092246
; Patent No. 6501314
; GENERAL INFORMATION:
;  APPLICANT: The Minister of National Defence, Government of Canada
;  APPLICANT:  Fulton, R E
;  APPLICANT:  Alvi, Azhar E
;  APPLICANT:  Nagata, Leslie
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mor
;  TITLE OF INVENTION:  scFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/092,246
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-9

  Query Match             59.4%;  Score 38;  DB 2;  Length 120;
  Best Local Similarity   66.7%;  Pred. No. 58;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              |:| || ||
Db        101 YYGNPWPAY 109


RESULT 45
US-10-096-246A-9
; Sequence 9, Application US/10096246A
; Patent No. 6818748
; GENERAL INFORMATION:
;  APPLICANT: Fulton, R. Elaine
;  APPLICANT:  Nagata, Leslie
;  APPLICANT:  Alvi, Azhar Z.
;  TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
;  TITLE OF INVENTION:  Monoclonal ScFV Antibody Against Venezuelan Equine Encephalitis
;  TITLE OF INVENTION:  Virus (VEE)
;  FILE REFERENCE: NEL-0007
;  CURRENT APPLICATION NUMBER: US/10/096,246A
;  CURRENT FILING DATE:  2002-03-13
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
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;   LENGTH: 120
;   TYPE: PRT
;   ORGANISM: mouse
US-10-096-246A-9

  Query Match             59.4%;  Score 38;  DB 2;  Length 120;
  Best Local Similarity   66.7%;  Pred. No. 58;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              |:| || ||
Db        101 YYGNPWPAY 109


RESULT 46
US-09-902-540-15009
; Sequence 15009, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15009
;   LENGTH: 275
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-15009

  Query Match             59.4%;  Score 38;  DB 2;  Length 275;
  Best Local Similarity   62.5%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 FGFPWFAY 10
              :|| ||:|
Db         45 YGFNWFSY 52


RESULT 47
US-09-710-279-2558
; Sequence 2558, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/09/710,279
;  CURRENT FILING DATE:  2000-11-09
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2558
;   LENGTH: 357
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-09-710-279-2558

  Query Match             59.4%;  Score 38;  DB 2;  Length 357;
  Best Local Similarity   55.6%;  Pred. No. 1.8e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
                |: |:||:|
Db         43 LFHGWPWYA 51


RESULT 48
US-09-902-540-9903
; Sequence 9903, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9903
;   LENGTH: 357
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-9903

  Query Match             59.4%;  Score 38;  DB 2;  Length 357;
  Best Local Similarity   60.0%;  Pred. No. 1.8e+02;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              |: | ||||:
Db         15 LHTGRPWFAF 24


RESULT 49
US-09-134-001C-5101
; Sequence 5101, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
;  APPLICANT: Lynn Doucette-Stamm et al
;  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
;  TITLE OF INVENTION:  EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE: GTC-007
;  CURRENT APPLICATION NUMBER: US/09/134,001C
;  CURRENT FILING DATE:  1998-08-13
;  PRIOR APPLICATION NUMBER: US 60/064,964
;  PRIOR FILING DATE: 1997-11-08
;  PRIOR APPLICATION NUMBER: US 60/055,779
;  PRIOR FILING DATE: 1997-08-14
;  NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5101
;   LENGTH: 415
;   TYPE: PRT
;   ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5101

  Query Match             59.4%;  Score 38;  DB 2;  Length 415;
  Best Local Similarity   55.6%;  Pred. No. 2.1e+02;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
                |: |:||:|
Db        101 LFHGWPWYA 109


RESULT 50
US-09-949-016-9590
; Sequence 9590, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9590
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9590

Query Match 59.4%; Score 38; DB 2; Length 489;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LYPGFPW 7
||: |||
Db 293 LYYNFPW 299

Search completed: March 23, 2006, 02:08:54
Job time : 29.6438 secs

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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:42:16 ; Search time 70.137 Seconds
(without alignments)
59.573 Million cell updates/sec

Title: US-10-755-382-25
Perfect score: 64
Sequence: 1 LYFGFPWFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	64	100.0	10	3	US-09-253-794-25	Sequence 25, Appl
2	64	100.0	10	4	US-10-680-734-25	Sequence 25, Appl
3	64	100.0	10	5	US-10-755-382-25	Sequence 25, Appl
4	64	100.0	118	4	US-10-270-073-3	Sequence 3, Appli
5	64	100.0	119	3	US-09-253-794-2	Sequence 2, Appli
6	64	100.0	119	3	US-09-253-794-8	Sequence 8, Appli
7	64	100.0	119	3	US-09-253-794-9	Sequence 9, Appli
8	64	100.0	119	3	US-09-253-794-10	Sequence 10, Appl
9	64	100.0	119	3	US-09-253-794-11	Sequence 11, Appl
10	64	100.0	119	3	US-09-253-794-12	Sequence 12, Appl
11	64	100.0	119	3	US-09-253-794-13	Sequence 13, Appl
12	64	100.0	119	3	US-09-253-794-14	Sequence 14, Appl
13	64	100.0	119	3	US-09-253-794-15	Sequence 15, Appl
14	64	100.0	119	3	US-09-253-794-17	Sequence 17, Appl
15	64	100.0	119	3	US-09-253-794-57	Sequence 57, Appl
16	64	100.0	119	3	US-09-253-794-58	Sequence 58, Appl
17	64	100.0	119	4	US-10-680-734-2	Sequence 2, Appli
18	64	100.0	119	4	US-10-680-734-8	Sequence 8, Appli
19	64	100.0	119	4	US-10-680-734-9	Sequence 9, Appli
20	64	100.0	119	4	US-10-680-734-10	Sequence 10, Appl
21	64	100.0	119	4	US-10-680-734-11	Sequence 11, Appl
22	64	100.0	119	4	US-10-680-734-12	Sequence 12, Appl
23	64	100.0	119	4	US-10-680-734-13	Sequence 13, Appl
24	64	100.0	119	4	US-10-680-734-14	Sequence 14, Appl
25	64	100.0	119	4	US-10-680-734-15	Sequence 15, Appl
26	64	100.0	119	4	US-10-680-734-17	Sequence 17, Appl
27	64	100.0	119	4	US-10-680-734-26	Sequence 26, Appl
28	64	100.0	119	4	US-10-680-734-27	Sequence 27, Appl
29	64	100.0	119	5	US-10-755-382-2	Sequence 2, Appli
30	64	100.0	119	5	US-10-755-382-8	Sequence 8, Appli
31	64	100.0	119	5	US-10-755-382-9	Sequence 9, Appli
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34	64	100.0	119	5	US-10-755-382-12	Sequence 12, Appl
35	64	100.0	119	5	US-10-755-382-13	Sequence 13, Appl
36	64	100.0	119	5	US-10-755-382-14	Sequence 14, Appl
37	64	100.0	119	5	US-10-755-382-15	Sequence 15, Appl
38	64	100.0	119	5	US-10-755-382-17	Sequence 17, Appl
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49	64	100.0	267	4	US-10-270-071-30	Sequence 30, Appl
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65	42	65.6	422	5	US-10-482-503-2	Sequence 2, Appli
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68	42	65.6	423	4	US-10-067-477-1	Sequence 1, Appli
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71	42	65.6	423	4	US-10-168-262-3	Sequence 3, Appli
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73	42	65.6	423	5	US-10-482-503-4	Sequence 4, Appli
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83	40	62.5	127	4	US-10-425-115-306439	Sequence 306439,
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91	40	62.5	299	4	US-10-197-919-12	Sequence 12, Appl
92	40	62.5	299	6	US-11-041-419-31	Sequence 31, Appl
93	40	62.5	299	6	US-11-041-419-45	Sequence 45, Appl
94	40	62.5	299	6	US-11-111-953-158	Sequence 158, App
95	40	62.5	299	6	US-11-111-953-475	Sequence 475, App
96	40	62.5	309	4	US-10-264-049-3005	Sequence 3005, Ap
97	40	62.5	309	4	US-10-276-774-2283	Sequence 2283, Ap
98	40	62.5	445	3	US-09-738-626-3627	Sequence 3627, Ap
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115	39	60.9	345	4	US-10-241-742-334	Sequence 334, App
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119	39	60.9	369	5	US-10-470-048B-561	Sequence 561, App
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125	38.5	60.2	146	3	US-09-791-551-111	Sequence 111, App
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236	36	56.2	214	5	US-10-472-928-3452	Sequence 3452, Ap
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238	36	56.2	216	4	US-10-410-764-47	Sequence 47, Appl
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868	35	54.7	455	4	US-10-197-698-14	Sequence 14, Appl
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936	35	54.7	455	4	US-10-016-177A-430	Sequence 430, App
937	35	54.7	455	4	US-10-173-693-14	Sequence 14, Appl
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955	35	54.7	455	4	US-10-063-538-4	Sequence 4, Appli
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959	35	54.7	455	4	US-10-201-327-14	Sequence 14, Appl
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966	35	54.7	455	4	US-10-125-923A-14	Sequence 14, Appl
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971	35	54.7	455	4	US-10-197-691-14	Sequence 14, Appl
972	35	54.7	455	4	US-10-198-771-14	Sequence 14, Appl
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974	35	54.7	455	4	US-10-179-520-14	Sequence 14, Appl
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979	35	54.7	455	4	US-10-166-709A-430	Sequence 430, App
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981	35	54.7	455	4	US-10-179-511-14	Sequence 14, Appl
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994	35	54.7	455	4	US-10-206-918-14	Sequence 14, Appl
995	35	54.7	455	4	US-10-208-025-14	Sequence 14, Appl
996	35	54.7	455	4	US-10-063-580-4	Sequence 4, Appli
997	35	54.7	455	4	US-10-063-557-4	Sequence 4, Appli
998	35	54.7	455	4	US-10-225-567A-597	Sequence 597, App
999	35	54.7	455	4	US-10-198-760-14	Sequence 14, Appl
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ALIGNMENTS

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RESULT 1
US-09-253-794-25
; Sequence 25, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 25:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 10 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-253-794-25

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  Best Local Similarity   100.0%;  Pred. No. 0.0029;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
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Db          1 LYFGFPWFAY 10


RESULT 2
US-10-680-734-25
; Sequence 25, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 25
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-680-734-25

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  Best Local Similarity   100.0%;  Pred. No. 0.0029;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
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Db          1 LYFGFPWFAY 10


RESULT 3
US-10-755-382-25
; Sequence 25, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
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;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 25:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 10 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-755-382-25

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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
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Db          1 LYFGFPWFAY 10


RESULT 4
US-10-270-073-3
; Sequence 3, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14VH deduced amino acid sequence
US-10-270-073-3

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  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 5
US-09-253-794-2
; Sequence 2, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-253-794-2

  Query Match             100.0%;  Score 64;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 6
US-09-253-794-8
; Sequence 8, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
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;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/253,794
;              FILING DATE: 22-Feb-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US 08/318,157
;              FILING DATE: 05-OCT-1994
;         ATTORNEY/AGENT INFORMATION:
;              NAME: SAXE, Bernhard D.
;              REGISTRATION NUMBER: 28,665
;              REFERENCE/DOCKET NUMBER: 18733/464
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (202)672-5300
;              TELEFAX: (202)672-5399
;              TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 8:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 119 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: <Unknown>
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-253-794-8

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Qy          1 LYFGFPWFAY 10
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Db         99 LYFGFPWFAY 108


RESULT 7
US-09-253-794-9
; Sequence 9, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;         APPLICANT: HANSEN, Hans J.
;                    ARMOUR, Kathryn L.
;         TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                             MOUSE MONOCLONAL ANTIBODIES
;         NUMBER OF SEQUENCES: 58
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Foley & Lardner
;              STREET: 3000 K Street, N.W., Suite 500
;              CITY: Washington
;              STATE: D.C.
;              COUNTRY: USA
;              ZIP: 20007-5109
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
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;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/253,794
;              FILING DATE: 22-Feb-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US 08/318,157
;              FILING DATE: 05-OCT-1994
;         ATTORNEY/AGENT INFORMATION:
;              NAME: SAXE, Bernhard D.
;              REGISTRATION NUMBER: 28,665
;              REFERENCE/DOCKET NUMBER: 18733/464
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (202)672-5300
;              TELEFAX: (202)672-5399
;              TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 9:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 119 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: <Unknown>
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-253-794-9

  Query Match             100.0%;  Score 64;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 8
US-09-253-794-10
; Sequence 10, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;         APPLICANT: HANSEN, Hans J.
;                    ARMOUR, Kathryn L.
;         TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                             MOUSE MONOCLONAL ANTIBODIES
;         NUMBER OF SEQUENCES: 58
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: Foley & Lardner
;              STREET: 3000 K Street, N.W., Suite 500
;              CITY: Washington
;              STATE: D.C.
;              COUNTRY: USA
;              ZIP: 20007-5109
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.30
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/253,794
;              FILING DATE: 22-Feb-1999
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US 08/318,157
;              FILING DATE: 05-OCT-1994
;         ATTORNEY/AGENT INFORMATION:
;              NAME: SAXE, Bernhard D.
;              REGISTRATION NUMBER: 28,665
;              REFERENCE/DOCKET NUMBER: 18733/464
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (202)672-5300
;              TELEFAX: (202)672-5399
;              TELEX: 904136
;    INFORMATION FOR SEQ ID NO: 10:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 119 amino acids
;              TYPE: amino acid
;              STRANDEDNESS: <Unknown>
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-253-794-10

  Query Match             100.0%;  Score 64;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108
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RESULT 9
US-09-253-794-11
; Sequence 11, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-253-794-11

  Query Match             100.0%;  Score 64;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 10
US-09-253-794-12
; Sequence 12, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-253-794-12

  Query Match             100.0%;  Score 64;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 11
US-09-253-794-13
; Sequence 13, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
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;           REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 119 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-253-794-13

  Query Match             100.0%;  Score 64;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 12
US-09-253-794-14
; Sequence 14, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Foley & Lardner
;           STREET: 3000 K Street, N.W., Suite 500
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/253,794
;           FILING DATE: 22-Feb-1999
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US 08/318,157
;           FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;           NAME: SAXE, Bernhard D.
;           REGISTRATION NUMBER: 28,665
;           REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 119 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-253-794-14

  Query Match             100.0%;  Score 64;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 13
US-09-253-794-15
; Sequence 15, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Foley & Lardner
;           STREET: 3000 K Street, N.W., Suite 500
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/253,794
;           FILING DATE: 22-Feb-1999
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US 08/318,157
;           FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;           NAME: SAXE, Bernhard D.
;           REGISTRATION NUMBER: 28,665
;           REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 119 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-253-794-15

  Query Match             100.0%;  Score 64;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 14
US-09-253-794-17
; Sequence 17, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
```

```
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-253-794-17

  Query Match             100.0%;  Score 64;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 15
US-09-253-794-57
; Sequence 57, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 57:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-253-794-57

  Query Match             100.0%;  Score 64;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 16
US-09-253-794-58
; Sequence 58, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Foley & Lardner
;            STREET: 3000 K Street, N.W., Suite 500
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/253,794
;            FILING DATE: 22-Feb-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/318,157
;            FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: SAXE, Bernhard D.
;            REGISTRATION NUMBER: 28,665
;            REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)672-5300
;            TELEFAX: (202)672-5399
;            TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 58:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 119 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-09-253-794-58
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  Query Match             100.0%;  Score 64;  DB 3;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 17
US-10-680-734-2
; Sequence 2, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Mus sp.
US-10-680-734-2

  Query Match             100.0%;  Score 64;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 18
US-10-680-734-8
; Sequence 8, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-8

  Query Match             100.0%;  Score 64;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 19
US-10-680-734-9
; Sequence 9, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-9

  Query Match             100.0%;  Score 64;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 20
US-10-680-734-10
; Sequence 10, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-10

  Query Match             100.0%;  Score 64;  DB 4;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 21
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US-10-680-734-11
; Sequence 11, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: HANSEN, HANS J.
; TITLE OF INVENTION: ANTIBODY THERAPY
; FILE REFERENCE: 40923-0051US5
; CURRENT APPLICATION NUMBER: US/10/680,734
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: 60/467,161
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: PCT/US02/32307
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/416,531
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 11
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-680-734-11

Query Match 100.0%; Score 64; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
||||||||||
Db 99 LYFGFPWFAY 108

RESULT 22
US-10-680-734-12
; Sequence 12, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: HANSEN, HANS J.
; TITLE OF INVENTION: ANTIBODY THERAPY
; FILE REFERENCE: 40923-0051US5
; CURRENT APPLICATION NUMBER: US/10/680,734
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: 60/467,161
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: PCT/US02/32307
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/416,531
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-680-734-12

Query Match 100.0%; Score 64; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
||||||||||
Db 99 LYFGFPWFAY 108

RESULT 23
US-10-680-734-13
; Sequence 13, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: HANSEN, HANS J.
; TITLE OF INVENTION: ANTIBODY THERAPY
; FILE REFERENCE: 40923-0051US5
; CURRENT APPLICATION NUMBER: US/10/680,734
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: 60/467,161
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: PCT/US02/32307
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/416,531
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-680-734-13

Query Match 100.0%; Score 64; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
||||||||||
Db 99 LYFGFPWFAY 108

RESULT 24
US-10-680-734-14
; Sequence 14, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: HANSEN, HANS J.
; TITLE OF INVENTION: ANTIBODY THERAPY
; FILE REFERENCE: 40923-0051US5
; CURRENT APPLICATION NUMBER: US/10/680,734
; CURRENT FILING DATE: 2003-10-08
; PRIOR APPLICATION NUMBER: 60/467,161
; PRIOR FILING DATE: 2003-05-02
; PRIOR APPLICATION NUMBER: PCT/US02/32307
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/416,531
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-680-734-14

Query Match 100.0%; Score 64; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
||||||||||
Db 99 LYFGFPWFAY 108

RESULT 25
US-10-680-734-15
; Sequence 15, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: HANSEN, HANS J.
; TITLE OF INVENTION: ANTIBODY THERAPY
; FILE REFERENCE: 40923-0051US5
; CURRENT APPLICATION NUMBER: US/10/680,734
; CURRENT FILING DATE: 2003-10-08

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;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 15
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-15

  Query Match           100.0%;  Score 64;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 26
US-10-680-734-17
; Sequence 17, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-17

  Query Match           100.0%;  Score 64;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 27
US-10-680-734-26
; Sequence 26, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 26
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-26

  Query Match           100.0%;  Score 64;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 28
US-10-680-734-27
; Sequence 27, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 27
;   LENGTH: 119
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-27

  Query Match           100.0%;  Score 64;  DB 4;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 29
US-10-755-382-2
; Sequence 2, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;
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;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/755,382
;           FILING DATE: 13-Jan-2004
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/09/253,794
;           FILING DATE: 22-Feb-1999
;           APPLICATION NUMBER: US 08/318,157
;           FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;           NAME: SAXE, Bernhard D.
;           REGISTRATION NUMBER: 28,665
;           REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 119 amino acids
;           TYPE: amino acid
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-755-382-2

  Query Match           100.0%;  Score 64;  DB 5;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 30
US-10-755-382-8
; Sequence 8, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Foley & Lardner
;           STREET: 3000 K Street, N.W., Suite 500
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/755,382
;           FILING DATE: 13-Jan-2004
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/09/253,794
;           FILING DATE: 22-Feb-1999
;           APPLICATION NUMBER: US 08/318,157
;           FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;           NAME: SAXE, Bernhard D.
;           REGISTRATION NUMBER: 28,665
;           REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 119 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-755-382-8

  Query Match           100.0%;  Score 64;  DB 5;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 31
US-10-755-382-9
; Sequence 9, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Foley & Lardner
;           STREET: 3000 K Street, N.W., Suite 500
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/10/755,382
;           FILING DATE: 13-Jan-2004
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: US/09/253,794
;           FILING DATE: 22-Feb-1999
;           APPLICATION NUMBER: US 08/318,157
;           FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;           NAME: SAXE, Bernhard D.
;           REGISTRATION NUMBER: 28,665
;           REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202)672-5300
;           TELEFAX: (202)672-5399
;           TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 119 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: <Unknown>
;           TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-755-382-9

  Query Match           100.0%;  Score 64;  DB 5;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 32
US-10-755-382-10
; Sequence 10, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-755-382-10

  Query Match             100.0%;  Score 64;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 33
US-10-755-382-11
; Sequence 11, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-755-382-11

  Query Match             100.0%;  Score 64;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 34
US-10-755-382-12
; Sequence 12, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
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;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-755-382-12

  Query Match             100.0%;  Score 64;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 35
US-10-755-382-13
; Sequence 13, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-755-382-13

  Query Match             100.0%;  Score 64;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 36
US-10-755-382-14
; Sequence 14, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 14:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-755-382-14

  Query Match             100.0%;  Score 64;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
```

```
                  ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 37
US-10-755-382-15
; Sequence 15, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 15:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-755-382-15

  Query Match             100.0%;  Score 64;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 38
US-10-755-382-17
; Sequence 17, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 17:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-755-382-17

  Query Match             100.0%;  Score 64;  DB 5;  Length 119;
  Best Local Similarity   100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 39
US-10-755-382-57
; Sequence 57, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
```

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;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 57:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-10-755-382-57

  Query Match            100.0%;  Score 64;  DB 5;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 40
US-10-755-382-58
; Sequence 58, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;       APPLICANT: HANSEN, Hans J.
;                  ARMOUR, Kathryn L.
;       TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                           MOUSE MONOCLONAL ANTIBODIES
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;       ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 58:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 119 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-755-382-58

  Query Match            100.0%;  Score 64;  DB 5;  Length 119;
  Best Local Similarity  100.0%;  Pred. No. 0.028;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db         99 LYFGFPWFAY 108


RESULT 41
US-10-006-771A-4
; Sequence 4, Application US/10006771A
; Publication No. US20020165360A1
; GENERAL INFORMATION:
;  APPLICANT: Junghans, Richard P.
;  TITLE OF INVENTION: Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen
;  FILE REFERENCE: 002
;  CURRENT APPLICATION NUMBER: US/10/006,771A
;  CURRENT FILING DATE:  2002-06-04
;  PRIOR APPLICATION NUMBER: 60/250,090
;  PRIOR FILING DATE: 2000-11-30
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 138
;   TYPE: PRT
;   ORGANISM: Homo sapiens and Mus sp.
US-10-006-771A-4

  Query Match            100.0%;  Score 64;  DB 4;  Length 138;
  Best Local Similarity  100.0%;  Pred. No. 0.032;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        118 LYFGFPWFAY 127


RESULT 42
US-10-270-073-6
; Sequence 6, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 256
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14-0 amino acid sequence
US-10-270-073-6
```

```
  Query Match             100.0%;  Score 64;  DB 4;  Length 256;
  Best Local Similarity   100.0%;  Pred. No. 0.057;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        122 LYFGFPWFAY 131


RESULT 43
US-10-270-073-8
; Sequence 8, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 257
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14-1G amino acid sequence
US-10-270-073-8

  Query Match             100.0%;  Score 64;  DB 4;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 0.057;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        122 LYFGFPWFAY 131


RESULT 44
US-10-270-071-18
; Sequence 18, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
;  FILE REFERENCE: 042418/0110
;  CURRENT APPLICATION NUMBER: US/10/270,071
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
;   OTHER INFORMATION: sequence of hMN14VK
US-10-270-071-18

  Query Match             100.0%;  Score 64;  DB 4;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 0.058;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        122 LYFGFPWFAY 131


RESULT 45
US-10-270-073-2
; Sequence 2, Application US/10270073
; Publication No. US20030148409A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID
;  TITLE OF INVENTION: DIRECT TARGETING BINDING PROTEINS
;  FILE REFERENCE: 042418/0112
;  CURRENT APPLICATION NUMBER: US/10/270,073
;  CURRENT FILING DATE:  2002-10-15
;  PRIOR APPLICATION NUMBER: 60/328,835
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: 60/341,881
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: 60/345,641
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: 60/404,919
;  PRIOR FILING DATE: 2002-08-22
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: hMN-14scFv-L5 amino acid sequence
US-10-270-073-2

  Query Match             100.0%;  Score 64;  DB 4;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 0.058;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||||||||||
Db        122 LYFGFPWFAY 131


RESULT 46
US-10-328-190-6
; Sequence 6, Application US/10328190
; Publication No. US20030162709A1
; GENERAL INFORMATION:
;  APPLICANT: ROSSI, EDMUND A.
;  APPLICANT:  CHANG, CHIEN-HSING KEN
;  APPLICANT:  GOLDENBERG, DAVID M.
;  TITLE OF INVENTION: METHODS OF GENERATING MULTISPECIFIC, MULTIVALENT AGENTS
;  TITLE OF INVENTION:  FROM VH AND VL DOMAINS
;  FILE REFERENCE: 042418/0115
;  CURRENT APPLICATION NUMBER: US/10/328,190
;  CURRENT FILING DATE:  2003-04-03
;  PRIOR APPLICATION NUMBER: 60/342,103
;  PRIOR FILING DATE: 2001-12-26
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 261
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hMN14-scFv-L5
; OTHER INFORMATION: protein sequence
US-10-328-190-6

 Query Match 100.0%; Score 64; DB 4; Length 261;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
 ||||||||||
Db 122 LYFGFPWFAY 131

RESULT 47
US-10-270-071-22
; Sequence 22, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
; APPLICANT: ROSSI, EDMUND
; APPLICANT: CHANG, CHIEN-HSING KEN
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
; FILE REFERENCE: 042418/0110
; CURRENT APPLICATION NUMBER: US/10/270,071
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/328,835
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/341,881
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; OTHER INFORMATION: sequence of polypeptide 2 of BS1
US-10-270-071-22

 Query Match 100.0%; Score 64; DB 4; Length 267;
 Best Local Similarity 100.0%; Pred. No. 0.059;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
 ||||||||||
Db 122 LYFGFPWFAY 131

RESULT 48
US-10-270-071-26
; Sequence 26, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
; APPLICANT: ROSSI, EDMUND
; APPLICANT: CHANG, CHIEN-HSING KEN
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
; FILE REFERENCE: 042418/0110
; CURRENT APPLICATION NUMBER: US/10/270,071
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/328,835
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/341,881
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; OTHER INFORMATION: sequence of polypeptide 2 of BS1.5
US-10-270-071-26

 Query Match 100.0%; Score 64; DB 4; Length 267;
 Best Local Similarity 100.0%; Pred. No. 0.059;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
 ||||||||||
Db 122 LYFGFPWFAY 131

RESULT 49
US-10-270-071-30
; Sequence 30, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
; APPLICANT: ROSSI, EDMUND
; APPLICANT: CHANG, CHIEN-HSING KEN
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
; FILE REFERENCE: 042418/0110
; CURRENT APPLICATION NUMBER: US/10/270,071
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/328,835
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/341,881
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; OTHER INFORMATION: sequence of polypeptide 2 of BS2
US-10-270-071-30

 Query Match 100.0%; Score 64; DB 4; Length 267;
 Best Local Similarity 100.0%; Pred. No. 0.059;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 122 LYFGFPWFAY 131

RESULT 50
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; Sequence 36, Application US/10270071
; Publication No. US20030113333A1
; GENERAL INFORMATION:
; APPLICANT: ROSSI, EDMUND
; APPLICANT: CHANG, CHIEN-HSING KEN
; TITLE OF INVENTION: AFFINITY ENHANCEMENT AGENTS
; FILE REFERENCE: 042418/0110
; CURRENT APPLICATION NUMBER: US/10/270,071
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: 60/328,835
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/341,881
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
; OTHER INFORMATION: sequence for polypetide 1 of BS1.5H (h679XhMN14 bispecific
; OTHER INFORMATION: diabody)
US-10-270-071-36

Query Match 100.0%; Score 64; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: March 23, 2006, 02:52:47
Job time : 84.2798 secs

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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:44:01 ; Search time 8.49315 Seconds
(without alignments)
33.701 Million cell updates/sec

Title: US-10-755-382-25
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Scoring table: BLOSUM62
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Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	40	62.5	117	7	US-11-097-812-29	Sequence 29, Appl
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8	39	60.9	363	6	US-10-793-626-302	Sequence 302, App
9	39	60.9	1075	7	US-11-089-551A-23	Sequence 23, Appl
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242	31	48.4	117	7	US-11-004-590-217	Sequence 217, App
243	31	48.4	117	7	US-11-004-590-221	Sequence 221, App
244	31	48.4	117	7	US-11-004-590-222	Sequence 222, App

245	31	48.4	117	7	US-11-004-590-223	Sequence 223, App
246	31	48.4	117	7	US-11-004-590-226	Sequence 226, App
247	31	48.4	117	7	US-11-004-590-227	Sequence 227, App
248	31	48.4	117	7	US-11-004-590-228	Sequence 228, App
249	31	48.4	145	6	US-10-504-389A-45	Sequence 45, Appl
250	31	48.4	150	7	US-11-096-568A-10114	Sequence 10114, A
251	31	48.4	156	6	US-10-467-657-1280	Sequence 1280, Ap
252	31	48.4	185	7	US-11-096-568A-10113	Sequence 10113, A
253	31	48.4	205	6	US-10-689-742-72	Sequence 72, Appl
254	31	48.4	214	7	US-11-096-051-16	Sequence 16, Appl
255	31	48.4	241	6	US-10-467-657-7266	Sequence 7266, Ap
256	31	48.4	241	7	US-11-096-568A-10112	Sequence 10112, A
257	31	48.4	242	6	US-10-524-647-6	Sequence 6, Appli
258	31	48.4	242	6	US-10-524-647-8	Sequence 8, Appli
259	31	48.4	242	6	US-10-524-647-10	Sequence 10, Appl
260	31	48.4	242	6	US-10-524-647-100	Sequence 100, App
261	31	48.4	242	6	US-10-524-972-6	Sequence 6, Appli
262	31	48.4	242	6	US-10-524-972-8	Sequence 8, Appli
263	31	48.4	242	6	US-10-524-972-10	Sequence 10, Appl
264	31	48.4	242	6	US-10-524-972-84	Sequence 84, Appl
265	31	48.4	242	7	US-11-129-143-181	Sequence 181, App
266	31	48.4	242	7	US-11-070-080-33	Sequence 33, Appl
267	31	48.4	257	7	US-11-098-686-10104	Sequence 10104, A
268	31	48.4	261	7	US-11-096-568A-3864	Sequence 3864, Ap
269	31	48.4	279	7	US-11-087-099-2670	Sequence 2670, Ap
270	31	48.4	318	7	US-11-087-099-6672	Sequence 6672, Ap
271	31	48.4	337	6	US-10-875-716-2	Sequence 2, Appli
272	31	48.4	337	7	US-11-174-816-13	Sequence 13, Appl
273	31	48.4	337	7	US-11-174-816-43	Sequence 43, Appl
274	31	48.4	337	7	US-11-174-816-58	Sequence 58, Appl
275	31	48.4	337	7	US-11-174-819-11	Sequence 11, Appl
276	31	48.4	337	7	US-11-174-819-69	Sequence 69, Appl
277	31	48.4	337	7	US-11-174-751-14	Sequence 14, Appl
278	31	48.4	339	7	US-11-174-816-40	Sequence 40, Appl
279	31	48.4	339	7	US-11-174-816-55	Sequence 55, Appl
280	31	48.4	339	7	US-11-174-819-5	Sequence 5, Appli
281	31	48.4	339	7	US-11-174-819-74	Sequence 74, Appl
282	31	48.4	344	7	US-11-174-819-77	Sequence 77, Appl
283	31	48.4	347	7	US-11-087-099-2230	Sequence 2230, Ap
284	31	48.4	347	7	US-11-096-568A-32503	Sequence 32503, A
285	31	48.4	351	7	US-11-174-816-5	Sequence 5, Appli
286	31	48.4	351	7	US-11-174-819-68	Sequence 68, Appl
287	31	48.4	351	7	US-11-174-751-6	Sequence 6, Appli
288	31	48.4	358	7	US-11-087-099-7013	Sequence 7013, Ap
289	31	48.4	366	6	US-10-467-657-1700	Sequence 1700, Ap
290	31	48.4	380	7	US-11-087-099-8062	Sequence 8062, Ap
291	31	48.4	387	7	US-11-087-099-935	Sequence 935, App
292	31	48.4	393	7	US-11-054-281-301	Sequence 301, App
293	31	48.4	396	7	US-11-087-099-1287	Sequence 1287, Ap
294	31	48.4	417	6	US-10-793-626-950	Sequence 950, App
295	31	48.4	428	6	US-10-821-234-997	Sequence 997, App
296	31	48.4	444	7	US-11-004-590-232	Sequence 232, App
297	31	48.4	444	7	US-11-004-590-233	Sequence 233, App
298	31	48.4	447	7	US-11-004-590-230	Sequence 230, App
299	31	48.4	447	7	US-11-004-590-231	Sequence 231, App
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308	31	48.4	481	7	US-11-096-568A-31400	Sequence 31400, A
309	31	48.4	481	7	US-11-096-568A-33459	Sequence 33459, A
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313	31	48.4	529	7	US-11-096-568A-31399	Sequence 31399, A
314	31	48.4	534	6	US-10-646-283-2	Sequence 2, Appli
315	31	48.4	553	7	US-11-087-099-1793	Sequence 1793, Ap
316	31	48.4	555	7	US-11-096-568A-33458	Sequence 33458, A
317	31	48.4	560	7	US-11-096-568A-33457	Sequence 33457, A
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319	31	48.4	576	7	US-11-087-099-10787	Sequence 10787, A
320	31	48.4	579	7	US-11-087-099-8402	Sequence 8402, Ap
321	31	48.4	583	7	US-11-087-099-6900	Sequence 6900, Ap
322	31	48.4	584	7	US-11-087-099-5098	Sequence 5098, Ap
323	31	48.4	584	7	US-11-087-099-5436	Sequence 5436, Ap
324	31	48.4	586	7	US-11-096-568A-32501	Sequence 32501, A
325	31	48.4	615	7	US-11-136-244-13	Sequence 13, Appl
326	31	48.4	631	7	US-11-087-099-10959	Sequence 10959, A
327	31	48.4	637	7	US-11-096-568A-27876	Sequence 27876, A
328	31	48.4	668	7	US-11-098-686-11201	Sequence 11201, A
329	31	48.4	704	7	US-11-096-568A-27875	Sequence 27875, A
330	31	48.4	732	7	US-11-096-568A-27874	Sequence 27874, A
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332	31	48.4	818	7	US-11-120-308-94	Sequence 94, Appl
333	31	48.4	850	7	US-11-087-099-10238	Sequence 10238, A
334	31	48.4	887	7	US-11-096-568A-29796	Sequence 29796, A
335	31	48.4	917	7	US-11-096-568A-29795	Sequence 29795, A
336	31	48.4	961	7	US-11-096-568A-29794	Sequence 29794, A
337	31	48.4	1076	7	US-11-096-568A-29101	Sequence 29101, A
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340	31	48.4	1208	6	US-10-330-773-244	Sequence 244, App
341	31	48.4	1327	7	US-11-096-568A-29099	Sequence 29099, A
342	31	48.4	2440	6	US-10-766-317-10	Sequence 10, Appl
343	31	48.4	5712	7	US-11-143-980-47	Sequence 47, Appl
344	31	48.4	7968	7	US-11-143-980-49	Sequence 49, Appl
345	30.5	47.7	247	6	US-10-821-234-1174	Sequence 1174, Ap
346	30.5	47.7	342	7	US-11-087-099-3637	Sequence 3637, Ap
347	30.5	47.7	350	7	US-11-087-099-1811	Sequence 1811, Ap
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349	30	46.9	13	6	US-10-511-559-415	Sequence 415, App
350	30	46.9	13	6	US-10-511-559-416	Sequence 416, App
351	30	46.9	13	6	US-10-511-559-417	Sequence 417, App
352	30	46.9	18	6	US-10-939-890-132	Sequence 132, App
353	30	46.9	19	6	US-10-467-657-8958	Sequence 8958, Ap
354	30	46.9	49	7	US-11-123-896-78	Sequence 78, Appl
355	30	46.9	49	7	US-11-123-896-285	Sequence 285, App
356	30	46.9	54	6	US-10-974-534-2	Sequence 2, Appli
357	30	46.9	59	6	US-10-467-657-6296	Sequence 6296, Ap
358	30	46.9	76	7	US-11-000-463-318	Sequence 318, App
359	30	46.9	76	7	US-11-000-463-790	Sequence 790, App
360	30	46.9	82	7	US-11-123-896-284	Sequence 284, App
361	30	46.9	84	7	US-11-096-568A-14275	Sequence 14275, A
362	30	46.9	85	5	US-09-978-360A-601	Sequence 601, App
363	30	46.9	85	5	US-09-978-360A-602	Sequence 602, App
364	30	46.9	85	5	US-09-978-360A-779	Sequence 779, App
365	30	46.9	85	7	US-11-123-896-77	Sequence 77, Appl
366	30	46.9	93	7	US-11-087-099-8624	Sequence 8624, Ap
367	30	46.9	115	7	US-11-217-562-8	Sequence 8, Appli
368	30	46.9	115	7	US-11-107-219-8	Sequence 8, Appli
369	30	46.9	118	7	US-11-096-568A-4036	Sequence 4036, Ap
370	30	46.9	119	7	US-11-183-205-53	Sequence 53, Appl
371	30	46.9	119	7	US-11-183-205-54	Sequence 54, Appl
372	30	46.9	120	7	US-11-097-812-68	Sequence 68, Appl
373	30	46.9	122	7	US-11-096-568A-14274	Sequence 14274, A
374	30	46.9	127	7	US-11-096-568A-14273	Sequence 14273, A
375	30	46.9	142	6	US-10-467-657-926	Sequence 926, App
376	30	46.9	142	6	US-10-467-657-5200	Sequence 5200, Ap
377	30	46.9	145	7	US-11-096-568A-20503	Sequence 20503, A
378	30	46.9	151	7	US-11-087-099-2616	Sequence 2616, Ap
379	30	46.9	151	7	US-11-087-099-2809	Sequence 2809, Ap
380	30	46.9	151	7	US-11-087-099-8085	Sequence 8085, Ap
381	30	46.9	151	7	US-11-087-099-8771	Sequence 8771, Ap
382	30	46.9	151	7	US-11-087-099-8994	Sequence 8994, Ap
383	30	46.9	151	7	US-11-087-099-10783	Sequence 10783, A
384	30	46.9	151	7	US-11-087-099-11943	Sequence 11943, A
385	30	46.9	156	7	US-11-087-099-5494	Sequence 5494, Ap
386	30	46.9	158	7	US-11-098-686-11246	Sequence 11246, A
387	30	46.9	171	7	US-11-087-099-11564	Sequence 11564, A
388	30	46.9	173	7	US-11-087-099-4481	Sequence 4481, Ap
389	30	46.9	177	6	US-10-467-657-456	Sequence 456, App
390	30	46.9	194	7	US-11-087-099-10091	Sequence 10091, A

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394	30	46.9	228	7	US-11-098-686-10964	Sequence 10964, A
395	30	46.9	234	7	US-11-072-512-3869	Sequence 3869, Ap
396	30	46.9	236	7	US-11-096-568A-23039	Sequence 23039, A
397	30	46.9	241	6	US-10-793-626-2574	Sequence 2574, Ap
398	30	46.9	243	7	US-11-087-099-9740	Sequence 9740, Ap
399	30	46.9	244	7	US-11-087-099-9456	Sequence 9456, Ap
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401	30	46.9	273	7	US-11-096-568A-23037	Sequence 23037, A
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403	30	46.9	281	7	US-11-087-099-358	Sequence 358, App
404	30	46.9	288	7	US-11-072-512-3120	Sequence 3120, Ap
405	30	46.9	294	7	US-11-112-882-85	Sequence 85, Appl
406	30	46.9	301	7	US-11-087-099-12187	Sequence 12187, A
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408	30	46.9	306	7	US-11-087-099-9166	Sequence 9166, Ap
409	30	46.9	308	7	US-11-174-816-50	Sequence 50, Appl
410	30	46.9	322	7	US-11-096-568A-7498	Sequence 7498, Ap
411	30	46.9	323	7	US-11-087-099-2157	Sequence 2157, Ap
412	30	46.9	324	7	US-11-092-140-34	Sequence 34, Appl
413	30	46.9	332	7	US-11-174-816-39	Sequence 39, Appl
414	30	46.9	332	7	US-11-174-816-54	Sequence 54, Appl
415	30	46.9	332	7	US-11-174-819-3	Sequence 3, Appli
416	30	46.9	333	6	US-10-055-877-178	Sequence 178, App
417	30	46.9	333	6	US-10-527-500-27	Sequence 27, Appl
418	30	46.9	335	7	US-11-174-819-73	Sequence 73, Appl
419	30	46.9	338	6	US-10-467-657-3178	Sequence 3178, Ap
420	30	46.9	338	6	US-10-055-877-175	Sequence 175, App
421	30	46.9	338	7	US-11-174-816-63	Sequence 63, Appl
422	30	46.9	338	7	US-11-174-819-82	Sequence 82, Appl
423	30	46.9	339	7	US-11-127-877-49	Sequence 49, Appl
424	30	46.9	339	7	US-11-174-816-3	Sequence 3, Appli
425	30	46.9	339	7	US-11-174-819-67	Sequence 67, Appl
426	30	46.9	339	7	US-11-174-751-3	Sequence 3, Appli
427	30	46.9	339	7	US-11-174-751-46	Sequence 46, Appl
428	30	46.9	342	7	US-11-174-816-56	Sequence 56, Appl
429	30	46.9	342	7	US-11-174-819-75	Sequence 75, Appl
430	30	46.9	342	7	US-11-096-568A-7497	Sequence 7497, Ap
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432	30	46.9	343	7	US-11-174-751-9	Sequence 9, Appli
433	30	46.9	344	7	US-11-174-816-46	Sequence 46, Appl
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435	30	46.9	344	7	US-11-174-816-60	Sequence 60, Appl
436	30	46.9	344	7	US-11-174-816-61	Sequence 61, Appl
437	30	46.9	344	7	US-11-174-816-62	Sequence 62, Appl
438	30	46.9	344	7	US-11-174-819-30	Sequence 30, Appl
439	30	46.9	344	7	US-11-174-819-32	Sequence 32, Appl
440	30	46.9	344	7	US-11-174-819-79	Sequence 79, Appl
441	30	46.9	344	7	US-11-174-819-80	Sequence 80, Appl
442	30	46.9	344	7	US-11-174-819-81	Sequence 81, Appl
443	30	46.9	344	7	US-11-096-568A-31491	Sequence 31491, A
444	30	46.9	348	7	US-11-082-389-218	Sequence 218, App
445	30	46.9	348	7	US-11-174-816-48	Sequence 48, Appl
446	30	46.9	348	7	US-11-174-819-34	Sequence 34, Appl
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448	30	46.9	348	7	US-11-096-568A-31490	Sequence 31490, A
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452	30	46.9	358	6	US-10-055-877-176	Sequence 176, App
453	30	46.9	358	6	US-10-055-877-177	Sequence 177, App
454	30	46.9	358	7	US-11-174-816-49	Sequence 49, Appl
455	30	46.9	358	7	US-11-174-816-52	Sequence 52, Appl
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457	30	46.9	358	7	US-11-174-816-64	Sequence 64, Appl
458	30	46.9	358	7	US-11-174-816-65	Sequence 65, Appl
459	30	46.9	358	7	US-11-174-816-66	Sequence 66, Appl
460	30	46.9	358	7	US-11-174-816-67	Sequence 67, Appl
461	30	46.9	358	7	US-11-174-816-68	Sequence 68, Appl
462	30	46.9	358	7	US-11-174-816-69	Sequence 69, Appl
463	30	46.9	358	7	US-11-174-819-15	Sequence 15, Appl
464	30	46.9	358	7	US-11-174-819-17	Sequence 17, Appl
465	30	46.9	358	7	US-11-174-819-24	Sequence 24, Appl
466	30	46.9	358	7	US-11-174-819-26	Sequence 26, Appl
467	30	46.9	358	7	US-11-174-819-83	Sequence 83, Appl
468	30	46.9	358	7	US-11-174-819-84	Sequence 84, Appl
469	30	46.9	358	7	US-11-174-819-85	Sequence 85, Appl
470	30	46.9	358	7	US-11-174-819-86	Sequence 86, Appl
471	30	46.9	358	7	US-11-174-819-87	Sequence 87, Appl
472	30	46.9	358	7	US-11-174-819-88	Sequence 88, Appl
473	30	46.9	358	7	US-11-174-819-89	Sequence 89, Appl
474	30	46.9	362	7	US-11-174-816-70	Sequence 70, Appl
475	30	46.9	368	7	US-11-096-568A-16642	Sequence 16642, A
476	30	46.9	373	7	US-11-096-568A-21984	Sequence 21984, A
477	30	46.9	375	7	US-11-098-686-10499	Sequence 10499, A
478	30	46.9	377	7	US-11-096-568A-16641	Sequence 16641, A
479	30	46.9	383	7	US-11-096-568A-16640	Sequence 16640, A
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483	30	46.9	394	7	US-11-074-176-310	Sequence 310, App
484	30	46.9	399	7	US-11-096-568A-7496	Sequence 7496, Ap
485	30	46.9	403	6	US-10-330-773-241	Sequence 241, App
486	30	46.9	410	7	US-11-096-568A-21983	Sequence 21983, A
487	30	46.9	414	7	US-11-074-176-46	Sequence 46, Appl
488	30	46.9	416	7	US-11-098-686-10708	Sequence 10708, A
489	30	46.9	442	7	US-11-024-959-373	Sequence 373, App
490	30	46.9	443	7	US-11-087-099-4443	Sequence 4443, Ap
491	30	46.9	444	7	US-11-024-959-337	Sequence 337, App
492	30	46.9	444	7	US-11-087-099-956	Sequence 956, App
493	30	46.9	446	7	US-11-072-512-2206	Sequence 2206, Ap
494	30	46.9	447	7	US-11-024-959-452	Sequence 452, App
495	30	46.9	447	7	US-11-024-959-505	Sequence 505, App
496	30	46.9	447	7	US-11-087-099-979	Sequence 979, App
497	30	46.9	448	7	US-11-183-205-56	Sequence 56, Appl
498	30	46.9	458	7	US-11-087-099-9621	Sequence 9621, Ap
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507	30	46.9	493	7	US-11-087-099-5102	Sequence 5102, Ap
508	30	46.9	507	7	US-11-087-099-10522	Sequence 10522, A
509	30	46.9	508	7	US-11-082-389-178	Sequence 178, App
510	30	46.9	517	7	US-11-098-686-11247	Sequence 11247, A
511	30	46.9	525	6	US-10-995-561-858	Sequence 858, App
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513	30	46.9	539	7	US-11-096-568A-13358	Sequence 13358, A
514	30	46.9	567	6	US-10-330-773-556	Sequence 556, App
515	30	46.9	577	7	US-11-072-175-187	Sequence 187, App
516	30	46.9	582	6	US-10-330-773-558	Sequence 558, App
517	30	46.9	589	6	US-10-501-035-202	Sequence 202, App
518	30	46.9	611	6	US-10-330-773-553	Sequence 553, App
519	30	46.9	622	7	US-11-087-099-4176	Sequence 4176, Ap
520	30	46.9	644	7	US-11-087-099-6153	Sequence 6153, Ap
521	30	46.9	811	7	US-11-200-296B-81	Sequence 81, Appl
522	30	46.9	863	6	US-10-793-626-2010	Sequence 2010, Ap
523	30	46.9	867	7	US-11-087-099-10404	Sequence 10404, A
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525	30	46.9	1006	6	US-10-793-626-154	Sequence 154, App
526	30	46.9	1010	6	US-10-959-611-2	Sequence 2, Appli
527	30	46.9	1049	6	US-10-131-826A-358	Sequence 358, App
528	30	46.9	1049	6	US-10-973-115B-358	Sequence 358, App
529	30	46.9	1076	7	US-11-098-686-11184	Sequence 11184, A
530	30	46.9	1227	6	US-10-858-730-223	Sequence 223, App
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532	30	46.9	1356	7	US-11-129-741-2939	Sequence 2939, Ap
533	30	46.9	1356	7	US-11-129-741-2941	Sequence 2941, Ap
534	30	46.9	1356	7	US-11-129-741-2943	Sequence 2943, Ap
535	30	46.9	1356	7	US-11-129-741-2945	Sequence 2945, Ap
536	30	46.9	1356	7	US-11-129-741-2949	Sequence 2949, Ap

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538	30	46.9	1356	7	US-11-129-741-4245	Sequence 4245, Ap
539	30	46.9	1362	6	US-10-895-064-420	Sequence 420, App
540	30	46.9	1362	7	US-11-129-741-420	Sequence 420, App
541	30	46.9	1476	6	US-10-647-956A-4	Sequence 4, Appli
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543	30	46.9	2096	6	US-10-995-561-606	Sequence 606, App
544	30	46.9	2351	6	US-10-995-561-608	Sequence 608, App
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546	30	46.9	2351	7	US-11-244-087-3	Sequence 3, Appli
547	30	46.9	2351	7	US-11-267-631-49	Sequence 49, Appl
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553	29.5	46.1	447	7	US-11-102-621-131	Sequence 131, App
554	29.5	46.1	447	7	US-11-102-621-132	Sequence 132, App
555	29.5	46.1	447	7	US-11-102-621-133	Sequence 133, App
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561	29	45.3	11	6	US-10-467-657-9000	Sequence 9000, Ap
562	29	45.3	13	7	US-11-004-399-1766	Sequence 1766, Ap
563	29	45.3	23	6	US-10-895-064-226	Sequence 226, App
564	29	45.3	23	7	US-11-129-741-226	Sequence 226, App
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568	29	45.3	60	7	US-11-096-568A-2648	Sequence 2648, Ap
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573	29	45.3	99	7	US-11-096-568A-5731	Sequence 5731, Ap
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575	29	45.3	121	7	US-11-136-559-12	Sequence 12, Appl
576	29	45.3	121	7	US-11-136-559-20	Sequence 20, Appl
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587	29	45.3	243	7	US-11-096-568A-24970	Sequence 24970, A
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590	29	45.3	255	6	US-10-454-437-152	Sequence 152, App
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594	29	45.3	261	6	US-10-793-626-2442	Sequence 2442, Ap
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599	29	45.3	284	7	US-11-096-568A-6984	Sequence 6984, Ap
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602	29	45.3	295	7	US-11-205-562-4	Sequence 4, Appli
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606	29	45.3	296	7	US-11-205-562-1	Sequence 1, Appli
607	29	45.3	296	7	US-11-205-562-3	Sequence 3, Appli
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616	29	45.3	338	7	US-11-087-099-12138	Sequence 12138, A
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625	29	45.3	371	7	US-11-096-568A-9324	Sequence 9324, Ap
626	29	45.3	371	7	US-11-096-568A-9325	Sequence 9325, Ap
627	29	45.3	372	7	US-11-096-568A-9323	Sequence 9323, Ap
628	29	45.3	373	7	US-11-096-568A-9322	Sequence 9322, Ap
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635	29	45.3	409	7	US-11-096-568A-22446	Sequence 22446, A
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637	29	45.3	412	7	US-11-096-568A-18439	Sequence 18439, A
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645	29	45.3	430	7	US-11-096-568A-5372	Sequence 5372, Ap
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647	29	45.3	451	7	US-11-087-099-2650	Sequence 2650, Ap
648	29	45.3	453	6	US-10-131-826A-270	Sequence 270, App
649	29	45.3	453	6	US-10-973-115B-270	Sequence 270, App
650	29	45.3	457	6	US-10-821-234-1185	Sequence 1185, Ap
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652	29	45.3	464	7	US-11-087-099-8095	Sequence 8095, Ap
653	29	45.3	468	6	US-10-467-657-1112	Sequence 1112, Ap
654	29	45.3	471	7	US-11-061-869-20	Sequence 20, Appl
655	29	45.3	471	7	US-11-197-721-34	Sequence 34, Appl
656	29	45.3	477	7	US-11-096-568A-5370	Sequence 5370, Ap
657	29	45.3	482	7	US-11-096-568A-8958	Sequence 8958, Ap
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659	29	45.3	483	7	US-11-116-881A-165	Sequence 165, App
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663	29	45.3	533	7	US-11-145-035-15	Sequence 15, Appl
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666	29	45.3	576	7	US-11-096-568A-8959	Sequence 8959, Ap
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668	29	45.3	590	6	US-10-501-035-321	Sequence 321, App
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670	29	45.3	598	7	US-11-145-035-14	Sequence 14, Appl
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674	29	45.3	724	6	US-10-873-632A-16	Sequence 16, Appl
675	29	45.3	724	7	US-11-184-380-4	Sequence 4, Appli
676	29	45.3	724	7	US-11-145-035-36	Sequence 36, Appl
677	29	45.3	724	7	US-11-143-866-2	Sequence 2, Appli
678	29	45.3	726	6	US-10-873-632A-17	Sequence 17, Appl
679	29	45.3	726	7	US-11-143-866-4	Sequence 4, Appli
680	29	45.3	735	6	US-10-873-632A-13	Sequence 13, Appl
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682	29	45.3	735	7	US-11-145-035-13	Sequence 13, Appl

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685	29	45.3	736	6	US-10-873-632A-19	Sequence 19, Appl
686	29	45.3	736	6	US-10-873-632A-20	Sequence 20, Appl
687	29	45.3	736	7	US-11-145-035-20	Sequence 20, Appl
688	29	45.3	736	7	US-11-145-035-22	Sequence 22, Appl
689	29	45.3	736	7	US-11-145-035-26	Sequence 26, Appl
690	29	45.3	737	7	US-11-145-035-38	Sequence 38, Appl
691	29	45.3	738	6	US-10-873-632A-21	Sequence 21, Appl
692	29	45.3	738	7	US-11-145-035-40	Sequence 40, Appl
693	29	45.3	738	7	US-11-145-035-41	Sequence 41, Appl
694	29	45.3	748	7	US-11-087-099-4575	Sequence 4575, Ap
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698	29	45.3	796	6	US-10-995-561-954	Sequence 954, App
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702	29	45.3	832	7	US-11-221-470-63	Sequence 63, Appl
703	29	45.3	832	7	US-11-221-470-64	Sequence 64, Appl
704	29	45.3	842	7	US-11-221-470-50	Sequence 50, Appl
705	29	45.3	842	7	US-11-221-470-51	Sequence 51, Appl
706	29	45.3	843	7	US-11-221-470-45	Sequence 45, Appl
707	29	45.3	843	7	US-11-221-470-47	Sequence 47, Appl
708	29	45.3	843	7	US-11-221-470-48	Sequence 48, Appl
709	29	45.3	843	7	US-11-221-470-53	Sequence 53, Appl
710	29	45.3	843	7	US-11-221-470-54	Sequence 54, Appl
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712	29	45.3	843	7	US-11-221-470-56	Sequence 56, Appl
713	29	45.3	843	7	US-11-221-470-59	Sequence 59, Appl
714	29	45.3	845	7	US-11-221-470-11	Sequence 11, Appl
715	29	45.3	845	7	US-11-221-470-46	Sequence 46, Appl
716	29	45.3	845	7	US-11-221-470-57	Sequence 57, Appl
717	29	45.3	845	7	US-11-221-470-58	Sequence 58, Appl
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723	29	45.3	1255	7	US-11-052-554A-266	Sequence 266, App
724	29	45.3	1255	7	US-11-052-554A-267	Sequence 267, App
725	29	45.3	1255	7	US-11-052-554A-268	Sequence 268, App
726	29	45.3	1255	7	US-11-052-554A-269	Sequence 269, App
727	29	45.3	1255	7	US-11-052-554A-270	Sequence 270, App
728	29	45.3	1255	7	US-11-052-554A-271	Sequence 271, App
729	29	45.3	1255	7	US-11-052-554A-272	Sequence 272, App
730	29	45.3	1255	7	US-11-052-554A-273	Sequence 273, App
731	29	45.3	1255	7	US-11-052-554A-274	Sequence 274, App
732	29	45.3	1255	7	US-11-052-554A-275	Sequence 275, App
733	29	45.3	1255	7	US-11-004-399-4026	Sequence 4026, Ap
734	29	45.3	1257	7	US-11-004-399-1737	Sequence 1737, Ap
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736	29	45.3	1313	7	US-11-091-668-4	Sequence 4, Appli
737	29	45.3	1351	7	US-11-129-741-2937	Sequence 2937, Ap
738	29	45.3	1351	7	US-11-129-741-2947	Sequence 2947, Ap
739	29	45.3	1385	7	US-11-129-741-3655	Sequence 3655, Ap
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741	29	45.3	1468	6	US-10-467-657-1088	Sequence 1088, Ap
742	29	45.3	1565	6	US-10-467-657-2704	Sequence 2704, Ap
743	29	45.3	2280	7	US-11-022-562-211	Sequence 211, App
744	29	45.3	3011	6	US-10-985-205-3	Sequence 3, Appli
745	29	45.3	3116	6	US-10-995-561-826	Sequence 826, App
746	29	45.3	3712	7	US-11-019-711-48	Sequence 48, Appl
747	29	45.3	3712	7	US-11-019-711-51	Sequence 51, Appl
748	28.5	44.5	69	5	US-09-978-360A-704	Sequence 704, App
749	28.5	44.5	81	6	US-10-821-234-1613	Sequence 1613, Ap
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753	28.5	44.5	468	7	US-11-087-099-3450	Sequence 3450, Ap
754	28.5	44.5	552	7	US-11-087-099-10983	Sequence 10983, A
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757	28	43.8	9	6	US-10-510-101-10	Sequence 10, Appl
758	28	43.8	9	7	US-11-033-039-297	Sequence 297, App
759	28	43.8	10	7	US-11-097-224B-8	Sequence 8, Appli
760	28	43.8	10	7	US-11-250-411-11	Sequence 11, Appl
761	28	43.8	10	7	US-11-097-252A-8	Sequence 8, Appli
762	28	43.8	13	7	US-11-152-974A-299	Sequence 299, App
763	28	43.8	13	7	US-11-152-974A-551	Sequence 551, App
764	28	43.8	13	7	US-11-153-143A-299	Sequence 299, App
765	28	43.8	13	7	US-11-153-143A-551	Sequence 551, App
766	28	43.8	16	6	US-10-517-904-2	Sequence 2, Appli
767	28	43.8	18	7	US-11-033-039-1215	Sequence 1215, Ap
768	28	43.8	18	7	US-11-033-039-1231	Sequence 1231, Ap
769	28	43.8	22	7	US-11-066-967-108	Sequence 108, App
770	28	43.8	30	7	US-11-116-943-8	Sequence 8, Appli
771	28	43.8	51	7	US-11-172-571-29	Sequence 29, Appl
772	28	43.8	51	7	US-11-096-568A-1244	Sequence 1244, Ap
773	28	43.8	76	7	US-11-172-571-28	Sequence 28, Appl
774	28	43.8	101	7	US-11-072-512-1979	Sequence 1979, Ap
775	28	43.8	107	6	US-10-507-662-64	Sequence 64, Appl
776	28	43.8	111	7	US-11-184-005-5	Sequence 5, Appli
777	28	43.8	114	7	US-11-055-163-18	Sequence 18, Appl
778	28	43.8	116	7	US-11-055-163-17	Sequence 17, Appl
779	28	43.8	116	7	US-11-152-366-283	Sequence 283, App
780	28	43.8	118	6	US-10-537-061-7	Sequence 7, Appli
781	28	43.8	119	7	US-11-250-411-97	Sequence 97, Appl
782	28	43.8	119	7	US-11-250-411-101	Sequence 101, App
783	28	43.8	120	7	US-11-096-568A-20952	Sequence 20952, A
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785	28	43.8	127	6	US-10-793-626-242	Sequence 242, App
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787	28	43.8	138	7	US-11-250-411-90	Sequence 90, Appl
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ALIGNMENTS

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RESULT 1
US-11-190-188-6
; Sequence 6, Application US/11190188
; Publication No. US20060035331A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  PATTERSON, Chandra
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  SHIH, Leo L.
;  APPLICANT:  TRIBOULEY, Catherine
;  APPLICANT:  LU, Dyung Aina M.
;  APPLICANT:  YUE, Henry
;  APPLICANT:  KHAN, Farrah A.
;  APPLICANT:  POLICKY, Jennifer L.
;  APPLICANT:  AU-YOUNG, Janice
;  APPLICANT:  YANG, Junming
;  APPLICANT:  HARLAND, Lee
;  APPLICANT:  WALSH, Roderick T.
;  APPLICANT:  LO, Terence P.
;  APPLICANT:  BOROWSKY, Mark L.
;  TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
;  FILE REFERENCE: PI-0044 PCT
;  CURRENT APPLICATION NUMBER: US/11/190,188
;  CURRENT FILING DATE:  2005-07-27
;  PRIOR APPLICATION NUMBER: US/10/220,382
;  PRIOR FILING DATE: 2001-03-01
;  PRIOR APPLICATION NUMBER: 60/186,854; 60/188,384; 60/190,453; 60/190,730
;  PRIOR FILING DATE: 2000-03-03; 2000-03-10; 2000-03-17; 2000-03-20
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PERL Program
; SEQ ID NO 6
;   LENGTH: 153
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 5376785CD1
US-11-190-188-6

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  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db         56 LYFAFHWFA 64


RESULT 2
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; Sequence 16, Application US/11037199
; Publication No. US20060030015A1
; GENERAL INFORMATION:
;  APPLICANT: Japan Science and Technology Corporation
;  TITLE OF INVENTION: Novel methods of producing antibody-enzyme, the antibody-enzymes,
;  TITLE OF INVENTION:  and the use thereof
;  FILE REFERENCE: A251-01/PCT
;  CURRENT APPLICATION NUMBER: US/11/037,199
;  CURRENT FILING DATE:  2005-01-19
;  PRIOR APPLICATION NUMBER: JP 2002-211756
;  PRIOR FILING DATE: 2002-7-19
;  PRIOR APPLICATION NUMBER: JP 2002-211768
;  PRIOR FILING DATE: 2002-7-19
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;  PRIOR FILING DATE: 2003-7-17
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.1
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;   ORGANISM: Helicobacter pylori
US-11-037-199-16

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RESULT 3
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; Sequence 23, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
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; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-23

Query Match 62.5%; Score 40; DB 7; Length 117;
Best Local Similarity 50.0%; Pred. No. 8.1;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
|::|: || |
Db 100 LFYGYAWFNY 109

RESULT 4
US-11-097-812-29
; Sequence 29, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 117
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-29

Query Match 62.5%; Score 40; DB 7; Length 117;
Best Local Similarity 50.0%; Pred. No. 8.1;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
|::|: || |
Db 100 LFYGYAWFNY 109

RESULT 5
US-11-097-812-33
; Sequence 33, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Kretz-Rommel, Anke
; APPLICANT: Dakappagari, Naveen
; TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
; TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
; FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
; CURRENT APPLICATION NUMBER: US/11/097,812
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 11/016,647
; PRIOR FILING DATE: 2004-12-17
; PRIOR APPLICATION NUMBER: PCT/US04/06570
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/548,385
; PRIOR FILING DATE: 2004-02-28
; PRIOR APPLICATION NUMBER: US 60/529,500
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 60/451,816
; PRIOR FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 117
; TYPE: PRT
; ORGANISM: mouse
US-11-097-812-33

Query Match 62.5%; Score 40; DB 7; Length 117;
Best Local Similarity 50.0%; Pred. No. 8.1;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LYFGFPWFAY 10
|::|: || |
Db 100 LFYGYAWFNY 109

RESULT 6
US-11-136-559-8
; Sequence 8, Application US/11136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
; FILE REFERENCE: P07069US04/BAS
; CURRENT APPLICATION NUMBER: US/11/136,559
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US/10/056,052
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: 60/308,116
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/298,413
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/274,611
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: 60/264,072
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-11-136-559-8

Query Match 62.5%; Score 40; DB 7; Length 118;
Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YFGFPWFAY 10
|:| ||||
Db 99 YYGNSWFAY 107

RESULT 7
US-11-136-559-16
; Sequence 16, Application US/11136559
; Publication No. US20050287164A1
; GENERAL INFORMATION:
; APPLICANT: PATTI, Joseph M
; APPLICANT: HUTCHINS, Jeff T
; APPLICANT: DOMANSKI, Paul
; APPLICANT: PATEL, Pratiksha
; APPLICANT: HALL, Andrea

```
;  TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE CLFA PROTEIN . . .
;  FILE REFERENCE: P07069US04/BAS
;  CURRENT APPLICATION NUMBER: US/11/136,559
;  CURRENT FILING DATE:  2005-05-25
;  PRIOR APPLICATION NUMBER: US/10/056,052
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: 60/308,116
;  PRIOR FILING DATE: 2001-07-30
;  PRIOR APPLICATION NUMBER: 60/298,413
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: 60/274,611
;  PRIOR FILING DATE: 2001-03-12
;  PRIOR APPLICATION NUMBER: 60/264,072
;  PRIOR FILING DATE: 2001-01-26
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
;   LENGTH: 118
;   TYPE: PRT
;   ORGANISM: Staphylococcus aureus
US-11-136-559-16

  Query Match             62.5%;  Score 40;  DB 7;  Length 118;
  Best Local Similarity   66.7%;  Pred. No. 8.2;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              |:|  ||||
Db         99 YYGNSWFAY 107


RESULT 8
US-10-793-626-302
; Sequence 302, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 302
;   LENGTH: 363
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-10-793-626-302

  Query Match             60.9%;  Score 39;  DB 6;  Length 363;
  Best Local Similarity   66.7%;  Pred. No. 29;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              ||   ||||
Db        317 LYLSIPWFA 325


RESULT 9
US-11-089-551A-23
; Sequence 23, Application US/11089551A
; Publication No. US20050266242A1
; GENERAL INFORMATION:
;  APPLICANT: Lindquist et al.
;  TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
;  FILE REFERENCE: 30554/40025A
;  CURRENT APPLICATION NUMBER: US/11/089,551A
;  CURRENT FILING DATE:  2005-03-24
;  PRIOR APPLICATION NUMBER: US 60/559,286
;  PRIOR FILING DATE: 2004-03-31
;  NUMBER OF SEQ ID NOS: 65
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
;   LENGTH: 1075
;   TYPE: PRT
;   ORGANISM: Saccharomyces cerevisiae
US-11-089-551A-23

  Query Match             60.9%;  Score 39;  DB 7;  Length 1075;
  Best Local Similarity   60.0%;  Pred. No. 69;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              | |||||  ::
Db        671 LKFGFPWNSF 680


RESULT 10
US-10-793-626-2558
; Sequence 2558, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2558
;   LENGTH: 357
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
US-10-793-626-2558

  Query Match             59.4%;  Score 38;  DB 6;  Length 357;
  Best Local Similarity   55.6%;  Pred. No. 41;
  Matches    5;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              |: |:||:|
Db         43 LFHGWPWYA 51


RESULT 11
US-11-124-367A-393
; Sequence 393, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
;  APPLICANT: Michele Cargill
;  APPLICANT:  Hongjin Huang
;  TITLE OF INVENTION: Genetic Polymorphisms Associated with
;  TITLE OF INVENTION:  Fibrosis Methods of Detection and Uses Thereof
;  FILE REFERENCE: CL001519.ORD
;  CURRENT APPLICATION NUMBER: US/11/124,367A
;  CURRENT FILING DATE:  2005-05-09
;  PRIOR APPLICATION NUMBER: US 60/568,846
;  PRIOR FILING DATE: 2004-05-07
;  PRIOR APPLICATION NUMBER: US 60/582,609
;  PRIOR FILING DATE: 2004-06-25
;  PRIOR APPLICATION NUMBER: US 60/599,554
;  PRIOR FILING DATE: 2004-08-09
;  NUMBER OF SEQ ID NOS: 34460
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 393
;   LENGTH: 485
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-124-367A-393

  Query Match             59.4%;  Score 38;  DB 7;  Length 485;
  Best Local Similarity   71.4%;  Pred. No. 53;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LYFGFPW 7
              ||: |||
Db        289 LYYNFPW 295


RESULT 12
US-11-087-099-969
; Sequence 969, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 969
;   LENGTH: 801
;   TYPE: PRT
;   ORGANISM: Neurospora crassa
US-11-087-099-969

  Query Match             59.4%;  Score 38;  DB 7;  Length 801;
  Best Local Similarity   71.4%;  Pred. No. 79;
  Matches    5;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GFPWFAY 10
              ||||:|:
Db        504 GFPWWAF 510


RESULT 13
US-11-152-569-18
; Sequence 18, Application US/11152569
; Publication No. US20060005278A1
; GENERAL INFORMATION:
;  APPLICANT: Ecker, Joseph R.
;  APPLICANT:  Nehring, Ramlah
;  APPLICANT:  McGrath, Robert B.
;  TITLE OF INVENTION: ETHYLENE INSENSITIVE PLANTS
;  FILE REFERENCE: 532792001210
;  CURRENT APPLICATION NUMBER: US/11/152,569
;  CURRENT FILING DATE:  2005-06-13
;  PRIOR APPLICATION NUMBER: 10/144,156
;  PRIOR FILING DATE: 2002-10-05
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 295
;   TYPE: PRT
;   ORGANISM: Caenorhabditis elegans
US-11-152-569-18

  Query Match             58.6%;  Score 37.5;  DB 7;  Length 295;
  Best Local Similarity   57.1%;  Pred. No. 42;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    5;  Gaps    1;

Qy          1 LYFG-----FPWFA 9
              ||||     ||| |
Db        164 LYFGMYKTTFPWHA 177


RESULT 14
US-11-096-568A-28225
; Sequence 28225, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28225
;   LENGTH: 426
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(426)
;   OTHER INFORMATION: Ceres Seq. ID no. 2708137
US-11-096-568A-28225

  Query Match             57.8%;  Score 37;  DB 7;  Length 426;
  Best Local Similarity   71.4%;  Pred. No. 68;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 FGFPWFA 9
              | :||||
Db         59 FNYPWFA 65


RESULT 15
US-11-096-568A-28224
; Sequence 28224, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 28224
;   LENGTH: 427
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(427)
;   OTHER INFORMATION: Ceres Seq. ID no. 2708136
US-11-096-568A-28224

  Query Match             57.8%;  Score 37;  DB 7;  Length 427;
  Best Local Similarity   71.4%;  Pred. No. 68;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 FGFPWFA 9
              | :||||
Db         60 FNYPWFA 66


RESULT 16
US-11-087-099-6677
; Sequence 6677, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 6677
;   LENGTH: 479
;   TYPE: PRT
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;   ORGANISM: Pseudomonas putida KT2440
US-11-087-099-6677

  Query Match             57.8%;  Score 37;  DB 7;  Length 479;
  Best Local Similarity   60.0%;  Pred. No. 75;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              |||| |: |:
Db        441 LYFGLPFIAW 450


RESULT 17
US-11-072-512-3830
; Sequence 3830, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
;  APPLICANT: ISOGAI, TAKAO
;  APPLICANT:  SUGIYAMA, TOMOYASU
;  APPLICANT:  OTSUKI, TETSUJI
;  APPLICANT:  WAKAMATSU, AI
;  APPLICANT:  SATO, HIROYUKI
;  APPLICANT:  ISHII, SHIZUKO
;  APPLICANT:  YAMAMOTO, JUN-ICHI
;  APPLICANT:  ISONO, YUUKO
;  APPLICANT:  HIO, YURI
;  APPLICANT:  OTSUKA, KAORU
;  APPLICANT:  NAGAI, KEIICHI
;  APPLICANT:  IRIE, RYOTARO
;  APPLICANT:  TAMECHIKA, ICHIRO
;  APPLICANT:  SEKI, NAOHIKO
;  APPLICANT:  YOSHIKAWA, TSUTOMU
;  APPLICANT:  OTSUKA, MOTOYUKI
;  APPLICANT:  NAGAHARI, KENJI
;  APPLICANT:  MASUHO, YASUHIKO
;  TITLE OF INVENTION: Novel full length cDNA
;  FILE REFERENCE: 084335-0191
;  CURRENT APPLICATION NUMBER: US/11/072,512
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: US 60/350,978
;  PRIOR FILING DATE: 2002-01-25
;  PRIOR APPLICATION NUMBER: JP 2001-379298
;  PRIOR FILING DATE: 2001-11-05
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3830
;   LENGTH: 1064
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-072-512-3830

  Query Match             57.8%;  Score 37;  DB 7;  Length 1064;
  Best Local Similarity   55.6%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              |:| ||  |
Db        345 YYGVPWGVY 353


RESULT 18
US-11-229-371-123
; Sequence 123, Application US/11229371
; Publication No. US20060021092A1
; GENERAL INFORMATION:
;  APPLICANT: McCourt, Peter
;  APPLICANT:  Ghassemian, Majid
;  APPLICANT:  Cutler, Sean
;  APPLICANT:  Bonetta, Dario
;  TITLE OF INVENTION: Stress Tolerance and Delayed Senescence in Plants
;  FILE REFERENCE: 22542-007CIP2CON1
;  CURRENT APPLICATION NUMBER: US/11/229,371
;  CURRENT FILING DATE:  2005-09-16
;  PRIOR APPLICATION NUMBER: 10/229,541
;  PRIOR FILING DATE: 2002-08-27
;  PRIOR APPLICATION NUMBER: 10/160,764
;  PRIOR FILING DATE: 2002-05-31
;  PRIOR APPLICATION NUMBER: 60/294,766
;  PRIOR FILING DATE: 2001-05-31
;  PRIOR APPLICATION NUMBER: 60/348,909
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: 10/210,760
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: 60/309,396
;  PRIOR FILING DATE: 2001-08-01
;  PRIOR APPLICATION NUMBER: 60/337,084
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: 09/191,687
;  PRIOR FILING DATE: 1998-11-13
;  NUMBER OF SEQ ID NOS: 178
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
;   LENGTH: 400
;   TYPE: PRT
;   ORGANISM: Glycine max
US-11-229-371-123

  Query Match             57.0%;  Score 36.5;  DB 7;  Length 400;
  Best Local Similarity   77.8%;  Pred. No. 78;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 LYFG-FPWF 8
              ||||  |||
Db         78 LYFGVLPWF 86


RESULT 19
US-11-228-923-123
; Sequence 123, Application US/11228923
; Publication No. US20060031966A1
; GENERAL INFORMATION:
;  APPLICANT: McCourt, Peter
;  APPLICANT:  Ghassemian, Majid
;  APPLICANT:  Cutler, Sean
;  APPLICANT:  Bonetta, Dario
;  TITLE OF INVENTION: Stress Tolerance and Delayed Senescence in Plants
;  FILE REFERENCE: 22542-007CIP2CON2
;  CURRENT APPLICATION NUMBER: US/11/228,923
;  CURRENT FILING DATE:  2005-09-16
;  PRIOR APPLICATION NUMBER: 10/229,541
;  PRIOR FILING DATE: 2002-08-27
;  PRIOR APPLICATION NUMBER: 10/160,764
;  PRIOR FILING DATE: 2002-05-31
;  PRIOR APPLICATION NUMBER: 60/294,766
;  PRIOR FILING DATE: 2001-05-31
;  PRIOR APPLICATION NUMBER: 60/348,909
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: 10/210,760
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: 60/309,396
;  PRIOR FILING DATE: 2001-08-01
;  PRIOR APPLICATION NUMBER: 60/337,084
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: 09/191,687
;  PRIOR FILING DATE: 1998-11-13
;  NUMBER OF SEQ ID NOS: 178
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
;   LENGTH: 400
;   TYPE: PRT
;   ORGANISM: Glycine max
US-11-228-923-123

  Query Match             57.0%;  Score 36.5;  DB 7;  Length 400;
  Best Local Similarity   77.8%;  Pred. No. 78;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;
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Qy          1 LYFG-FPWF 8
              ||||  |||
Db         78 LYFGVLPWF 86


RESULT 20
US-11-228-875-123
; Sequence 123, Application US/11228875
; Publication No. US20060037108A1
; GENERAL INFORMATION:
;  APPLICANT: McCourt, Peter
;  APPLICANT:  Ghassemian, Majid
;  APPLICANT:  Cutler, Sean
;  APPLICANT:  Bonetta, Dario
;  TITLE OF INVENTION: Stress Tolerance and Delayed Senescence in Plants
;  FILE REFERENCE: 22542-007CIP2CON3
;  CURRENT APPLICATION NUMBER: US/11/228,875
;  CURRENT FILING DATE:  2005-09-16
;  PRIOR APPLICATION NUMBER: 10/229,541
;  PRIOR FILING DATE: 2002-08-27
;  PRIOR APPLICATION NUMBER: 10/160,764
;  PRIOR FILING DATE: 2002-05-31
;  PRIOR APPLICATION NUMBER: 60/294,766
;  PRIOR FILING DATE: 2001-05-31
;  PRIOR APPLICATION NUMBER: 60/348,909
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: 10/210,760
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: 60/309,396
;  PRIOR FILING DATE: 2001-08-01
;  PRIOR APPLICATION NUMBER: 60/337,084
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: 09/191,687
;  PRIOR FILING DATE: 1998-11-13
;  NUMBER OF SEQ ID NOS: 178
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
;   LENGTH: 400
;   TYPE: PRT
;   ORGANISM: Glycine max
US-11-228-875-123

  Query Match             57.0%;  Score 36.5;  DB 7;  Length 400;
  Best Local Similarity   77.8%;  Pred. No. 78;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 LYFG-FPWF 8
              ||||  |||
Db         78 LYFGVLPWF 86


RESULT 21
US-11-229-371-113
; Sequence 113, Application US/11229371
; Publication No. US20060021092A1
; GENERAL INFORMATION:
;  APPLICANT: McCourt, Peter
;  APPLICANT:  Ghassemian, Majid
;  APPLICANT:  Cutler, Sean
;  APPLICANT:  Bonetta, Dario
;  TITLE OF INVENTION: Stress Tolerance and Delayed Senescence in Plants
;  FILE REFERENCE: 22542-007CIP2CON1
;  CURRENT APPLICATION NUMBER: US/11/229,371
;  CURRENT FILING DATE:  2005-09-16
;  PRIOR APPLICATION NUMBER: 10/229,541
;  PRIOR FILING DATE: 2002-08-27
;  PRIOR APPLICATION NUMBER: 10/160,764
;  PRIOR FILING DATE: 2002-05-31
;  PRIOR APPLICATION NUMBER: 60/294,766
;  PRIOR FILING DATE: 2001-05-31
;  PRIOR APPLICATION NUMBER: 60/348,909
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: 10/210,760
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: 60/309,396
;  PRIOR FILING DATE: 2001-08-01
;  PRIOR APPLICATION NUMBER: 60/337,084
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: 09/191,687
;  PRIOR FILING DATE: 1998-11-13
;  NUMBER OF SEQ ID NOS: 178
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
;   LENGTH: 424
;   TYPE: PRT
;   ORGANISM: Glycine max
US-11-229-371-113

  Query Match             57.0%;  Score 36.5;  DB 7;  Length 424;
  Best Local Similarity   77.8%;  Pred. No. 82;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 LYFG-FPWF 8
              ||||  |||
Db         78 LYFGVLPWF 86


RESULT 22
US-11-228-923-113
; Sequence 113, Application US/11228923
; Publication No. US20060031966A1
; GENERAL INFORMATION:
;  APPLICANT: McCourt, Peter
;  APPLICANT:  Ghassemian, Majid
;  APPLICANT:  Cutler, Sean
;  APPLICANT:  Bonetta, Dario
;  TITLE OF INVENTION: Stress Tolerance and Delayed Senescence in Plants
;  FILE REFERENCE: 22542-007CIP2CON2
;  CURRENT APPLICATION NUMBER: US/11/228,923
;  CURRENT FILING DATE:  2005-09-16
;  PRIOR APPLICATION NUMBER: 10/229,541
;  PRIOR FILING DATE: 2002-08-27
;  PRIOR APPLICATION NUMBER: 10/160,764
;  PRIOR FILING DATE: 2002-05-31
;  PRIOR APPLICATION NUMBER: 60/294,766
;  PRIOR FILING DATE: 2001-05-31
;  PRIOR APPLICATION NUMBER: 60/348,909
;  PRIOR FILING DATE: 2001-10-22
;  PRIOR APPLICATION NUMBER: 10/210,760
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: 60/309,396
;  PRIOR FILING DATE: 2001-08-01
;  PRIOR APPLICATION NUMBER: 60/337,084
;  PRIOR FILING DATE: 2001-12-04
;  PRIOR APPLICATION NUMBER: 09/191,687
;  PRIOR FILING DATE: 1998-11-13
;  NUMBER OF SEQ ID NOS: 178
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
;   LENGTH: 424
;   TYPE: PRT
;   ORGANISM: Glycine max
US-11-228-923-113

  Query Match             57.0%;  Score 36.5;  DB 7;  Length 424;
  Best Local Similarity   77.8%;  Pred. No. 82;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy          1 LYFG-FPWF 8
              ||||  |||
Db         78 LYFGVLPWF 86


RESULT 23
US-11-228-875-113
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; Sequence 113, Application US/11228875
; Publication No. US20060037108A1
; GENERAL INFORMATION:
; APPLICANT: McCourt, Peter
; APPLICANT: Ghassemian, Majid
; APPLICANT: Cutler, Sean
; APPLICANT: Bonetta, Dario
; TITLE OF INVENTION: Stress Tolerance and Delayed Senescence in Plants
; FILE REFERENCE: 22542-007CIP2CON3
; CURRENT APPLICATION NUMBER: US/11/228,875
; CURRENT FILING DATE: 2005-09-16
; PRIOR APPLICATION NUMBER: 10/229,541
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 10/160,764
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/294,766
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: 60/348,909
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 10/210,760
; PRIOR FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: 60/309,396
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/337,084
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/191,687
; PRIOR FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 178
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 113
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Glycine max
US-11-228-875-113

Query Match 57.0%; Score 36.5; DB 7; Length 424;
Best Local Similarity 77.8%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 LYFG-FPWF 8
|||| |||
Db 78 LYFGVLPWF 86

RESULT 24
US-11-004-399-61
; Sequence 61, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against SA
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pCV1
US-11-004-399-61

Query Match 56.2%; Score 36; DB 7; Length 43;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FGFPW 7
|||||
Db 14 FGFPW 18

RESULT 25
US-11-004-399-431
; Sequence 431, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against SAI
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 431
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pCV8
US-11-004-399-431

Query Match 56.2%; Score 36; DB 7; Length 43;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FGFPW 7
|||||
Db 14 FGFPW 18

RESULT 26
US-11-004-399-3864
; Sequence 3864, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-CoV Viral Nucleotide
; TITLE OF INVENTION: Sequences and Methods of Use Thereof For Immunization Against SAI
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3864
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pCV6
US-11-004-399-3864

Query Match 56.2%; Score 36; DB 7; Length 43;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 FGFPW 7
              |||||
Db         14 FGFPW 18


RESULT 27
US-11-051-720-1306
; Sequence 1306, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
;  APPLICANT: Compugen Ltd
;  TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
;  TITLE OF INVENTION:  THEREOF FOR DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 1847.1002
;  CURRENT APPLICATION NUMBER: US/11/051,720
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1306
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-051-720-1306

  Query Match             56.2%;  Score 36;  DB 7;  Length 180;
  Best Local Similarity   100.0%;  Pred. No. 49;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 FGFPW 7
              |||||
Db        132 FGFPW 136


RESULT 28
US-11-087-099-9944
; Sequence 9944, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 9944
;   LENGTH: 225
;   TYPE: PRT
;   ORGANISM: Oryza sativa (japonica cultivar-group)
US-11-087-099-9944

  Query Match             56.2%;  Score 36;  DB 7;  Length 225;
  Best Local Similarity   55.6%;  Pred. No. 59;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              |::| || |
Db         59 LWYGLPWVA 67


RESULT 29
US-11-098-686-10102
; Sequence 10102, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
;  APPLICANT: Kapur, Vivek and Gebhart, Connie J.
;  TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
;  TITLE OF INVENTION:  FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
;  FILE REFERENCE: 09531-128001
;  CURRENT APPLICATION NUMBER: US/11/098,686
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: PCT/US03/31318
;  PRIOR FILING DATE: 2003-10-01
;  PRIOR APPLICATION NUMBER: US 60/416,395
;  PRIOR FILING DATE: 2002-10-04
;  NUMBER OF SEQ ID NOS: 11433
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10102
;   LENGTH: 276
;   TYPE: PRT
;   ORGANISM: Lawsonia intracellularis
US-11-098-686-10102

  Query Match             56.2%;  Score 36;  DB 7;  Length 276;
  Best Local Similarity   66.7%;  Pred. No. 69;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              || |||:|:
Db        210 LYAGFPFFS 218


RESULT 30
US-11-067-121-2
; Sequence 2, Application US/11067121
; Publication No. US20050261185A1
; GENERAL INFORMATION:
;  APPLICANT: Martijn, Cecile
;  APPLICANT:  Rondahl, Lena
;  TITLE OF INVENTION: THERAPEUTIC PROTEINS
;  FILE REFERENCE: 18909-002001
;  CURRENT APPLICATION NUMBER: US/11/067,121
;  CURRENT FILING DATE:  2005-02-25
;  PRIOR APPLICATION NUMBER: US 60/576,445
;  PRIOR FILING DATE: 2004-06-02
;  PRIOR APPLICATION NUMBER: SE 0400489-1
;  PRIOR FILING DATE: 2004-02-27
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 295
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-11-067-121-2

  Query Match             56.2%;  Score 36;  DB 7;  Length 295;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 FGFPW 7
              |||||
Db        132 FGFPW 136


RESULT 31
US-11-067-121-11
; Sequence 11, Application US/11067121
; Publication No. US20050261185A1
; GENERAL INFORMATION:
;  APPLICANT: Martijn, Cecile
;  APPLICANT:  Rondahl, Lena
;  TITLE OF INVENTION: THERAPEUTIC PROTEINS
;  FILE REFERENCE: 18909-002001
;  CURRENT APPLICATION NUMBER: US/11/067,121
;  CURRENT FILING DATE:  2005-02-25
;  PRIOR APPLICATION NUMBER: US 60/576,445
;  PRIOR FILING DATE: 2004-06-02
;  PRIOR APPLICATION NUMBER: SE 0400489-1
;  PRIOR FILING DATE: 2004-02-27
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 295
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-067-121-11
```

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  Query Match             56.2%;  Score 36;  DB 7;  Length 295;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 FGFPW 7
              |||||
Db        132 FGFPW 136


RESULT 32
US-11-051-720-1701
; Sequence 1701, Application US/11051720
; Publication No. US20060046257A1
; GENERAL INFORMATION:
;  APPLICANT: Compugen Ltd
;  TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS
;  TITLE OF INVENTION:  THEREOF FOR DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 1847.1002
;  CURRENT APPLICATION NUMBER: US/11/051,720
;  CURRENT FILING DATE:  2005-01-27
;  NUMBER OF SEQ ID NOS: 1780
; SEQ ID NO 1701
;   LENGTH: 295
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-051-720-1701

  Query Match             56.2%;  Score 36;  DB 7;  Length 295;
  Best Local Similarity   100.0%;  Pred. No. 73;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 FGFPW 7
              |||||
Db        132 FGFPW 136


RESULT 33
US-11-087-099-2355
; Sequence 2355, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2355
;   LENGTH: 477
;   TYPE: PRT
;   ORGANISM: Lactococcus lactis subsp. lactis
US-11-087-099-2355

  Query Match             56.2%;  Score 36;  DB 7;  Length 477;
  Best Local Similarity   71.4%;  Pred. No. 1.1e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LYFGFPW 7
              ||||: |
Db        453 LYFGYKW 459


RESULT 34
US-11-087-099-5222
; Sequence 5222, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 5222
;   LENGTH: 555
;   TYPE: PRT
;   ORGANISM: Linum usitatissimum
US-11-087-099-5222

  Query Match             56.2%;  Score 36;  DB 7;  Length 555;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              | | || ||
Db        458 YLGRPWKAY 466


RESULT 35
US-11-097-812-58
; Sequence 58, Application US/11097812
; Publication No. US20050281828A1
; GENERAL INFORMATION:
;  APPLICANT: Bowdish, Katherine S.
;  APPLICANT:  Kretz-Rommel, Anke
;  APPLICANT:  Dakappagari, Naveen
;  TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
;  TITLE OF INVENTION:  PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
;  FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
;  CURRENT APPLICATION NUMBER: US/11/097,812
;  CURRENT FILING DATE:  2005-04-01
;  PRIOR APPLICATION NUMBER: US 11/016,647
;  PRIOR FILING DATE: 2004-12-17
;  PRIOR APPLICATION NUMBER: PCT/US04/06570
;  PRIOR FILING DATE: 2004-03-04
;  PRIOR APPLICATION NUMBER: US 60/548,385
;  PRIOR FILING DATE: 2004-02-28
;  PRIOR APPLICATION NUMBER: US 60/529,500
;  PRIOR FILING DATE: 2003-12-15
;  PRIOR APPLICATION NUMBER: US 60/451,816
;  PRIOR FILING DATE: 2003-03-04
;  NUMBER OF SEQ ID NOS: 207
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: mouse
US-11-097-812-58

  Query Match             54.7%;  Score 35;  DB 7;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 7;
  Matches    4;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWF 8
              |::|: ||
Db          2 LFYGYAWF 9


RESULT 36
US-11-096-568A-33695
; Sequence 33695, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 33695
;   LENGTH: 173
;   TYPE: PRT
;   ORGANISM: Arabidopsis thaliana
;   FEATURE:
;   NAME/KEY: misc_feature
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;   LOCATION: (1)..(173)
;   OTHER INFORMATION: Ceres Seq. ID no. 13603886
US-11-096-568A-33695

  Query Match            54.7%;  Score 35;  DB 7;  Length 173;
  Best Local Similarity  50.0%;  Pred. No. 69;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              |: || || :
Db         79 LFLGFRWFFF 88


RESULT 37
US-10-467-657-5258
; Sequence 5258, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5258
;   LENGTH: 266
;   TYPE: PRT
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5258

  Query Match            54.7%;  Score 35;  DB 6;  Length 266;
  Best Local Similarity  66.7%;  Pred. No. 97;
  Matches    6;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFA 9
              || | || |
Db         79 LYCGSPWLA 87


RESULT 38
US-11-096-568A-12995
; Sequence 12995, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 12995
;   LENGTH: 332
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(332)
;   OTHER INFORMATION: Ceres Seq. ID no. 14316024
US-11-096-568A-12995

  Query Match            54.7%;  Score 35;  DB 7;  Length 332;
  Best Local Similarity  71.4%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GFPWFAY 10
                |||| |:
Db        226 GFPWSAF 232


RESULT 39
US-11-096-568A-12994
; Sequence 12994, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 12994
;   LENGTH: 341
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(341)
;   OTHER INFORMATION: Ceres Seq. ID no. 14316023
US-11-096-568A-12994

  Query Match            54.7%;  Score 35;  DB 7;  Length 341;
  Best Local Similarity  71.4%;  Pred. No. 1.2e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GFPWFAY 10
                |||| |:
Db        235 GFPWSAF 241


RESULT 40
US-11-096-568A-12993
; Sequence 12993, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides F
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 12993
;   LENGTH: 372
;   TYPE: PRT
;   ORGANISM: Triticum aestivum
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(372)
;   OTHER INFORMATION: Ceres Seq. ID no. 14316022
US-11-096-568A-12993

  Query Match            54.7%;  Score 35;  DB 7;  Length 372;
  Best Local Similarity  71.4%;  Pred. No. 1.3e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 GFPWFAY 10
                |||| |:
Db        266 GFPWSAF 272


RESULT 41
US-11-087-099-2545
; Sequence 2545, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
;  APPLICANT: Abad, Mark S. et al.
;  TITLE OF INVENTION: Genes and Uses for Plant Improvement
```

```
;  FILE REFERENCE: 38-21(53450)B EP
;  CURRENT APPLICATION NUMBER: US/11/087,099
;  CURRENT FILING DATE:  2005-03-22
;  NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 2545
;   LENGTH: 418
;   TYPE: PRT
;   ORGANISM: Chlorella vulgaris
US-11-087-099-2545

  Query Match             54.7%;  Score 35;  DB 7;  Length 418;
  Best Local Similarity   70.0%;  Pred. No. 1.4e+02;
  Matches    7;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              | | || |||
Db        210 LLFPFPLFAY 219


RESULT 42
US-10-063-703-4
; Sequence 4, Application US/10063703
; Publication No. US20060008901A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,703
;  CURRENT FILING DATE:  2002-05-08
;      Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 4
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-063-703-4

  Query Match             54.7%;  Score 35;  DB 6;  Length 455;
  Best Local Similarity   50.0%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              |:||| |  :
Db         16 LFFGFGWLFF 25


RESULT 43
US-11-102-240-4
; Sequence 4, Application US/11102240
; Publication No. US20050260647A1
; GENERAL INFORMATION:
;  APPLICANT: Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: ANTIBODIES TO POLYPEPTIDES ENCODED BY A NUCLEIC ACID UNDEREXPRESS
;  TITLE OF INVENTION:  ESOPHAGEAL TUMOR
;  FILE REFERENCE: P3230R1C106C
;  CURRENT APPLICATION NUMBER: US/11/102,240
;  CURRENT FILING DATE:  2005-04-08
;  PRIOR APPLICATION NUMBER: 10/063662
;  PRIOR FILING DATE: 2002-05-07
;  PRIOR APPLICATION NUMBER: 10/006867
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: 60/170262
;  PRIOR FILING DATE: 199-12-09
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 4
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-11-102-240-4

  Query Match             54.7%;  Score 35;  DB 7;  Length 455;
  Best Local Similarity   50.0%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              |:||| |  :
Db         16 LFFGFGWLFF 25


RESULT 44
US-11-103-195-4
; Sequence 4, Application US/11103195
; Publication No. US20060051779A1
; GENERAL INFORMATION:
;  APPLICANT: Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230C166C1
;  CURRENT APPLICATION NUMBER: US/11/103,195
;  CURRENT FILING DATE:  2005-04-11
;  PRIOR APPLICATION NUMBER: 10/063743
;  PRIOR FILING DATE: 2002-05-09
;  PRIOR APPLICATION NUMBER: 10/006867
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: 60/082797
;  PRIOR FILING DATE: 1998-04-22
;  PRIOR APPLICATION NUMBER: PCT/US00/23328
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: 60/170262
;  PRIOR FILING DATE: 1999-12-09
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 4
;   LENGTH: 455
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-11-103-195-4

  Query Match             54.7%;  Score 35;  DB 7;  Length 455;
  Best Local Similarity   50.0%;  Pred. No. 1.5e+02;
  Matches    5;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              |:||| |  :
Db         16 LFFGFGWLFF 25


RESULT 45
US-11-057-058-59
; Sequence 59, Application US/11057058
; Publication No. US20050244400A1
; GENERAL INFORMATION:
;  APPLICANT: LeBowitz, Jonathan
;  APPLICANT:  Maga, John
;  TITLE OF INVENTION: ACID ALPHA-GLUCOSIDASE AND FRAGMENTS THEREOF
;  FILE REFERENCE: SYM-011
;  CURRENT APPLICATION NUMBER: US/11/057,058
;  CURRENT FILING DATE:  2005-02-10
```

```
;  PRIOR APPLICATION NUMBER: US 60/543,812
;  PRIOR FILING DATE: 2004-02-10
;  NUMBER OF SEQ ID NOS: 68
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 59
;   LENGTH: 932
;   TYPE: PRT
;   ORGANISM: Coturnix japonica
US-11-057-058-59

  Query Match            54.7%;  Score 35;  DB 7;  Length 932;
  Best Local Similarity  71.4%;  Pred. No. 2.7e+02;
  Matches    5;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LYFGFPW 7
              |:| |||
Db        725 LFFEFPW 731


RESULT 46
US-11-096-568A-6062
; Sequence 6062, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
;  APPLICANT: Alexandrov, Nickolai et al.
;  TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
;  TITLE OF INVENTION:  Therby
;  FILE REFERENCE: 2750-1592PUS2
;  CURRENT APPLICATION NUMBER: US/11/096,568A
;  CURRENT FILING DATE:  2005-04-01
;  NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 6062
;   LENGTH: 212
;   TYPE: PRT
;   ORGANISM: Glycine max
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(212)
;   OTHER INFORMATION: Ceres Seq. ID no. 14313586
US-11-096-568A-6062

  Query Match            53.1%;  Score 34;  DB 7;  Length 212;
  Best Local Similarity  60.0%;  Pred. No. 1.2e+02;
  Matches    6;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 LYFGFPWFAY 10
              ||  | || |
Db        181 LYKEFTWFEY 190


RESULT 47
US-11-098-686-10686
; Sequence 10686, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
;  APPLICANT: Kapur, Vivek and Gebhart, Connie J.
;  TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
;  TITLE OF INVENTION:  FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
;  FILE REFERENCE: 09531-128001
;  CURRENT APPLICATION NUMBER: US/11/098,686
;  CURRENT FILING DATE:  2005-04-04
;  PRIOR APPLICATION NUMBER: PCT/US03/31318
;  PRIOR FILING DATE: 2003-10-01
;  PRIOR APPLICATION NUMBER: US 60/416,395
;  PRIOR FILING DATE: 2002-10-04
;  NUMBER OF SEQ ID NOS: 11433
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10686
;   LENGTH: 234
;   TYPE: PRT
;   ORGANISM: Lawsonia intracellularis
US-11-098-686-10686

  Query Match            53.1%;  Score 34;  DB 7;  Length 234;
  Best Local Similarity  66.7%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 YFGFPW 7
              | |:||
Db         38 YIGYPW 43


RESULT 48
US-11-112-882-35
; Sequence 35, Application US/11112882
; Publication No. US20050273885A1
; GENERAL INFORMATION:
;  APPLICANT: Commonwealth Scientific and Industrial Research Organisation
;  TITLE OF INVENTION: Synthesis of Long-Chain Polyunsaturated Fatty Acids in Recombinant
;  FILE REFERENCE: 503244
;  CURRENT APPLICATION NUMBER: US/11/112,882
;  CURRENT FILING DATE:  2005-04-22
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 263
;   TYPE: PRT
;   ORGANISM: Isochrysis galbana
US-11-112-882-35

  Query Match            53.1%;  Score 34;  DB 7;  Length 263;
  Best Local Similarity  55.6%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              :|| ||  |
Db        143 HFGAPWDVY 151


RESULT 49
US-11-166-993-120
; Sequence 120, Application US/11166993
; Publication No. US20050287652A1
; GENERAL INFORMATION:
;  APPLICANT: E. I. du Pont de Nemours and Company
;  APPLICANT:  Damude, Howard G.
;  APPLICANT:  Zhu, Quinn
;  TITLE OF INVENTION: Delta-8 desaturase and its use in making polyunsaturated
;  TITLE OF INVENTION:  fatty acids
;  FILE REFERENCE: CL3150
;  CURRENT APPLICATION NUMBER: US/11/166,993
;  CURRENT FILING DATE:  2005-06-24
;  PRIOR APPLICATION NUMBER: US 60/583041
;  PRIOR FILING DATE: 2004-06-25
;  PRIOR APPLICATION NUMBER: US 60/624812
;  PRIOR FILING DATE: 2004-11-04
;  NUMBER OF SEQ ID NOS: 151
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 120
;   LENGTH: 263
;   TYPE: PRT
;   ORGANISM: Isochrysis galbana
US-11-166-993-120

  Query Match            53.1%;  Score 34;  DB 7;  Length 263;
  Best Local Similarity  55.6%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 YFGFPWFAY 10
              :|| ||  |
Db        143 HFGAPWDVY 151


RESULT 50
US-11-146-428-78
; Sequence 78, Application US/11146428
```

; Publication No. US20060051847A1
; GENERAL INFORMATION:
; APPLICANT: GUNNARSSON, NINA KATARINA
; APPLICANT: FORSTER, JOCHEN
; APPLICANT: NEILSEN, JENS BREDAL
; TITLE OF INVENTION: METABOLICALLY ENGINEERED CELLS FOR THE
; TITLE OF INVENTION: PRODUCTION OF POLYUNSATURATED FATTY ACIDS
; FILE REFERENCE: 671306-2001.1
; CURRENT APPLICATION NUMBER: US/11/146,428
; CURRENT FILING DATE: 2005-06-06
; PRIOR APPLICATION NUMBER: 60/577,245
; PRIOR FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 78
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Isochrysis galbana
US-11-146-428-78

Query Match 53.1%; Score 34; DB 7; Length 263;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 YFGFPWFAY 10
              :|| ||  |
Db        143 HFGAPWDVY 151
```

Search completed: March 23, 2006, 02:53:12
Job time : 10.4932 secs

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OM protein - protein search, using sw model

Run on: March 23, 2006, 00:44:09 ; Search time 68.1085 Seconds
(without alignments)
148.377 Million cell updates/sec

Title: US-10-755-382-26
Perfect score: 112
Sequence: 1 DIQLTQSPSSLSASVGDRVTITC 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	112	100.0	23	2	AAR97319	Aar97319 Humanised
2	112	100.0	23	9	ADY31301	Ady31301 Human ant
3	112	100.0	23	9	ADY31292	Ady31292 Human ant
4	112	100.0	56	5	ABG30476	Abg30476 Human ant
5	112	100.0	86	2	AAY39533	Aay39533 Humanised
6	112	100.0	86	5	ABB83945	Abb83945 Humanised
7	112	100.0	86	6	ABG75598	Abg75598 REI frame
8	112	100.0	92	6	ABU09366	Abu09366 Human REI
9	112	100.0	92	6	ABU10141	Abu10141 Human REI
10	112	100.0	95	7	ADF09971	Adf09971 Antibody
11	112	100.0	95	7	ADF09970	Adf09970 Antibody
12	112	100.0	95	7	ADF10076	Adf10076 VEGF anti
13	112	100.0	95	7	ADF10178	Adf10178 Antibody
14	112	100.0	95	7	ADF10177	Adf10177 Antibody
15	112	100.0	95	7	ADF10075	Adf10075 VEGF anti
16	112	100.0	95	9	AEB13577	Aeb13577 Human var
17	112	100.0	95	9	AEB13578	Aeb13578 Human var
18	112	100.0	95	9	AEB13630	Aeb13630 Human var
19	112	100.0	95	9	AEB13631	Aeb13631 Human var
20	112	100.0	101	2	AAY34316	Aay34316 IgG antib
21	112	100.0	103	7	ADD69249	Add69249 Human lig
22	112	100.0	103	7	ADF09995	Adf09995 Antibody
23	112	100.0	103	7	ADF10099	Adf10099 VEGF anti
24	112	100.0	106	2	AAR97337	Aar97337 Humanised
25	112	100.0	106	5	AAU99540	Aau99540 Humanised
26	112	100.0	106	5	AAU99543	Aau99543 Humanised
27	112	100.0	106	5	AAU99523	Aau99523 Humanised
28	112	100.0	106	5	AAU76651	Aau76651 Protein t
29	112	100.0	106	6	AAE33534	Aae33534 Human AQC
30	112	100.0	106	8	ADM95100	Adm95100 Humanised
31	112	100.0	106	8	ADM98322	Adm98322 Humanised
32	112	100.0	107	2	AAW41400	Aaw41400 Humanised
33	112	100.0	107	5	ABG30494	Abg30494 Human ant
34	112	100.0	107	5	AAO17151	Aao17151 Human end
35	112	100.0	107	6	AAO27204	Aao27204 Chimeric
36	112	100.0	107	6	AAO27196	Aao27196 Chimeric
37	112	100.0	107	8	ADL02314	Adl02314 Humanised
38	112	100.0	107	8	ADS84366	Ads84366 Human ant
39	112	100.0	107	8	ADR68508	Adr68508 Anti-EPO-
40	112	100.0	108	4	AAU02534	Aau02534 Anti-adip
41	112	100.0	108	6	AAO16704	Aao16704 Human ant
42	112	100.0	108	6	AAO16706	Aao16706 Human ant
43	112	100.0	108	6	ADA89164	Ada89164 Human ant
44	112	100.0	108	6	ADA89176	Ada89176 Human ant
45	112	100.0	108	8	ADG31770	Adg31770 V(L) doma

ALIGNMENTS

RESULT 1
AAR97319
ID AAR97319 standard; peptide; 23 AA.
XX
AC AAR97319;
XX
DT 15-OCT-1996 (first entry)
XX
DE Humanised monoclonal antibody light chain framework region.
XX
KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW complementary determining region; anti-carcinoembryonic antigen; CEA;
KW diagnosis; imaging; therapy; immune response.
XX
OS Homo sapiens.
XX
PN WO9611013-A1.
XX
PD 18-APR-1996.
XX
PF 28-SEP-1995; 95WO-US011964.
XX
PR 05-OCT-1994; 94US-00318157.
XX
PA (IMMU-) IMMUNOMEDICS INC.
XX
PI Hansen HJ, Armour KL;
XX
DR WPI; 1996-209653/21.
XX
PT New humanised anti-CEA monoclonal antibody - having engrafted murine
PT CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS Claim 7; Page 39; 62pp; English.
XX
CC New humanised monoclonal antibodies (MAbs) comprising the complementary
CC determining regions (CDRs) of a parental murine class III anti-
CC carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC heterologous antibody which can be derived from any species including
CC human, retain the anti-CEA binding specificity of the parental murine MAb
CC but are less immunogenic in a human subject than the parental MAb. The
CC humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC -producing cancers and patients receiving the humanised antibodies and
CC conjugates show improved therapeutic results, decreased immune responses
CC and decreased immune-mediated adverse effects compared to the parent
CC antibody. This sequence corresponds to the first framework region of the
CC light chain of the humanised MAb. See AAR97313-97333

```
XX
SQ   Sequence 23 AA;

  Query Match             100.0%;  Score 112;  DB 2;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 2
ADY31301
ID   ADY31301 standard; peptide; 23 AA.
XX
AC   ADY31301;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Human antibody kappa chain framework peptide - SEQ ID 133.
XX
KW   DNA library; humanized antibody; antibody engineering;
KW   kappa chain framework.
XX
OS   Homo sapiens.
XX
PN   US2005042664-A1.
XX
PD   24-FEB-2005.
XX
PF   20-AUG-2004; 2004US-00923068.
XX
PR   22-AUG-2003; 2003US-0497213P.
PR   13-OCT-2003; 2003US-0510741P.
XX
PA   (MEDI-) MEDIMMUNE INC.
XX
PI   Wu H,  Dall-Acqua W,  Damschroder M;
XX
DR   WPI; 2005-180802/19.
XX
PT   New library of nucleic acid sequences comprises nucleotide sequences
PT   encoding humanized heavy chain variable regions and humanized light chain
PT   variable regions, useful for producing humanized antibodies.
XX
PS   Disclosure; SEQ ID NO 133; 179pp; English.
XX
CC   The invention comprises a library of nucleotide sequences encoding
CC   humanized antibody heavy chain variable regions and humanized antibody
CC   light chain variable regions. The library of the invention is useful for
CC   producing humanized antibodies, or for re-engineering or reshaping an
CC   antibody from a first species for use in a second species. The present
CC   amino acid sequence represents a human germline kappa chain framework
CC   peptide.
XX
SQ   Sequence 23 AA;

  Query Match             100.0%;  Score 112;  DB 9;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 3
ADY31292
ID   ADY31292 standard; peptide; 23 AA.
XX
AC   ADY31292;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Human antibody kappa chain framework peptide - SEQ ID 124.
XX
KW   DNA library; humanized antibody; antibody engineering;
KW   kappa chain framework.
XX
OS   Homo sapiens.
XX
PN   US2005042664-A1.
XX
PD   24-FEB-2005.
XX
PF   20-AUG-2004; 2004US-00923068.
XX
PR   22-AUG-2003; 2003US-0497213P.
PR   13-OCT-2003; 2003US-0510741P.
XX
PA   (MEDI-) MEDIMMUNE INC.
XX
PI   Wu H,  Dall-Acqua W,  Damschroder M;
XX
DR   WPI; 2005-180802/19.
XX
PT   New library of nucleic acid sequences comprises nucleotide sequences
PT   encoding humanized heavy chain variable regions and humanized light chain
PT   variable regions, useful for producing humanized antibodies.
XX
PS   Disclosure; SEQ ID NO 124; 179pp; English.
XX
CC   The invention comprises a library of nucleotide sequences encoding
CC   humanized antibody heavy chain variable regions and humanized antibody
CC   light chain variable regions. The library of the invention is useful for
CC   producing humanized antibodies, or for re-engineering or reshaping an
CC   antibody from a first species for use in a second species. The present
CC   amino acid sequence represents a human germline kappa chain framework
CC   peptide.
XX
SQ   Sequence 23 AA;

  Query Match             100.0%;  Score 112;  DB 9;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 4
ABG30476
ID   ABG30476 standard; protein; 56 AA.
XX
AC   ABG30476;
XX
DT   07-OCT-2002  (first entry)
XX
DE   Human anti-CD40 monoclonal antibody 13E4 light chain #1.
XX
KW   Human; light chain; CD40; autoimmune disease; multiple sclerosis;
KW   systemic lupus erythematosus; psoriasis; inflammatory bowel disease;
KW   Crohn's disease; rheumatoid arthritis; organ rejection; lymphoma;
KW   non-Hodgkin's lymphoma; monoclonal antibody; B cell; glycoprotein;
KW   proliferation.
XX
OS   Homo sapiens.
XX
PN   WO200228904-A2.
XX
PD   11-APR-2002.
XX
PF   02-OCT-2001; 2001WO-US030857.
XX
```

PR 02-OCT-2000; 2000US-0237556P.
XX
PA (CHIR) CHIRON CORP.
XX
PI Chu K, Wang C, Yoshihara C, Donnelly JJ;
XX
DR WPI; 2002-405169/43.
XX
PT A human anti-CD40 monoclonal antibody or fragment useful for inhibiting
PT proliferation, growth or differentiation of a normal human B cells and
PT treating autoimmune disease such as rheumatoid arthritis or systemic
PT lupus erythematosus.
XX
PS Claim 1; Fig 5; 75pp; English.
XX
CC The invention relates to a human monoclonal antibody or fragment capable
CC of specifically binding to a human CD40 antigen (a glycoprotein expressed
CC on the surface of human B cells), where the antibody or fragment is free
CC of significant agonistic activity when it binds to the CD40 antigen, and
CC the growth or differentiation is inhibited. The fragments comprise the
CC complementarity determining region (CDR) of the light and heavy chains of
CC the monoclonal antibodies secreted by a hybridoma consisting of 15B8,
CC 20C4, 12D9, 9F7 and 13E4. Also included are the nucleic acids encoding
CC the antibody (or fragments). The antibodies or fragments are used for
CC inhibiting proliferation, growth or differentiation of a normal human B
CC cells and to inhibit antibody production by B cells. They may also be
CC useful for treating autoimmune diseases, such as systemic lupus
CC erythematosus, psoriasis, multiple sclerosis, inflammatory bowel disease
CC (Crohn's disease), rheumatoid arthritis, and lymphoma (especially Non-
CC Hodgkin's Lymphoma). The present sequence represents the antibody 13E4
CC light chain
XX
SQ Sequence 56 AA;

Query Match 100.0%; Score 112; DB 5; Length 56;
Best Local Similarity 100.0%; Pred. No. 5.5e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRVTITC 23
||||||||||||||||||||||||
Db 1 DIQLTQSPSSLSASVGDRVTITC 23

RESULT 5
AAY39533
ID AAY39533 standard; protein; 86 AA.
XX
AC AAY39533;
XX
DT 22-NOV-1999 (first entry)
XX
DE Humanised Murine COL1 VK chain (REIVK).
XX
KW Antibody; human; carcinoembryonic antigen; CEA; cancer; tumour imaging;
KW tumour identification; metastasis; diagnosis; mouse; VK chain.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
PN WO9943817-A1.
XX
PD 02-SEP-1999.
XX
PF 25-FEB-1998; 98WO-US003680.
XX
PR 25-FEB-1998; 98WO-US003680.
XX
PA (DOWC) DOW CHEM CO.
XX
PI Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
XX
DR WPI; 1999-550870/46.
XX
PT New antibody specific for treatment and diagnosis of cancer.
XX
PS Claim 2; Fig 2; 82pp; English.
XX
CC This sequence represents a humanised version of the murine COL1 VK chain,
CC designated REIVK, and was used to obtain the humanised antibody (Ab) of
CC the invention. The humanised Ab, or its fragment, specifically binds to
CC carcinoembryonic antigen (CEA). The Ab, optionally coupled to an effector
CC or label, is used to treat or prevent CEA-expressing cancers (e.g. of
CC breast, ovary, lung, stomach, or colon) and to detect CEA-expressing
CC cells, either in vitro (optionally on a solid support) or in vivo
CC (particularly by tumour imaging to identify tumours and metastases before
CC surgery), for diagnosis or prognosis. It is not significantly
CC immunogenic, i.e. the Ab does not induce a human anti-murine antibody or
CC allergic response, or non-specific cytotoxicity, so can be administered
CC repeatedly. It retains specificity for CEA, and has improved clearance
CC (allowing efficient targeting) and metabolic properties
XX
SQ Sequence 86 AA;

Query Match 100.0%; Score 112; DB 2; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.1e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRVTITC 23
||||||||||||||||||||||||
Db 1 DIQLTQSPSSLSASVGDRVTITC 23

RESULT 6
ABB83945
ID ABB83945 standard; protein; 86 AA.
XX
AC ABB83945;
XX
DT 30-OCT-2002 (first entry)
XX
DE Humanised monoclonal antibody chain REIVK.
XX
KW Mouse; COL1; humanised antibody; carcinoembryonic antigen; CEA; cancer;
KW cytostatic; antibody.
XX
OS Synthetic.
XX
PN US2002052479-A1.
XX
PD 02-MAY-2002.
XX
PF 18-FEB-1998; 98US-00025403.
XX
PR 31-OCT-1996; 96US-0029694P.
XX
PA (ANDE/) ANDERSON K W H.
PA (TEMP/) TEMPEST P.
PA (CARR/) CARR F J.
PA (HARR/) HARRIS W J.
PA (ARMO/) ARMOUR K.
XX
PI Anderson KWH, Tempest P, Carr FJ, Harris WJ, Armour K;
XX
DR WPI; 2002-415220/44.
XX
PT New humanized antibody or antibody fragment that is derived from murine
PT antibody, useful for treating and detecting carcinoembryonic antigen
PT expressing cancer in mammal.
XX
PS Claim 2; Fig 2; 34pp; English.
XX
CC The invention relates to a humanised antibody or humanised antibody
CC fragment (I) which specifically binds carcinoembryonic antigen (CEA) and
CC that is derived from a murine antibody that binds CEA. (I) is used for
CC treating (in vivo) and detecting a CEA-expressing cancer in a mammal. (I)

```
CC   is used for in vitro or in vivo immunodetection of CEA-expressing cancer
CC   cells. The present sequence is that of an antibody chain of the invention
XX
SQ   Sequence 86 AA;

  Query Match             100.0%;  Score 112;  DB 5;  Length 86;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 7
ABG75598
ID   ABG75598 standard; protein; 86 AA.
XX
AC   ABG75598;
XX
DT   25-APR-2003  (first entry)
XX
DE   REI framework region (FR) variable light domain template.
XX
KW   Human; humanised antibody; tumour antigen; carcinoembryonic antigen; CEA;
KW   carcinoma; breast; lung; gastrointestinal; stomach cancer; colon cancer;
KW   COL-1; cytostatic; variable light domain; VK; REI; framework region; FR;
KW   complementarity determining region; CDR.
XX
OS   Homo sapiens.
XX
PN   US2002165387-A1.
XX
PD   07-NOV-2002.
XX
PF   09-OCT-2001; 2001US-00974052.
XX
PR   31-OCT-1996;   96US-0029694P.
PR   30-OCT-1997;   97WO-US019642.
PR   18-FEB-1998;   98US-00025403.
PR   28-SEP-2000; 2000US-00672609.
XX
PA   (ANDE/) KERR ANDERSON W H.
PA   (TEMP/) TEMPEST P R.
PA   (CARR/) CARR F J.
PA   (HARR/) HARRIS W J.
PA   (ARMO/) ARMOUR K.
XX
PI   Kerr Anderson WH,  Tempest PR,  Carr FJ,  Harris WJ,  Armour K;
XX
DR   WPI; 2003-247263/24.
XX
PT   New humanized antibody or humanized antibody fragment that specifically
PT   binds carcinoembryonic antigen CEA, useful for treating CEA-expressing
PT   cancer.
XX
PS   Claim 2; Fig 2; 34pp; English.
XX
CC   The invention discloses a humanised antibody or humanised antibody
CC   fragment that specifically binds the tumour antigen, carcinoembryonic
CC   antigen (CEA). The antigen is expressed by various human carcinomas
CC   including breast, lung and gastrointestinal carcinomas such as stomach
CC   and colon cancers. The humanised antibody fragment is derived from a
CC   murine antibody, COL-1, which has a high affinity for CEA. Also disclosed
CC   is a nucleic acid sequence from which may be expressed the humanised
CC   antibody or humanised antibody fragment and a composition for treating,
CC   or detection of, cancer comprising the humanised antibody or humanised
CC   antibody fragment. The humanised antibody or humanised antibody fragment
CC   is useful for treating CEA-expressing cancer. The sequence presented is
CC   the human REI framework region (FR) variable light domain template. The
CC   FRs are regions of the antibody amino acid sequence interposed between
CC   the complementarity determining regions (CDRs)
XX
SQ   Sequence 86 AA;

  Query Match             100.0%;  Score 112;  DB 6;  Length 86;
  Best Local Similarity   100.0%;  Pred. No. 9.1e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 8
ABU09366
ID   ABU09366 standard; protein; 92 AA.
XX
AC   ABU09366;
XX
DT   08-JUL-2003  (first entry)
XX
DE   Human REI framework region (REIVK).
XX
KW   Human; humanised monoclonal antibody; TAG-72; colon cancer;
KW   tumour-associated glycoprotein-72; immunodetection; tumour cell;
KW   surgical excision; disease status; cytostatic; REIVK;
KW   REI framework region.
XX
OS   Homo sapiens.
XX
PN   US2003013856-A1.
XX
PD   16-JAN-2003.
XX
PF   31-OCT-2001; 2001US-00040997.
XX
PR   31-OCT-1996;   96US-0030173P.
PR   30-OCT-1997;   97WO-US019641.
PR   18-FEB-1998;   98US-00025203.
XX
PA   (ANDE/) ANDERSON W H K.
PA   (TEMP/) TEMPEST P R.
PA   (CARR/) CARR F J.
PA   (HARR/) HARRIS W J.
PA   (ARMO/) ARMOUR K.
XX
PI   Anderson WHK,  Tempest PR,  Carr FJ,  Harris WJ,  Armour K;
XX
DR   WPI; 2003-401607/38.
XX
PT   Novel humanized antibody derived from a murine antibody that specifically
PT   binds tumor-associated glycoprotein-72, useful for treating and detecting
PT   cancer.
XX
PS   Claim 2; Fig 2; 29pp; English.
XX
CC   The present invention relates to a novel humanised monoclonal antibody,
CC   and its fragments which specifically binds tumour-associated glycoprotein
CC   -72 (TAG-72), where the humanised monoclonal antibody is derived from a
CC   murine monoclonal antibody (e.g. CC49) that binds TAG-72. The humanised
CC   monoclonal antibody, and its fragments are useful for the treating and
CC   detection of TAG-72 cancers which express TAG-72 (e.g. colon cancer). The
CC   cancer is detected by the immunodetection of in vivo tumour cells, which
CC   may be removed by surgical excision. The humanised monoclonal antibody of
CC   the invention is useful as a immunodiagnostic agent both in vivo and in
CC   vitro, and also for repeated monitoring of the disease status of a
CC   patient. The present sequence represents human REI framework region
CC   (REIVK)
XX
SQ   Sequence 92 AA;

  Query Match             100.0%;  Score 112;  DB 6;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23
```

RESULT 9
ABU10141
ID ABU10141 standard; protein; 92 AA.
XX
AC ABU10141;
XX
DT 11-AUG-2003 (first entry)
XX
DE Human REI antibody framework region.
XX
KW Human; tumour-associated glycoprotein 72; TAG-72; antibody; REI; cancer;
KW tumour; tumour imaging; serum clearance.
XX
OS Homo sapiens.
XX
PN US2003013854-A1.
XX
PD 16-JAN-2003.
XX
PF 31-OCT-2001; 2001US-00999021.
XX
PR 31-OCT-1996; 96US-0030173P.
PR 30-OCT-1997; 97WO-US019641.
PR 18-FEB-1998; 98US-00025203.
XX
PA (ANDE/) ANDERSON W H K.
PA (TEMP/) TEMPEST P R.
PA (CARR/) CARR F J.
PA (HARR/) HARRIS W J.
PA (ARMO/) ARMOUR K.
XX
PI Anderson WHK, Tempest PR, Carr FJ, Harris WJ, Armour K;
XX
DR WPI; 2003-438920/41.
XX
PT Novel humanized monoclonal antibody which specifically binds tumor-
PT associated glycoprotein-72 useful for treating cancer and in vivo imaging
PT of tumors or cancer cells expressing the tumor-associated glycoprotein-
PT 72.
XX
PS Claim 2; Fig 2; 29pp; English.
XX
CC The invention relates to a humanised antibody (or its fragment) which
CC specifically binds tumour-associated glycoprotein 72 (TAG-72) (the
CC antibody or its fragment is derived from a murine antibody which
CC specifically binds TAG-72). The humanised antibody is useful for in vivo
CC treatment of cancer, by intravenously administering a radionuclide-
CC labelled antibody, detecting tumour cells using a radionuclide activity
CC probe, and removing the detected tumour cells by surgical excision. The
CC radionuclide is (125)I or (131)I. A composition containing the humanised
CC antibody is useful for in vivo treatment of a mammal having a TAG-72
CC expressing cancer. A composition containing the humanised antibody is
CC useful for in vitro immunodetection of TAG-72 expressing cancer cells,
CC where the antibody or its fragments of the composition are bound to a
CC solid support and also for in vivo tumour imaging. The humanised
CC antibodies have little or no reduced immunogenicity in humans over murine
CC and chimeric antibodies and have improved serum clearance and metabolic
CC properties. The antibodies can be used over prolonged time periods. The
CC present sequence represents the amino acid sequence of the human REI
CC antibody framework region
XX
SQ Sequence 92 AA;

```
  Query Match             100.0%;  Score 112;  DB 6;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23
```

RESULT 10
ADF09971
ID ADF09971 standard; protein; 95 AA.
XX
AC ADF09971;
XX
DT 12-FEB-2004 (first entry)
XX
DE Antibody light chain variable region VLk_1D-37.
XX
KW Antibody; stability; solubility; antigen binding affinity;
KW variable region; human.
XX
OS Homo sapiens.
XX
PN WO2003074679-A2.
XX
PD 12-SEP-2003.
XX
PF 03-MAR-2003; 2003WO-US006598.
XX
PR 01-MAR-2002; 2002US-0360843P.
PR 29-MAY-2002; 2002US-0384197P.
XX
PA (XENC-) XENCOR.
XX
PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR WPI; 2003-722066/68.
XX
PT Computer optimization of physicochemical properties of antibodies
PT comprises analyzing the interactions of amino acids at variable
PT positions.
XX
PS Disclosure; Fig 2b; 135pp; English.
XX
CC The present invention relates to a method for optimizing at least one
CC physico-chemical property of an antibody by a computational screening
CC method. The method comprises: receiving a template antibody structure;
CC selecting at least one variable position belonging to the antibody
CC structure; selecting at least one amino acid to be considered at the
CC variable position(s); analyzing the interaction of each selected amino
CC acid at each variable position with at least part of the remainder of the
CC antibody, including the selected amino acids at other variable positions;
CC and identifying a set of at least one antibody sequence with at least one
CC optimized physico-chemical property. The method is useful for optimizing
CC the physico-chemical properties of an antibody, especially the stability,
CC solubility, or antigen binding affinity. The optimized antibody may be
CC useful for treating a patient. The present sequence is an antibody
CC variable region sequence used to illustrate the invention.
XX
SQ Sequence 95 AA;

```
  Query Match             100.0%;  Score 112;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 1e-08;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23
```

RESULT 11
ADF09970
ID ADF09970 standard; protein; 95 AA.
XX
AC ADF09970;
XX
DT 12-FEB-2004 (first entry)

XX
DE Antibody light chain variable region VLk_1-37.
XX
KW Antibody; stability; solubility; antigen binding affinity;
KW variable region; human.
XX
OS Homo sapiens.
XX
PN WO2003074679-A2.
XX
PD 12-SEP-2003.
XX
PF 03-MAR-2003; 2003WO-US006598.
XX
PR 01-MAR-2002; 2002US-0360843P.
PR 29-MAY-2002; 2002US-0384197P.
XX
PA (XENC-) XENCOR.
XX
PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR WPI; 2003-722066/68.
XX
PT Computer optimization of physicochemical properties of antibodies
PT comprises analyzing the interactions of amino acids at variable
PT positions.
XX
PS Disclosure; Fig 2b; 135pp; English.
XX
CC The present invention relates to a method for optimizing at least one
CC physico-chemical property of an antibody by a computational screening
CC method. The method comprises: receiving a template antibody structure;
CC selecting at least one variable position belonging to the antibody
CC structure; selecting at least one amino acid to be considered at the
CC variable position(s); analyzing the interaction of each selected amino
CC acid at each variable position with at least part of the remainder of the
CC antibody, including the selected amino acids at other variable positions;
CC and identifying a set of at least one antibody sequence with at least one
CC optimized physico-chemical property. The method is useful for optimizing
CC the physico-chemical properties of an antibody, especially the stability,
CC solubility, or antigen binding affinity. The optimized antibody may be
CC useful for treating a patient. The present sequence is an antibody
CC variable region sequence used to illustrate the invention.
XX
SQ Sequence 95 AA;

Query Match 100.0%; Score 112; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRVTITC 23
||||||||||||||||||||||
Db 1 DIQLTQSPSSLSASVGDRVTITC 23

RESULT 12
ADF10076
ID ADF10076 standard; protein; 95 AA.
XX
AC ADF10076;
XX
DT 12-FEB-2004 (first entry)
XX
DE VEGF antibody light chain variable region VLk_1D-37.
XX
KW Antibody; stability; solubility; antigen binding affinity;
KW variable region; human; VEGF.
XX
OS Homo sapiens.
XX
PN WO2003074679-A2.
XX
PD 12-SEP-2003.
XX
PF 03-MAR-2003; 2003WO-US006598.
XX
PR 01-MAR-2002; 2002US-0360843P.
PR 29-MAY-2002; 2002US-0384197P.
XX
PA (XENC-) XENCOR.
XX
PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR WPI; 2003-722066/68.
XX
PT Computer optimization of physicochemical properties of antibodies
PT comprises analyzing the interactions of amino acids at variable
PT positions.
XX
PS Example 6; Fig 16b; 135pp; English.
XX
CC The present invention relates to a method for optimizing at least one
CC physico-chemical property of an antibody by a computational screening
CC method. The method comprises: receiving a template antibody structure;
CC selecting at least one variable position belonging to the antibody
CC structure; selecting at least one amino acid to be considered at the
CC variable position(s); analyzing the interaction of each selected amino
CC acid at each variable position with at least part of the remainder of the
CC antibody, including the selected amino acids at other variable positions;
CC and identifying a set of at least one antibody sequence with at least one
CC optimized physico-chemical property. The method is useful for optimizing
CC the physico-chemical properties of an antibody, especially the stability,
CC solubility, or antigen binding affinity. The optimized antibody may be
CC useful for treating a patient. The present sequence is an antibody
CC variable region sequence used to illustrate the invention.
XX
SQ Sequence 95 AA;

Query Match 100.0%; Score 112; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRVTITC 23
||||||||||||||||||||||
Db 1 DIQLTQSPSSLSASVGDRVTITC 23

RESULT 13
ADF10178
ID ADF10178 standard; protein; 95 AA.
XX
AC ADF10178;
XX
DT 12-FEB-2004 (first entry)
XX
DE Antibody light chain variable region VLk_1D-37.
XX
KW Antibody; stability; solubility; antigen binding affinity;
KW variable region; human.
XX
OS Homo sapiens.
XX
PN WO2003074679-A2.
XX
PD 12-SEP-2003.
XX
PF 03-MAR-2003; 2003WO-US006598.
XX
PR 01-MAR-2002; 2002US-0360843P.
PR 29-MAY-2002; 2002US-0384197P.
XX
PA (XENC-) XENCOR.
XX
PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR WPI; 2003-722066/68.

XX
PT Computer optimization of physicochemical properties of antibodies
PT comprises analyzing the interactions of amino acids at variable
PT positions.
XX
PS Example 16; Fig 40b; 135pp; English.
XX
CC The present invention relates to a method for optimizing at least one
CC physico-chemical property of an antibody by a computational screening
CC method. The method comprises: receiving a template antibody structure;
CC selecting at least one variable position belonging to the antibody
CC structure; selecting at least one amino acid to be considered at the
CC variable position(s); analyzing the interaction of each selected amino
CC acid at each variable position with at least part of the remainder of the
CC antibody, including the selected amino acids at other variable positions;
CC and identifying a set of at least one antibody sequence with at least one
CC optimized physico-chemical property. The method is useful for optimizing
CC the physico-chemical properties of an antibody, especially the stability,
CC solubility, or antigen binding affinity. The optimized antibody may be
CC useful for treating a patient. The present sequence is an antibody
CC variable region sequence used to illustrate the invention.
XX
SQ Sequence 95 AA;

Query Match 100.0%; Score 112; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRVTITC 23
||||||||||||||||||||||
Db 1 DIQLTQSPSSLSASVGDRVTITC 23

RESULT 14
ADF10177
ID ADF10177 standard; protein; 95 AA.
XX
AC ADF10177;
XX
DT 12-FEB-2004 (first entry)
XX
DE Antibody light chain variable region VLk_1-37.
XX
KW Antibody; stability; solubility; antigen binding affinity;
KW variable region; human.
XX
OS Homo sapiens.
XX
PN WO2003074679-A2.
XX
PD 12-SEP-2003.
XX
PF 03-MAR-2003; 2003WO-US006598.
XX
PR 01-MAR-2002; 2002US-0360843P.
PR 29-MAY-2002; 2002US-0384197P.
XX
PA (XENC-) XENCOR.
XX
PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR WPI; 2003-722066/68.
XX
PT Computer optimization of physicochemical properties of antibodies
PT comprises analyzing the interactions of amino acids at variable
PT positions.
XX
PS Example 16; Fig 40b; 135pp; English.
XX
CC The present invention relates to a method for optimizing at least one
CC physico-chemical property of an antibody by a computational screening
CC method. The method comprises: receiving a template antibody structure;
CC selecting at least one variable position belonging to the antibody
CC structure; selecting at least one amino acid to be considered at the
CC variable position(s); analyzing the interaction of each selected amino
CC acid at each variable position with at least part of the remainder of the
CC antibody, including the selected amino acids at other variable positions;
CC and identifying a set of at least one antibody sequence with at least one
CC optimized physico-chemical property. The method is useful for optimizing
CC the physico-chemical properties of an antibody, especially the stability,
CC solubility, or antigen binding affinity. The optimized antibody may be
CC useful for treating a patient. The present sequence is an antibody
CC variable region sequence used to illustrate the invention.
XX
SQ Sequence 95 AA;

Query Match 100.0%; Score 112; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRVTITC 23
||||||||||||||||||||||
Db 1 DIQLTQSPSSLSASVGDRVTITC 23

RESULT 15
ADF10075
ID ADF10075 standard; protein; 95 AA.
XX
AC ADF10075;
XX
DT 12-FEB-2004 (first entry)
XX
DE VEGF antibody light chain variable region VLk_1-37.
XX
KW Antibody; stability; solubility; antigen binding affinity;
KW variable region; human; VEGF.
XX
OS Homo sapiens.
XX
PN WO2003074679-A2.
XX
PD 12-SEP-2003.
XX
PF 03-MAR-2003; 2003WO-US006598.
XX
PR 01-MAR-2002; 2002US-0360843P.
PR 29-MAY-2002; 2002US-0384197P.
XX
PA (XENC-) XENCOR.
XX
PI Lazar GA, Desjarlais JR, Marshall SA, Dahiyat B;
XX
DR WPI; 2003-722066/68.
XX
PT Computer optimization of physicochemical properties of antibodies
PT comprises analyzing the interactions of amino acids at variable
PT positions.
XX
PS Example 6; Fig 16b; 135pp; English.
XX
CC The present invention relates to a method for optimizing at least one
CC physico-chemical property of an antibody by a computational screening
CC method. The method comprises: receiving a template antibody structure;
CC selecting at least one variable position belonging to the antibody
CC structure; selecting at least one amino acid to be considered at the
CC variable position(s); analyzing the interaction of each selected amino
CC acid at each variable position with at least part of the remainder of the
CC antibody, including the selected amino acids at other variable positions;
CC and identifying a set of at least one antibody sequence with at least one
CC optimized physico-chemical property. The method is useful for optimizing
CC the physico-chemical properties of an antibody, especially the stability,
CC solubility, or antigen binding affinity. The optimized antibody may be
CC useful for treating a patient. The present sequence is an antibody
CC variable region sequence used to illustrate the invention.
XX

SQ Sequence 95 AA;

Query Match 100.0%; Score 112; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23
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Job time : 70.1085 secs

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Title: US-10-755-382-26
Perfect score: 112
Sequence: 1 DIQLTQSPSSLSASVGDRVTITC 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	112	100.0	108	1	K1HUBN	Ig kappa chain V-I
2	112	100.0	117	2	S24207	Ig kappa chain V r
3	112	100.0	122	2	S40370	Ig kappa chain - h
4	110	98.2	57	2	PH0879	Ig kappa chain V r
5	110	98.2	62	2	S42265	Ig kappa chain V r
6	110	98.2	95	2	PH0864	Ig kappa chain V r
7	110	98.2	95	2	S69898	Ig kappa chain V r
8	110	98.2	95	2	PH0862	Ig kappa chain V r
9	110	98.2	95	2	PH0867	Ig kappa chain V r
10	110	98.2	95	2	PH0863	Ig kappa chain V r
11	110	98.2	107	2	JL0139	Ig kappa chain V r
12	110	98.2	107	2	S36275	Ig lambda chain V
13	110	98.2	107	2	S36269	Ig lambda chain V
14	110	98.2	107	2	S40366	Ig kappa chain V-J
15	110	98.2	108	1	K1HUAG	Ig kappa chain V-I
16	110	98.2	108	1	K1HUAU	Ig kappa chain V-I
17	110	98.2	108	1	K1HUHU	Ig kappa chain V-I
18	110	98.2	108	1	K1HURE	Ig kappa chain V-I
19	110	98.2	108	1	K1HURY	Ig kappa chain V-I
20	110	98.2	108	1	K1HUSW	Ig kappa chain V-I
21	110	98.2	108	1	K1HUWE	Ig kappa chain V-I
22	110	98.2	108	2	S44122	Ig kappa chain V r
23	110	98.2	108	2	I39154	Ig kappa chain (BR
24	110	98.2	108	2	B49047	Ig kappa chain V r
25	110	98.2	116	2	A27594	Ig kappa chain pre
26	110	98.2	117	1	K1HU11	Ig kappa chain pre
27	110	98.2	117	2	C21056	Ig kappa chain pre
28	110	98.2	117	2	S24206	Ig kappa chain V r
29	110	98.2	117	2	S21668	Ig kappa chain V r
30	110	98.2	117	2	S41809	Ig kappa chain V r
31	110	98.2	117	2	B21056	Ig kappa chain pre
32	110	98.2	117	2	S42263	Ig kappa chain V r
33	110	98.2	117	2	S43528	Ig kappa chain V r
34	110	98.2	120	2	S46370	Ig kappa chain V-J
35	110	98.2	122	2	S40314	Ig kappa chain - h
36	110	98.2	123	2	S40331	Ig kappa chain - h
37	110	98.2	123	2	S40313	Ig kappa chain V-J
38	110	98.2	125	2	S40353	Ig kappa chain V-J
39	110	98.2	125	2	S40350	Ig kappa chain - h
40	110	98.2	127	2	S40367	Ig kappa chain V-J
41	110	98.2	129	1	K1HUDI	Ig kappa chain pre
42	110	98.2	129	1	K1HUWK	Ig kappa chain pre
43	110	98.2	129	2	S52789	Ig kappa chain V r
44	110	98.2	129	2	S52792	Ig kappa chain V r
45	110	98.2	129	2	S52793	Ig kappa chain V r

ALIGNMENTS

RESULT 1
K1HUBN
Ig kappa chain V-I region (Ban) - human
C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A01878
R;Dwulet, F.E.; O'Connor, T.P.; Benson, M.D.
Mol. Immunol. 23, 73-78, 1986
A;Title: Polymorphism in a kappa I primary (AL) amyloid protein (BAN).
A;Reference number: A01878; MUID:86174817; PMID:3083240
A;Accession: A01878
A;Molecule type: protein
A;Residues: 1-108 <DWU>
A;Cross-references: UNIPROT:P04430; UNIPARC:UPI000012E150
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: amyloid; heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4
F;23-88/Disulfide bonds: #status predicted

Query Match 100.0%; Score 112; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRVTITC 23
||||||||||||||||||||||||
Db 1 DIQLTQSPSSLSASVGDRVTITC 23

RESULT 2
S24207
Ig kappa chain V region (Vx 014 and Vx 04) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: S24207; S24210
R;Pargent, W.; Meindl, A.; Thiebe, R.; Mitzel, S.; Zachau, H.G.
Eur. J. Immunol. 21, 1821-1827, 1991
A;Title: The human immunoglobulin kappa locus. Characterization of the duplicated O regio
A;Reference number: S24205; MUID:91330953; PMID:1907917
A;Accession: S24207

A;Molecule type: DNA
A;Residues: 1-117 <PAR>
A;Cross-references: UNIPARC:UPI0000176CB9; EMBL:X59316
A;Genetics: G1
A;Accession: S24210
A;Molecule type: DNA
A;Residues: 1-117 <PAW>
A;Cross-references: UNIPARC:UPI0000176CB9; EMBL:X59313
A;Genetics: G2
C;Genetics: <G1>
A;Gene: Vx 014
A;Map position: 2
A;Introns: 19/1
C;Genetics: <G2>
A;Gene: Vx 04
A;Map position: 2
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 112; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRVTITC 23
||||||||||||||||||||||||
Db 23 DIQLTQSPSSLSASVGDRVTITC 45

RESULT 3
S40370
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40370
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40370
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-122 <KLE>
A;Cross-references: UNIPARC:UPI0000116178; EMBL:X72480; NID:g441428; PIDN:CAA51148.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-104/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 112; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRVTITC 23
||||||||||||||||||||||||
Db 15 DIQLTQSPSSLSASVGDRVTITC 37

RESULT 4
PH0879
Ig kappa chain V region (MAR) - human (fragment)
N;Alternate names: myeloma protein
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-May-1997
C;Accession: PH0879
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0879
A;Molecule type: protein
A;Residues: 1-57 <MAN>
A;Cross-references: UNIPARC:UPI0000176D86
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2

Query Match 98.2%; Score 110; DB 2; Length 57;
Best Local Similarity 95.7%; Pred. No. 2.1e-09;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRVTITC 23
|||:||||||||||||||||||
Db 1 DIQMTQSPSSLSASVGDRVTITC 23

RESULT 5
S42265
Ig kappa chain V region (018) - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C;Accession: S42265
R;Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Quer
J. Immunol. 147, 4007-4013, 1991
A;Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus infl
A;Reference number: S42263; MUID:92043792; PMID:1940382
A;Accession: S42265
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-62 <SCO>
A;Cross-references: UNIPARC:UPI0000176D84; EMBL:M64856
C;Genetics:
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 98.2%; Score 110; DB 2; Length 62;
Best Local Similarity 95.7%; Pred. No. 2.2e-09;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRVTITC 23
|||:||||||||||||||||||
Db 1 DIQMTQSPSSLSASVGDRVTITC 23

RESULT 6
PH0864
Ig kappa chain V region (anti-DNA, IC4) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH0864
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0864
A;Molecule type: DNA
A;Residues: 1-95 <MAN>
A;Cross-references: UNIPARC:UPI0000176D9D
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3

Query Match 98.2%; Score 110; DB 2; Length 95;
Best Local Similarity 95.7%; Pred. No. 3.5e-09;
Matches 22; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 7
S69898
Ig kappa chain V region (clone RFSJ5L), rheumatoid factor - human
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000
C;Accession: S69898
R;Randen, I.; Pascual, V.; Victor, K.; Thompson, K.M.; Forre, O.; Capra, D.J.; Natvig, J
Eur. J. Immunol. 23, 1220-1225, 1993
A;Title: Synovial IgG rheumatoid factors show evidence of an antigen-driven immune respo
A;Reference number: S69896; MUID:93272805; PMID:8500520
A;Accession: S69898
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-95 <RAN>
A;Cross-references: UNIPARC:UPI000011664C; EMBL:Z34892; NID:g509801; PIDN:CAA84375.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             98.2%;  Score 110;  DB 2;  Length 95;
  Best Local Similarity   95.7%;  Pred. No. 3.5e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 8
PH0862
Ig kappa chain V region (anti-DNA, III-3R) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH0862
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0862
A;Molecule type: DNA
A;Residues: 1-95 <MAN>
A;Cross-references: UNIPARC:UPI0000176D9C
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3

  Query Match             98.2%;  Score 110;  DB 2;  Length 95;
  Best Local Similarity   95.7%;  Pred. No. 3.5e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 9
PH0867
Ig kappa chain V region (anti-DNA, R3.5H5G) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-Jul-2004
C;Accession: PH0867
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0867
A;Molecule type: DNA
A;Residues: 1-95 <MAN>
A;Cross-references: UNIPROT:Q96SA9; UNIPARC:UPI0000176DA4
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3

  Query Match             98.2%;  Score 110;  DB 2;  Length 95;
  Best Local Similarity   95.7%;  Pred. No. 3.5e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 10
PH0863
Ig kappa chain V region (anti-DNA, III-2R) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 31-Dec-2004
C;Accession: PH0863
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0863
A;Molecule type: DNA
A;Residues: 1-95 <MAN>
A;Cross-references: UNIPROT:Q9UL70; UNIPARC:UPI0000176DA0
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3

  Query Match             98.2%;  Score 110;  DB 2;  Length 95;
  Best Local Similarity   95.7%;  Pred. No. 3.5e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 11
JL0139
Ig kappa chain V region (AND) - human (fragment)
N;Alternate names: amyloid protein
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C;Accession: JL0139
R;Liepnieks, J.J.; Dwulet, F.E.; Benson, M.D.
Mol. Immunol. 27, 481-485, 1990
A;Title: Amino acid sequence of a kappa I primary (AL) amyloid protein (AND).
A;Reference number: JL0139; MUID:90340314; PMID:2116593
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A;Accession: JL0139
A;Molecule type: protein
A;Residues: 1-107 <LIE>
A;Cross-references: UNIPARC:UPI0000176B28
A;Experimental source: spleen
A;Note: this protein is isolated from amyloid fibrils
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-97/Region: complementarity-determining 3
F;98-107/Region: framework 4

  Query Match             98.2%;  Score 110;  DB 2;  Length 107;
  Best Local Similarity   95.7%;  Pred. No. 3.9e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 12
S36275
Ig lambda chain V region (clone alpha-FOG1-A4) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36275
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36275
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
A;Cross-references: UNIPARC:UPI0000118DED; EMBL:Z18827; NID:g33416; PIDN:CAA79279.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             98.2%;  Score 110;  DB 2;  Length 107;
  Best Local Similarity   95.7%;  Pred. No. 3.9e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 13
S36269
Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36269
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36269
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
A;Cross-references: UNIPARC:UPI0000118DF1; EMBL:Z18838; NID:g33422; PIDN:CAA79290.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             98.2%;  Score 110;  DB 2;  Length 107;
  Best Local Similarity   95.7%;  Pred. No. 3.9e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 14
S40366
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40366
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40366
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-107 <KLE>
A;Cross-references: UNIPARC:UPI0000116174; EMBL:X72476; NID:g441420; PIDN:CAA51144.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;28-102/Domain: immunoglobulin homology <IMM>

  Query Match             98.2%;  Score 110;  DB 2;  Length 107;
  Best Local Similarity   95.7%;  Pred. No. 3.9e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db         13 DIQMTQSPSSLSASVGDRVTITC 35


RESULT 15
K1HUAG
Ig kappa chain V-I region (Ag) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01861
R;Titani, K.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 244, 3550-3560, 1969
A;Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete s
A;Reference number: A92047; MUID:69234734; PMID:4893682
A;Accession: A01861
A;Molecule type: protein
A;Residues: 1-108 <TIT>
A;Cross-references: UNIPROT:P01593; UNIPARC:UPI000012E13D
A;Note: the sequence of the C region, which has the Inv (3) marker, is also given
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lar
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status experimental

  Query Match             98.2%;  Score 110;  DB 1;  Length 108;
  Best Local Similarity   95.7%;  Pred. No. 3.9e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23
```

Search completed: March 23, 2006, 00:57:30
Job time : 8.55814 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 00:45:29 ; Search time 52.5969 Seconds
(without alignments)
308.519 Million cell updates/sec

Title: US-10-755-382-26
Perfect score: 112
Sequence: 1 DIQLTQSPSSLSASVGDRVTITC 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	112	100.0	108	1	KV1V_HUMAN	P04430 homo sapien
2	110	98.2	107	2	Q9UL81_HUMAN	Q9ul81 homo sapien
3	110	98.2	107	2	Q96SA9_HUMAN	Q96sa9 homo sapien
4	110	98.2	108	1	KV1A_HUMAN	P01593 homo sapien
5	110	98.2	108	1	KV1B_HUMAN	P01594 homo sapien
6	110	98.2	108	1	KV1H_HUMAN	P01600 homo sapien
7	110	98.2	108	1	KV1O_HUMAN	P01607 homo sapien
8	110	98.2	108	1	KV1P_HUMAN	P01608 homo sapien
9	110	98.2	108	1	KV1Q_HUMAN	P01609 homo sapien
10	110	98.2	108	1	KV1R_HUMAN	P01610 homo sapien
11	110	98.2	108	1	KV1Y_HUMAN	P80362 homo sapien
12	110	98.2	108	2	Q9UL70_HUMAN	Q9ul70 homo sapien
13	110	98.2	108	2	Q9UL77_HUMAN	Q9ul77 homo sapien
14	110	98.2	117	1	KV1I_HUMAN	P01601 homo sapien
15	110	98.2	129	1	KV1W_HUMAN	P04431 homo sapien
16	110	98.2	129	1	KV1X_HUMAN	P04432 homo sapien
17	110	98.2	236	2	Q6GMX0_HUMAN	Q6gmx0 homo sapien
18	110	98.2	236	2	Q502W4_HUMAN	Q502w4 homo sapien
19	107	95.5	108	1	KV1F_HUMAN	P01598 homo sapien
20	107	95.5	108	1	KV1S_HUMAN	P01611 homo sapien
21	107	95.5	117	1	KV1J_HUMAN	P01602 homo sapien
22	107	95.5	236	2	Q6GMX8_HUMAN	Q6gmx8 homo sapien
23	106	94.6	50	2	Q6LBV5_HUMAN	Q6lbv5 homo sapien
24	106	94.6	108	1	KV1E_HUMAN	P01597 homo sapien
25	106	94.6	108	1	KV1M_HUMAN	P01605 homo sapien
26	106	94.6	108	1	KV1N_HUMAN	P01606 homo sapien
27	106	94.6	236	2	Q6PIH7_HUMAN	Q6pih7 homo sapien
28	106	94.6	240	2	Q65ZC9_HUMAN	Q65zc9 homo sapien
29	106	94.6	244	2	Q65ZC8_HUMAN	Q65zc8 homo sapien
30	104	92.9	108	1	KV1G_HUMAN	P01599 homo sapien
31	104	92.9	236	2	Q7Z3Y4_HUMAN	Q7z3y4 homo sapien
32	104	92.9	236	2	Q6GMW1_HUMAN	Q6gmw1 homo sapien
33	103	92.0	108	1	KV1K_HUMAN	P01603 homo sapien
34	103	92.0	109	1	KV1T_HUMAN	P01612 homo sapien
35	103	92.0	189	2	Q569I7_HUMAN	Q569i7 homo sapien
36	103	92.0	236	2	Q6GMX9_HUMAN	Q6gmx9 homo sapien
37	102	91.1	107	1	KV1D_HUMAN	P01596 homo sapien
38	102	91.1	236	2	Q6PIH4_HUMAN	Q6pih4 homo sapien
39	102	91.1	236	2	Q6PIT5_HUMAN	Q6pit5 homo sapien
40	100	89.3	108	1	KV5O_MOUSE	P01648 mus musculu
41	100	89.3	116	2	Q96PF6_HUMAN	Q96pf6 homo sapien
42	99	88.4	108	1	KV1C_HUMAN	P01595 homo sapien
43	99	88.4	112	1	KV1U_HUMAN	P01613 homo sapien
44	97	86.6	109	2	Q920E6_MOUSE	Q920e6 mus musculu
45	97	86.6	115	1	KV5C_MOUSE	P01635 mus musculu

ALIGNMENTS

RESULT 1
KV1V_HUMAN
ID KV1V_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig kappa chain V-I region BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240; DOI=10.1016/0161-5890(86)90173-2;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
CC ---
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC ---
DR PIR; A01878; K1HUBN.
DR HSSP; P80362; 1WTL.
DR SMR; P04430; 1-108.
DR GO; GO:0005576; C:extracellular region; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Amyloid; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region.
FT REGION 1 23 Framework-1.
FT REGION 24 34 Complementarity-determining-1.
FT REGION 35 49 Framework-2.
FT REGION 50 56 Complementarity-determining-2.
FT REGION 57 88 Framework-3.
FT REGION 89 97 Complementarity-determining-3.
FT REGION 98 107 Framework-4.
FT DISULFID 23 88 By similarity.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MW; CD3FD944FE96FD37 CRC64;

Query Match 100.0%; Score 112; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRVTITC 23

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                  ||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 2
Q9UL81_HUMAN
ID   Q9UL81_HUMAN PRELIMINARY;      PRT;   107 AA.
AC   Q9UL81;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035033; AAD56269.1; -; mRNA.
DR   HSSP; P01607; 1BWW.
DR   SMR; Q9UL81; 1-107.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11501 MW;  070549FDE0754748 CRC64;

  Query Match             98.2%;  Score 110;  DB 2;  Length 107;
  Best Local Similarity   95.7%;  Pred. No. 5.8e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 3
Q96SA9_HUMAN
ID   Q96SA9_HUMAN PRELIMINARY;      PRT;   107 AA.
AC   Q96SA9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE   variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98375893; PubMed=9712075;
RA   Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT   "Molecular analysis of polyreactive monoclonal antibodies from
RT   rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT   antibody V region genes.";
RL   J. Immunol. 161:2020-2031(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1516616;
RA   Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT   "Human monoclonal striational autoantibodies isolated from thymic B
RT   lymphocytes of patients with myasthenia gravis use VH and VL gene
RT   segments associated with the autoimmune repertoire.";
RL   Eur. J. Immunol. 22:2231-2236(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=8436174;
RA   Wagner S.D., Luzzatto L.;
RT   "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT   distributed over a large portion of the V kappa locus and do not show
RT   somatic mutation.";
RL   Eur. J. Immunol. 23:391-397(1993).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1660528;
RA   Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA   Diamond B.;
RT   "Molecular characteristics of antibodies bearing an anti-DNA-
RT   associated idiotype.";
RL   J. Exp. Med. 174:1639-1652(1991).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1903706;
RA   Blaison G., Kuntz J.L., Pasquali J.L.;
RT   "Molecular analysis of V kappa III variable regions of polyclonal
RT   rheumatoid factors during rheumatoid arthritis.";
RL   Eur. J. Immunol. 21:1221-1227(1991).
DR   EMBL; U96396; AAB68785.1; -; mRNA.
DR   PIR; B49047; B49047.
DR   PIR; PH0867; PH0867.
DR   PIR; S16840; S16840.
DR   PIR; S31977; S31977.
DR   PIR; S34083; S34083.
DR   PIR; S34086; S34086.
DR   HSSP; P01607; 1BWW.
DR   SMR; Q96SA9; 1-107.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11520 MW;  4BB43E9C5B577F16 CRC64;

  Query Match             98.2%;  Score 110;  DB 2;  Length 107;
  Best Local Similarity   95.7%;  Pred. No. 5.8e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 4
KV1A_HUMAN
ID   KV1A_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01593;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region AG.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=69234734; PubMed=4893682;
RA   Titani K., Shinoda T., Putnam F.W.;
RT   "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT   complete sequence and the location of the disulfide bridges.";
RL   J. Biol. Chem. 244:3550-3560(1969).
```

```
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ---------------------------------------------------------------------
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CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01861; K1HUAG.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01593; 1-108.
DR   Ensembl; ENSG00000173782; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11992 MW;  E3B3B246C18F0C4F CRC64;

  Query Match             98.2%;  Score 110;  DB 1;  Length 108;
  Best Local Similarity   95.7%;  Pred. No. 5.8e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 5
KV1B_HUMAN
ID   KV1B_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01594;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=72189444; PubMed=5028201;
RA   Schiechl H., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX   MEDLINE=77022433; PubMed=1234024;
RA   Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigemann W., Schramm H.J.;
RT   "The structure determination of the variable portion of the Bence-
RT   Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
CC   -!- MISCELLANEOUS: The structure of the V region was determined by
CC       molecular replacement methods using the known structure of the V
CC       region of the kappa chain REI.
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ---------------------------------------------------------------------
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CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A91653; K1HUAU.
DR   PDB; 1JV5; X-ray; A=1-107.
DR   Ensembl; ENSG00000173782; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin domain; Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
FT   STRAND        4      5
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       44     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       85     90
FT   STRAND       97     98
FT   STRAND      102    106
SQ   SEQUENCE   108 AA;  11939 MW;  E8011187EE6F6FB9 CRC64;

  Query Match             98.2%;  Score 110;  DB 1;  Length 108;
  Best Local Similarity   95.7%;  Pred. No. 5.8e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 6
KV1H_HUMAN
ID   KV1H_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01600;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Hau.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
```

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OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=71032830; PubMed=4097974;
RA   Watanabe S., Hilschmann N.;
RT   "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT   chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT   subgroups.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01868; K1HUHU.
DR   PDB; 1F6L; X-ray; L=1-108.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin domain; Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11671 MW;  08D3A6160D8D0618 CRC64;

  Query Match             98.2%;  Score 110;  DB 1;  Length 108;
  Best Local Similarity   95.7%;  Pred. No. 5.8e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 7
KV1O_HUMAN
ID   KV1O_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Rei.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC       marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A91663; K1HURE.
DR   PDB; 1AR2; X-ray; @=1-107.
DR   PDB; 1BWW; X-ray; A/B=1-107.
DR   PDB; 1REI; X-ray; A/B=1-107.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin domain; Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88
FT   NON_TER     108    108
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       45     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       84     90
FT   STRAND       97     98
FT   STRAND      102    106
SQ   SEQUENCE   108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;

  Query Match             98.2%;  Score 110;  DB 1;  Length 108;
  Best Local Similarity   95.7%;  Pred. No. 5.8e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 8
KV1P_HUMAN
ID   KV1P_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01608;
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DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Roy.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=68362076; PubMed=5595110;
RA   Hilschmann N.;
RT   "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT   Cum.).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN   [2]
RP   SEQUENCE REVISION TO 39 AND 41.
RA   Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA   Steinmetz-Kayne M., Suter L., Watanabe S.;
RL   (In) Franek F., Shugar D. (eds.);
RL   Gamma globulins: structure and function, pp.57-74, Academic Press, New
RL   York (1969).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC       marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A91638; K1HURY.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01608; 1-108.
DR   Ensembl; ENSG00000173782; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11782 MW;  F5ACEDE5A313DF3A CRC64;

  Query Match             98.2%;  Score 110;  DB 1;  Length 108;
  Best Local Similarity   95.7%;  Pred. No. 5.8e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 9
KV1Q_HUMAN
ID   KV1Q_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01609;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Scw.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=75059271; PubMed=4435756;
RA   Eulitz M., Hilschmann N.;
RT   "The primary structure of a human immunoglobulin L-chain of kappa-type
RT   (Bence-Jones protein Scw.), II: the chymotryptic peptides and the
RT   complete amino acid sequence.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 355:842-866(1974).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC       marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01875; K1HUSW.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01609; 1-107.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11764 MW;  32CECDDDF9644414 CRC64;

  Query Match             98.2%;  Score 110;  DB 1;  Length 108;
  Best Local Similarity   95.7%;  Pred. No. 5.8e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 10
KV1R_HUMAN
ID   KV1R_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01610;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region WEA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=83273707; PubMed=6410398;
RA   Goni F., Frangione B.;
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```
RT   "Amino acid sequence of the Fv region of a human monoclonal IgM
RT   (protein WEA) with antibody activity against 3,4-pyruvylated galactose
RT   in Klebsiella polysaccharides K30 and K33.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC   -!- MISCELLANEOUS: This chain was obtained from a monoclonal antibody
CC       against 3,4-pyruvylated galactose and isolated from a patient with
CC       Waldenstrom's macroglobulinemia.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01876; K1HUWE.
DR   HSSP; P80362; 1WTL.
DR   SMR; P01610; 1-108.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region; Monoclonal antibody.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11840 MW;  9249B61F0945618C CRC64;

  Query Match             98.2%;  Score 110;  DB 1;  Length 108;
  Best Local Similarity   95.7%;  Pred. No. 5.8e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 11
KV1Y_HUMAN
ID   KV1Y_HUMAN     STANDARD;      PRT;   108 AA.
AC   P80362;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region WAT.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX   MEDLINE=95086080; PubMed=7993911;
RA   Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA   Solomon A., Stevens F.J., Schiffer M.;
RT   "Comparison of crystal structures of two homologous proteins:
RT   structural origin of altered domain interactions in immunoglobulin
RT   light-chain dimers.";
RL   Biochemistry 33:14848-14857(1994).
RN   [2]
RP   PROTEIN SEQUENCE OF 1-35.
RX   MEDLINE=81267384; PubMed=6167731;
RA   Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA   Popp R.A., Solomon A.;
RT   "Characterization and preliminary crystallographic data on the VL-
RT   related fragment of the human kI Bence Jones protein Wat.";
RL   J. Mol. Biol. 147:185-193(1981).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PDB; 1WTL; X-ray; A/B=1-108.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin domain; Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   CONFLICT     30     31       TN -> SD (in Ref. 2).
FT   NON_TER     108    108
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       45     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       84     90
FT   STRAND       98     98
FT   STRAND      102    106
SQ   SEQUENCE   108 AA;  11737 MW;  D9D941B3F0FAE697 CRC64;

  Query Match             98.2%;  Score 110;  DB 1;  Length 108;
  Best Local Similarity   95.7%;  Pred. No. 5.8e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 12
Q9UL70_HUMAN
ID   Q9UL70_HUMAN PRELIMINARY;      PRT;   108 AA.
AC   Q9UL70;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1660528;
RA   Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA   Diamond B.;
RT   "Molecular characteristics of antibodies bearing an anti-DNA-
RT   associated idiotype.";
RL   J. Exp. Med. 174:1639-1652(1991).
DR   EMBL; AF035044; AAD56280.1; -; mRNA.
DR   PIR; PH0863; PH0863.
DR   HSSP; P01607; 1BWW.
DR   SMR; Q9UL70; 1-108.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11633 MW;  B7BEDC3E41FCCA37 CRC64;

  Query Match             98.2%;  Score 110;  DB 2;  Length 108;
  Best Local Similarity   95.7%;  Pred. No. 5.8e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 13
Q9UL77_HUMAN
ID   Q9UL77_HUMAN PRELIMINARY;      PRT;   108 AA.
AC   Q9UL77;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1516616;
RA   Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT   "Human monoclonal striational autoantibodies isolated from thymic B
RT   lymphocytes of patients with myasthenia gravis use VH and VL gene
RT   segments associated with the autoimmune repertoire.";
RL   Eur. J. Immunol. 22:2231-2236(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=8436174;
RA   Wagner S.D., Luzzatto L.;
RT   "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT   distributed over a large portion of the V kappa locus and do not show
RT   somatic mutation.";
RL   Eur. J. Immunol. 23:391-397(1993).
DR   EMBL; AF035037; AAD56273.1; -; mRNA.
DR   PIR; B49047; B49047.
DR   PIR; S34083; S34083.
DR   HSSP; P01607; 1BWW.
DR   SMR; Q9UL77; 1-108.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11738 MW;  C06681716C4D16F3 CRC64;

  Query Match             98.2%;  Score 110;  DB 2;  Length 108;
  Best Local Similarity   95.7%;  Pred. No. 5.8e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db          1 DIQMTQSPSSLSASVGDRVTITC 23


RESULT 14
KV1I_HUMAN
ID   KV1I_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01601;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region HK101 precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=81098966; PubMed=6779204;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Human immunoglobulin variable region genes -- DNA sequences of two V
RT   kappa genes and a pseudogene.";
RL   Nature 288:730-733(1980).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=83129397; PubMed=6402305; DOI=10.1016/0092-8674(83)90508-1;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Evolution of immunoglobulin V genes: evidence indicating that
RT   recently duplicated human V kappa sequences have diverged by gene
RT   conversion.";
RL   Cell 32:181-189(1983).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; K01322; AAA58930.1; -; Genomic_DNA.
DR   EMBL; K01324; AAA58932.1; -; Genomic_DNA.
DR   EMBL; V00558; CAA23824.1; -; Genomic_DNA.
DR   PIR; A01881; K1HU11.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01601; 23-116.
DR   Ensembl; ENSG00000122156; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
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DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
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FT   CHAIN        23   >117       Ig kappa chain V-I region HK101.
FT   REGION       23     45       Framework-1.
FT   REGION       46     56       Complementarity-determining-1.
FT   REGION       57     71       Framework-2.
FT   REGION       72     78       Complementarity-determining-2.
FT   REGION       79    110       Framework-3.
FT   REGION      111   >117       Complementarity-determining-3.
FT   DISULFID     45    110       By similarity.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12800 MW;  D7D0FF3718CEF587 CRC64;

  Query Match             98.2%;  Score 110;  DB 1;  Length 117;
  Best Local Similarity   95.7%;  Pred. No. 6.4e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||:||||||||||||||||||||
Db         23 DIQMTQSPSSLSASVGDRVTITC 45


RESULT 15
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ID   KV1W_HUMAN     STANDARD;      PRT;   129 AA.
AC   P04431;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Walker precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X00965; CAA25477.1; ALT_TERM; Genomic_DNA.
DR   PIR; A01883; K1HUWK.
DR   HSSP; P01607; 1BWW.
DR   SMR; P04431; 23-129.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       Ig kappa chain V-I region Walker.
FT   REGION       23     45       Framework-1.
FT   REGION       46     56       Complementarity-determining-1.
FT   REGION       57     71       Framework-2.
FT   REGION       72     78       Complementarity-determining-2.
FT   REGION       79    110       Framework-3.
FT   REGION      111    119       Complementarity-determining-3.
FT   REGION      120    129       Framework-4.
FT   DISULFID     45    110       By similarity.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14069 MW;  F941FA07D4AFC2F9 CRC64;

  Query Match             98.2%;  Score 110;  DB 1;  Length 129;
  Best Local Similarity   95.7%;  Pred. No. 7.1e-09;
  Matches   22;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
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Db         23 DIQMTQSPSSLSASVGDRVTITC 45


Search completed: March 23, 2006, 00:56:37
Job time : 52.5969 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 00:56:54 ; Search time 11.9457 Seconds
(without alignments)
159.182 Million cell updates/sec

Title: US-10-755-382-26
Perfect score: 112
Sequence: 1 DIQLTQSPSSLSASVGDRVTITC 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	112	100.0	23	1	US-08-318-157B-26	Sequence 26, Appl
2	112	100.0	23	2	US-09-253-794-26	Sequence 26, Appl
3	112	100.0	106	1	US-08-318-157B-19	Sequence 19, Appl
4	112	100.0	106	2	US-09-253-794-19	Sequence 19, Appl
5	112	100.0	107	1	US-08-318-157B-6	Sequence 6, Appli
6	112	100.0	107	2	US-09-171-945-61	Sequence 61, Appl
7	112	100.0	107	2	US-09-253-794-6	Sequence 6, Appli
8	112	100.0	107	2	US-09-910-059-61	Sequence 61, Appl
9	112	100.0	108	1	US-08-378-939-16	Sequence 16, Appl
10	112	100.0	108	1	US-08-378-939-18	Sequence 18, Appl
11	112	100.0	108	1	US-08-378-939-24	Sequence 24, Appl
12	112	100.0	108	1	US-08-378-939-30	Sequence 30, Appl
13	112	100.0	110	1	US-08-207-996-23	Sequence 23, Appl
14	112	100.0	110	1	US-08-207-996-24	Sequence 24, Appl
15	112	100.0	110	1	US-08-207-996-25	Sequence 25, Appl
16	112	100.0	110	1	US-08-760-840A-23	Sequence 23, Appl
17	112	100.0	110	1	US-08-760-840A-24	Sequence 24, Appl
18	112	100.0	110	1	US-08-760-840A-25	Sequence 25, Appl
19	112	100.0	110	2	US-09-266-119-23	Sequence 23, Appl
20	112	100.0	110	2	US-09-266-119-24	Sequence 24, Appl
21	112	100.0	110	2	US-09-266-119-25	Sequence 25, Appl
22	112	100.0	110	2	US-09-672-609-14	Sequence 14, Appl
23	112	100.0	110	2	US-09-602-709-23	Sequence 23, Appl
24	112	100.0	110	2	US-09-602-709-24	Sequence 24, Appl
25	112	100.0	110	2	US-09-602-709-25	Sequence 25, Appl
26	112	100.0	110	2	US-09-025-403A-14	Sequence 14, Appl
27	112	100.0	110	2	US-09-440-781-95	Sequence 95, Appl
28	112	100.0	110	2	US-08-908-469-103	Sequence 103, App
29	112	100.0	110	2	US-08-908-469-105	Sequence 105, App
30	112	100.0	110	2	US-08-908-469-107	Sequence 107, App
31	112	100.0	110	2	US-08-908-469-109	Sequence 109, App
32	112	100.0	110	2	US-08-908-469-111	Sequence 111, App
33	112	100.0	110	2	US-08-908-469-113	Sequence 113, App
34	112	100.0	110	2	US-08-908-469-115	Sequence 115, App
35	112	100.0	110	2	US-08-908-469-117	Sequence 117, App
36	112	100.0	111	1	US-08-887-352B-6	Sequence 6, Appli
37	112	100.0	111	2	US-09-109-207C-6	Sequence 6, Appli
38	112	100.0	111	2	US-09-296-005-6	Sequence 6, Appli
39	112	100.0	111	2	US-09-920-171-6	Sequence 6, Appli
40	112	100.0	111	2	US-09-716-028-6	Sequence 6, Appli
41	112	100.0	111	2	US-10-113-996-6	Sequence 6, Appli
42	112	100.0	112	2	US-08-435-516-4	Sequence 4, Appli
43	112	100.0	113	2	US-09-025-203-8	Sequence 8, Appli
44	112	100.0	113	2	US-09-999-021-8	Sequence 8, Appli
45	112	100.0	113	2	US-09-999-025-8	Sequence 8, Appli

ALIGNMENTS

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RESULT 1
US-08-318-157B-26
; Sequence 26, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-26

  Query Match             100.0%;  Score 112;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 8e-11;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
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Db          1 DIQLTQSPSSLSASVGDRVTITC 23
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RESULT 2
US-09-253-794-26
; Sequence 26, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 23 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-253-794-26

  Query Match             100.0%;  Score 112;  DB 2;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 8e-11;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
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Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 3
US-08-318-157B-19
; Sequence 19, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  106 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-19

  Query Match             100.0%;  Score 112;  DB 1;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-10;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 4
US-09-253-794-19
; Sequence 19, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
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;   INFORMATION FOR SEQ ID NO: 19:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 106 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-253-794-19

  Query Match             100.0%;  Score 112;  DB 2;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-10;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
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Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 5
US-08-318-157B-6
; Sequence 6, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  107 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-6

  Query Match             100.0%;  Score 112;  DB 1;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-10;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
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Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 6
US-09-171-945-61
; Sequence 61, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
;  APPLICANT:  Emery, Stephen
;  APPLICANT:  Copley, Clive Graham
;  APPLICANT:  Edge, Michael Derek
;  TITLE OF INVENTION:  Monoclonal Antibody to CEA, Conjugates Comprising Said
;  TITLE OF INVENTION:  Antibody, and Their Therapeutic Use in an Adept System
;  FILE REFERENCE:  Monoclonal Antibody to CEA
;  CURRENT APPLICATION NUMBER: US/09/171,945
;  CURRENT FILING DATE:  1998-10-29
;  PRIOR APPLICATION NUMBER:  GB9703103.3
;  PRIOR FILING DATE:  1997-02-14
;  PRIOR APPLICATION NUMBER:  GB9609405.7
;  PRIOR FILING DATE:  1996-05-04
;  PRIOR APPLICATION NUMBER:  PCT/GB97/01165
;  PRIOR FILING DATE:  1997-04-29
;  NUMBER OF SEQ ID NOS:  131
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 61
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-61

  Query Match             100.0%;  Score 112;  DB 2;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-10;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
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Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 7
US-09-253-794-6
; Sequence 6, Application US/09253794
; Patent No. 6676924
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 6:
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;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 107 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-253-794-6

  Query Match             100.0%;  Score 112;  DB 2;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-10;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 8
US-09-910-059-61
; Sequence 61, Application US/09910059
; Patent No. 6903203
; GENERAL INFORMATION:
;  APPLICANT: Copley, Clive G
;  APPLICANT:  Edge, Michael Derek
;  APPLICANT:  Emery, Stephen Charles
;  TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
;  TITLE OF INVENTION:  Their Therapeutic use in an Adept System
;  FILE REFERENCE: 1991-209
;  CURRENT APPLICATION NUMBER: US/09/910,059
;  CURRENT FILING DATE:  2001-07-23
;  PRIOR APPLICATION NUMBER: US 09/171,945
;  PRIOR FILING DATE: 1998-10-29
;  PRIOR APPLICATION NUMBER: PCT/GB97/01165
;  PRIOR FILING DATE: 1997-04-29
;  PRIOR APPLICATION NUMBER: GB 9703103.3
;  PRIOR FILING DATE: 1997-02-14
;  PRIOR APPLICATION NUMBER: GB9609405.7
;  PRIOR FILING DATE: 1996-05-04
;  NUMBER OF SEQ ID NOS: 131
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: humanised light chain variable region variant
US-09-910-059-61

  Query Match             100.0%;  Score 112;  DB 2;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-10;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 9
US-08-378-939-16
; Sequence 16, Application US/08378939
; Patent No. 5876961
;  GENERAL INFORMATION:
;    APPLICANT:  CROWE, JAMES SCOTT
;    APPLICANT:  LEWIS, ALAN PETER
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
;      STREET:  555 THIRTEENTH ST. N.W.
;      CITY:  WASHINGTON
;      STATE:  D. C.
;      COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,939
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/952640
;      FILING DATE:  01-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ERNST, BARBARA G
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1808-118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 783-6040
;      TELEFAX:  (202) 783-6031
;  INFORMATION FOR SEQ ID NO:  16:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-939-16

  Query Match             100.0%;  Score 112;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-10;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 10
US-08-378-939-18
; Sequence 18, Application US/08378939
; Patent No. 5876961
;  GENERAL INFORMATION:
;    APPLICANT:  CROWE, JAMES SCOTT
;    APPLICANT:  LEWIS, ALAN PETER
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
;      STREET:  555 THIRTEENTH ST. N.W.
;      CITY:  WASHINGTON
;      STATE:  D. C.
;      COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,939
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/952640
;      FILING DATE:  01-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ERNST, BARBARA G
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1808-118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 783-6040
;      TELEFAX:  (202) 783-6031
;  INFORMATION FOR SEQ ID NO:  18:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-939-18

  Query Match             100.0%;  Score 112;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-10;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 11
US-08-378-939-24
; Sequence 24, Application US/08378939
; Patent No. 5876961
;  GENERAL INFORMATION:
;    APPLICANT:  CROWE, JAMES SCOTT
;    APPLICANT:  LEWIS, ALAN PETER
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
;      STREET:  555 THIRTEENTH ST. N.W.
;      CITY:  WASHINGTON
;      STATE:  D. C.
;      COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,939
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/952640
;      FILING DATE:  01-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ERNST, BARBARA G
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1808-118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 783-6040
;      TELEFAX:  (202) 783-6031
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-939-24

  Query Match             100.0%;  Score 112;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-10;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 12
US-08-378-939-30
; Sequence 30, Application US/08378939
; Patent No. 5876961
;  GENERAL INFORMATION:
;    APPLICANT:  CROWE, JAMES SCOTT
;    APPLICANT:  LEWIS, ALAN PETER
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
;      STREET:  555 THIRTEENTH ST. N.W.
;      CITY:  WASHINGTON
;      STATE:  D. C.
;      COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,939
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/952640
;      FILING DATE:  01-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ERNST, BARBARA G
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1808-118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 783-6040
;      TELEFAX:  (202) 783-6031
;  INFORMATION FOR SEQ ID NO:  30:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  108 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-378-939-30

  Query Match             100.0%;  Score 112;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-10;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 13
US-08-207-996-23
; Sequence 23, Application US/08207996
; Patent No. 5646253
;  GENERAL INFORMATION:
;    APPLICANT:  Scotgen Biopharmaceuticals,  Inc.
;    APPLICANT:  1014 Hamilton Court
;    APPLICANT:  Menlo Park, California 94025
;    APPLICANT:  United States of America
;    APPLICANT:  1345 Avenue of the Americas
;    APPLICANT:  New York, New York 10105
;    APPLICANT:  United States of America
;    TITLE OF INVENTION:  RECOMBINANT HUMAN ANTI-LK26
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;      SOFTWARE:  WordPerfect 6.0/ASCII standard
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/207,996
;      FILING DATE:  08-MAR-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pasqualini, Patricia A.
;      REGISTRATION NUMBER:  34,894
;      REFERENCE/DOCKET NUMBER:  LUD-5363
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-688-9200
;      TELEFAX:  212-838-3884
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  110 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-207-996-23

  Query Match             100.0%;  Score 112;  DB 1;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 5e-10;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 14
US-08-207-996-24
; Sequence 24, Application US/08207996
; Patent No. 5646253
;  GENERAL INFORMATION:
;    APPLICANT:  Scotgen Biopharmaceuticals,  Inc.
;    APPLICANT:  1014 Hamilton Court
;    APPLICANT:  Menlo Park, California 94025
;    APPLICANT:  United States of America
;    APPLICANT:  1345 Avenue of the Americas
;    APPLICANT:  New York, New York 10105
;    APPLICANT:  United States of America
;    TITLE OF INVENTION:  RECOMBINANT HUMAN ANTI-LK26
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.0/ASCII standard
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/207,996
;      FILING DATE:  08-MAR-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pasqualini, Patricia A.
;      REGISTRATION NUMBER:  34,894
;      REFERENCE/DOCKET NUMBER:  LUD-5363
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-688-9200
;      TELEFAX:  212-838-3884
;  INFORMATION FOR SEQ ID NO:  24:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  110 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-207-996-24

  Query Match             100.0%;  Score 112;  DB 1;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 5e-10;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 15
US-08-207-996-25
; Sequence 25, Application US/08207996
; Patent No. 5646253
;  GENERAL INFORMATION:
;    APPLICANT:  Scotgen Biopharmaceuticals,  Inc.
;    APPLICANT:  1014 Hamilton Court
;    APPLICANT:  Menlo Park, California 94025
;    APPLICANT:  United States of America
;    APPLICANT:  1345 Avenue of the Americas
;    APPLICANT:  New York, New York 10105
;    APPLICANT:  United States of America
;    TITLE OF INVENTION:  RECOMBINANT HUMAN ANTI-LK26
;    TITLE OF INVENTION:  ANTIBODIES
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 6.0/ASCII standard
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/207,996
;      FILING DATE:  08-MAR-1994
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pasqualini, Patricia A.
;      REGISTRATION NUMBER:  34,894
;      REFERENCE/DOCKET NUMBER:  LUD-5363
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-688-9200
;      TELEFAX:  212-838-3884
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  110 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-207-996-25

  Query Match             100.0%;  Score 112;  DB 1;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 5e-10;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


Search completed: March 23, 2006, 00:58:43
Job time : 12.9457 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:12:29 ; Search time 40.4729 Seconds
(without alignments)
237.445 Million cell updates/sec

Title: US-10-755-382-26
Perfect score: 112
Sequence: 1 DIQLTQSPSSLSASVGDRVTITC 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	112	100.0	23	3	US-09-253-794-26	Sequence 26, Appl
2	112	100.0	23	5	US-10-923-068-124	Sequence 124, App
3	112	100.0	23	5	US-10-923-068-133	Sequence 133, App
4	112	100.0	23	5	US-10-755-382-26	Sequence 26, Appl
5	112	100.0	95	4	US-10-379-392-75	Sequence 75, Appl
6	112	100.0	95	4	US-10-379-392-76	Sequence 76, Appl
7	112	100.0	103	4	US-10-379-392-100	Sequence 100, App
8	112	100.0	103	4	US-10-379-392-121	Sequence 121, App
9	112	100.0	103	4	US-10-379-392-123	Sequence 123, App
10	112	100.0	103	4	US-10-379-392-125	Sequence 125, App
11	112	100.0	103	4	US-10-379-392-129	Sequence 129, App
12	112	100.0	103	4	US-10-379-392-131	Sequence 131, App
13	112	100.0	106	3	US-09-253-794-19	Sequence 19, Appl
14	112	100.0	106	4	US-10-474-832-58	Sequence 58, Appl
15	112	100.0	106	4	US-10-680-734-19	Sequence 19, Appl
16	112	100.0	106	5	US-10-755-382-19	Sequence 19, Appl
17	112	100.0	107	3	US-09-253-794-6	Sequence 6, Appli
18	112	100.0	107	3	US-09-910-059-61	Sequence 61, Appl
19	112	100.0	107	3	US-09-892-613C-26	Sequence 26, Appl
20	112	100.0	107	4	US-10-363-349-4	Sequence 4, Appli
21	112	100.0	107	4	US-10-269-711-5	Sequence 5, Appli
22	112	100.0	107	4	US-10-684-109-5	Sequence 5, Appli
23	112	100.0	107	4	US-10-680-734-6	Sequence 6, Appli
24	112	100.0	107	5	US-10-631-722-42	Sequence 42, Appl
25	112	100.0	107	5	US-10-631-722-45	Sequence 45, Appl
26	112	100.0	107	5	US-10-631-722-46	Sequence 46, Appl
27	112	100.0	107	5	US-10-482-759-26	Sequence 26, Appl
28	112	100.0	107	5	US-10-755-382-6	Sequence 6, Appli
29	112	100.0	107	5	US-10-822-306A-17	Sequence 17, Appl
30	112	100.0	108	4	US-10-153-159-4	Sequence 4, Appli
31	112	100.0	108	4	US-10-153-176-4	Sequence 4, Appli
32	112	100.0	108	4	US-10-371-942-8	Sequence 8, Appli
33	112	100.0	108	4	US-10-371-942-20	Sequence 20, Appl
34	112	100.0	108	4	US-10-443-134A-4	Sequence 4, Appli
35	112	100.0	108	5	US-10-805-177-20	Sequence 20, Appl
36	112	100.0	109	5	US-10-818-068-11	Sequence 11, Appl
37	112	100.0	109	5	US-10-724-274-11	Sequence 11, Appl
38	112	100.0	109	5	US-10-830-956-11	Sequence 11, Appl
39	112	100.0	110	3	US-09-056-160B-103	Sequence 103, App
40	112	100.0	110	3	US-09-056-160B-105	Sequence 105, App
41	112	100.0	110	3	US-09-056-160B-107	Sequence 107, App
42	112	100.0	110	3	US-09-056-160B-109	Sequence 109, App
43	112	100.0	110	3	US-09-056-160B-111	Sequence 111, App
44	112	100.0	110	3	US-09-056-160B-113	Sequence 113, App
45	112	100.0	110	3	US-09-056-160B-115	Sequence 115, App

ALIGNMENTS

RESULT 1
US-09-253-794-26
; Sequence 26, Application US/09253794
; Patent No. US20020018750A1
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-253-794-26

Query Match 100.0%; Score 112; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 2
US-10-923-068-124
; Sequence 124, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-124

  Query Match             100.0%;  Score 112;  DB 5;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 3
US-10-923-068-133
; Sequence 133, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-133

  Query Match             100.0%;  Score 112;  DB 5;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 4
US-10-755-382-26
; Sequence 26, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 23 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-755-382-26

  Query Match             100.0%;  Score 112;  DB 5;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 5
US-10-379-392-75
; Sequence 75, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
;  APPLICANT: Lazar, Gregory Alan
;  APPLICANT:  Desjarlais, John Rudolf
;  APPLICANT:  Marshall, Shannon Alicia
;  APPLICANT:  Dahiyat, Bassil I.
;  TITLE OF INVENTION: ANTIBODY OPTIMIZATION
;  FILE REFERENCE: A-71386-3 463077-236
;  CURRENT APPLICATION NUMBER: US/10/379,392
;  CURRENT FILING DATE:  2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/360,843
;  PRIOR FILING DATE: 2002-03-01
;  PRIOR APPLICATION NUMBER: US 60/384,197
;  PRIOR FILING DATE: 2002-05-29
;  NUMBER OF SEQ ID NOS: 184
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 75
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-379-392-75
```

Query Match 100.0%; Score 112; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23
```

RESULT 6
US-10-379-392-76
; Sequence 76, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 76
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-392-76

Query Match 100.0%; Score 112; DB 4; Length 95;
Best Local Similarity 100.0%; Pred. No. 9.6e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23
```

RESULT 7
US-10-379-392-100
; Sequence 100, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 100
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Humanized
US-10-379-392-100

Query Match 100.0%; Score 112; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23
```

RESULT 8
US-10-379-392-121
; Sequence 121, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 121
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-379-392-121

Query Match 100.0%; Score 112; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23
```

RESULT 9
US-10-379-392-123
; Sequence 123, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 103
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-379-392-123

Query Match 100.0%; Score 112; DB 4; Length 103;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 10
US-10-379-392-125
; Sequence 125, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
;  APPLICANT: Lazar, Gregory Alan
;  APPLICANT:  Desjarlais, John Rudolf
;  APPLICANT:  Marshall, Shannon Alicia
;  APPLICANT:  Dahiyat, Bassil I.
;  TITLE OF INVENTION: ANTIBODY OPTIMIZATION
;  FILE REFERENCE: A-71386-3 463077-236
;  CURRENT APPLICATION NUMBER: US/10/379,392
;  CURRENT FILING DATE:  2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/360,843
;  PRIOR FILING DATE: 2002-03-01
;  PRIOR APPLICATION NUMBER: US 60/384,197
;  PRIOR FILING DATE: 2002-05-29
;  NUMBER OF SEQ ID NOS: 184
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 125
;   LENGTH: 103
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (32)..(32)
;   OTHER INFORMATION: Xaa at position 32 can be Tyr, Met, Phe, Glu, Lys, Leu, Gln, or
;   OTHER INFORMATION: Arg
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (36)..(36)
;   OTHER INFORMATION: Xaa at position 36 can be Tyr, Phe, or Met
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (43)..(43)
;   OTHER INFORMATION: Xaa at position 43 can be Tyr, Phe, His or Ala
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (49)..(50)
;   OTHER INFORMATION: Xaa at positions 49 and 50 can be Phe, Tyr or Met
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (87)..(87)
;   OTHER INFORMATION: Xaa at position 87 can be Phe, Tyr or Met
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (91)..(91)
;   OTHER INFORMATION: Xaa at position 91 can be Phe, Tyr or Trp
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (98)..(98)
;   OTHER INFORMATION: Xaa at position 98 can be Phe or Met
US-10-379-392-125

  Query Match           100.0%;  Score 112;  DB 4;  Length 103;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-08;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 11
US-10-379-392-129
; Sequence 129, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
;  APPLICANT: Lazar, Gregory Alan
;  APPLICANT:  Desjarlais, John Rudolf
;  APPLICANT:  Marshall, Shannon Alicia
;  APPLICANT:  Dahiyat, Bassil I.
;  TITLE OF INVENTION: ANTIBODY OPTIMIZATION
;  FILE REFERENCE: A-71386-3 463077-236
;  CURRENT APPLICATION NUMBER: US/10/379,392
;  CURRENT FILING DATE:  2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/360,843
;  PRIOR FILING DATE: 2002-03-01
;  PRIOR APPLICATION NUMBER: US 60/384,197
;  PRIOR FILING DATE: 2002-05-29
;  NUMBER OF SEQ ID NOS: 184
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 129
;   LENGTH: 103
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (36)..(36)
;   OTHER INFORMATION: Xaa at position 36 can be Tyr, Phe, Met or Leu
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (43)..(43)
;   OTHER INFORMATION: Xaa at position 43 can be Tyr, Phe, His, Asp, Thr, Ala, Asn or
;   OTHER INFORMATION: Ser
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (87)..(87)
;   OTHER INFORMATION: Xaa at position 87 can be Phe, Tyr or Met
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (89)..(89)
;   OTHER INFORMATION: Xaa at position 89 can be Met or Gln
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (98)..(98)
;   OTHER INFORMATION: Xaa at position 98 can be Phe or Tyr
US-10-379-392-129

  Query Match           100.0%;  Score 112;  DB 4;  Length 103;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-08;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 12
US-10-379-392-131
; Sequence 131, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
;  APPLICANT: Lazar, Gregory Alan
;  APPLICANT:  Desjarlais, John Rudolf
;  APPLICANT:  Marshall, Shannon Alicia
;  APPLICANT:  Dahiyat, Bassil I.
;  TITLE OF INVENTION: ANTIBODY OPTIMIZATION
;  FILE REFERENCE: A-71386-3 463077-236
;  CURRENT APPLICATION NUMBER: US/10/379,392
;  CURRENT FILING DATE:  2003-03-03
;  PRIOR APPLICATION NUMBER: US 60/360,843
;  PRIOR FILING DATE: 2002-03-01
;  PRIOR APPLICATION NUMBER: US 60/384,197
;  PRIOR FILING DATE: 2002-05-29
;  NUMBER OF SEQ ID NOS: 184
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;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 131
;   LENGTH: 103
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic
US-10-379-392-131

  Query Match             100.0%;  Score 112;  DB 4;  Length 103;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-08;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 13
US-09-253-794-19
; Sequence 19, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 19:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 106 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-253-794-19

  Query Match             100.0%;  Score 112;  DB 3;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-08;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 14
US-10-474-832-58
; Sequence 58, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
;  APPLICANT: BIOGEN, INC.
;  TITLE OF INVENTION: ANTIBODIES TO VLA-1
;  FILE REFERENCE: A101 PCT
;  CURRENT APPLICATION NUMBER: US/10/474,832
;  CURRENT FILING DATE:  2003-10-14
;  PRIOR APPLICATION NUMBER: 60/283,794
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/303,689
;  PRIOR FILING DATE: 2001-07-06
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
;   LENGTH: 106
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: polypeptide
US-10-474-832-58

  Query Match             100.0%;  Score 112;  DB 4;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-08;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 15
US-10-680-734-19
; Sequence 19, Application US/10680734
; Publication No. US20040191248A1
; GENERAL INFORMATION:
;  APPLICANT: GOLDENBERG, DAVID M.
;  APPLICANT:  HANSEN, HANS J.
;  TITLE OF INVENTION: ANTIBODY THERAPY
;  FILE REFERENCE: 40923-0051US5
;  CURRENT APPLICATION NUMBER: US/10/680,734
;  CURRENT FILING DATE:  2003-10-08
;  PRIOR APPLICATION NUMBER: 60/467,161
;  PRIOR FILING DATE: 2003-05-02
;  PRIOR APPLICATION NUMBER: PCT/US02/32307
;  PRIOR FILING DATE: 2002-10-11
;  PRIOR APPLICATION NUMBER: 60/416,531
;  PRIOR FILING DATE: 2002-10-08
;  NUMBER OF SEQ ID NOS: 27
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 19
;   LENGTH: 106
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-680-734-19

  Query Match             100.0%;  Score 112;  DB 4;  Length 106;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-08;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


Search completed: March 23, 2006, 01:17:11
Job time : 41.4729 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:13:29 ; Search time 5.34884 Seconds
(without alignments)
123.078 Million cell updates/sec

Title: US-10-755-382-26
Perfect score: 112
Sequence: 1 DIQLTQSPSSLSASVGDRVTITC 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	112	100.0	95	7	US-11-004-590-70	Sequence 70, Appl
2	112	100.0	95	7	US-11-004-590-71	Sequence 71, Appl
3	112	100.0	96	7	US-11-084-554-144	Sequence 144, App
4	112	100.0	96	7	US-11-084-554-147	Sequence 147, App
5	112	100.0	96	7	US-11-136-250-144	Sequence 144, App
6	112	100.0	96	7	US-11-136-250-147	Sequence 147, App
7	112	100.0	107	7	US-11-107-028-40	Sequence 40, Appl
8	112	100.0	107	7	US-11-107-028-42	Sequence 42, Appl
9	112	100.0	107	7	US-11-102-424-17	Sequence 17, Appl
10	112	100.0	110	6	US-10-648-816-2	Sequence 2, Appli
11	112	100.0	110	6	US-10-648-816-3	Sequence 3, Appli
12	112	100.0	110	6	US-10-648-816-4	Sequence 4, Appli
13	112	100.0	110	6	US-10-648-816-5	Sequence 5, Appli
14	112	100.0	110	6	US-10-648-816-6	Sequence 6, Appli
15	112	100.0	110	6	US-10-648-816-7	Sequence 7, Appli
16	112	100.0	110	6	US-10-648-816-8	Sequence 8, Appli
17	112	100.0	111	7	US-11-077-978-1	Sequence 1, Appli
18	112	100.0	114	6	US-10-923-327-1	Sequence 1, Appli
19	112	100.0	114	6	US-10-923-327-2	Sequence 2, Appli
20	112	100.0	114	6	US-10-923-327-3	Sequence 3, Appli
21	112	100.0	128	7	US-11-096-074-20	Sequence 20, Appl
22	112	100.0	128	7	US-11-095-822-20	Sequence 20, Appl
23	112	100.0	218	6	US-10-923-327-6	Sequence 6, Appli
24	112	100.0	218	6	US-10-923-327-8	Sequence 8, Appli
25	112	100.0	218	6	US-10-923-327-10	Sequence 10, Appl
26	112	100.0	218	6	US-10-923-327-12	Sequence 12, Appl
27	112	100.0	218	6	US-10-923-327-17	Sequence 17, Appl
28	112	100.0	218	7	US-11-084-554-11	Sequence 11, Appl
29	112	100.0	218	7	US-11-136-250-11	Sequence 11, Appl
30	112	100.0	248	6	US-10-923-327-15	Sequence 15, Appl
31	112	100.0	248	6	US-10-923-327-16	Sequence 16, Appl
32	112	100.0	248	7	US-11-054-515-1360	Sequence 1360, Ap
33	110	98.2	23	6	US-10-839-799-121	Sequence 121, App
34	110	98.2	23	7	US-11-105-268-39	Sequence 39, Appl
35	110	98.2	29	6	US-10-925-366A-301	Sequence 301, App
36	110	98.2	29	6	US-10-925-366A-310	Sequence 310, App
37	110	98.2	29	6	US-10-925-366A-313	Sequence 313, App
38	110	98.2	30	6	US-10-925-366A-304	Sequence 304, App
39	110	98.2	31	6	US-10-925-366A-318	Sequence 318, App
40	110	98.2	31	6	US-10-925-366A-321	Sequence 321, App
41	110	98.2	33	6	US-10-925-366A-294	Sequence 294, App
42	110	98.2	49	6	US-10-925-366A-307	Sequence 307, App
43	110	98.2	49	6	US-10-925-366A-324	Sequence 324, App
44	110	98.2	49	6	US-10-925-366A-327	Sequence 327, App
45	110	98.2	80	6	US-10-982-357-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-11-004-590-70
; Sequence 70, Application US/11004590
; Publication No. US20060008883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF
; FILE REFERENCE: 185832/US/5
; CURRENT APPLICATION NUMBER: US/11/004,590
; CURRENT FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,167
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/581,613
; PRIOR FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US 60/601,665
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US 60/619,483
; PRIOR FILING DATE: 2004-10-14
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 70
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-590-70

Query Match 100.0%; Score 112; DB 7; Length 95;
Best Local Similarity 100.0%; Pred. No. 7.1e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DIQLTQSPSSLSASVGDRVTITC 23
||||||||||||||||||||||||
Db 1 DIQLTQSPSSLSASVGDRVTITC 23

RESULT 2
US-11-004-590-71
; Sequence 71, Application US/11004590
; Publication No. US20060008883A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John R.
; APPLICANT: Hammond, Phillip W.
; TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
; TITLE OF INVENTION: CONTENT AND COMPOSITIONS THEREOF

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;  FILE REFERENCE: 185832/US/5
;  CURRENT APPLICATION NUMBER: US/11/004,590
;  CURRENT FILING DATE:  2004-12-03
;  PRIOR APPLICATION NUMBER: US 60/527,167
;  PRIOR FILING DATE: 2003-12-04
;  PRIOR APPLICATION NUMBER: US 60/581,613
;  PRIOR FILING DATE: 2004-06-21
;  PRIOR APPLICATION NUMBER: US 60/601,665
;  PRIOR FILING DATE: 2004-08-13
;  PRIOR APPLICATION NUMBER: US 60/619,483
;  PRIOR FILING DATE: 2004-10-14
;  NUMBER OF SEQ ID NOS: 458
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 71
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-004-590-71

  Query Match            100.0%;  Score 112;  DB 7;  Length 95;
  Best Local Similarity  100.0%;  Pred. No. 7.1e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 3
US-11-084-554-144
; Sequence 144, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 144
;   LENGTH: 96
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-144

  Query Match            100.0%;  Score 112;  DB 7;  Length 96;
  Best Local Similarity  100.0%;  Pred. No. 7.1e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 4
US-11-084-554-147
; Sequence 147, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 147
;   LENGTH: 96
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-147

  Query Match            100.0%;  Score 112;  DB 7;  Length 96;
  Best Local Similarity  100.0%;  Pred. No. 7.1e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 5
US-11-136-250-144
; Sequence 144, Application US/11136250
; Publication No. US20060021074A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A2
;  CURRENT APPLICATION NUMBER: US/11/136,250
;  CURRENT FILING DATE:  2005-05-23
;  PRIOR APPLICATION NUMBER: 11/084,554
;  PRIOR FILING DATE: 2005-03-17
;  PRIOR APPLICATION NUMBER: PCT/US2005/009306
;  PRIOR FILING DATE: 2005-03-17
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 144
;   LENGTH: 96
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-136-250-144

  Query Match            100.0%;  Score 112;  DB 7;  Length 96;
  Best Local Similarity  100.0%;  Pred. No. 7.1e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 6
US-11-136-250-147
; Sequence 147, Application US/11136250
; Publication No. US20060021074A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A2
;  CURRENT APPLICATION NUMBER: US/11/136,250
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;  CURRENT FILING DATE:  2005-05-23
;  PRIOR APPLICATION NUMBER: 11/084,554
;  PRIOR FILING DATE: 2005-03-17
;  PRIOR APPLICATION NUMBER: PCT/US2005/009306
;  PRIOR FILING DATE: 2005-03-17
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 147
;    LENGTH: 96
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-11-136-250-147

  Query Match             100.0%;  Score 112;  DB 7;  Length 96;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 7
US-11-107-028-40
; Sequence 40, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
;  APPLICANT: CHAN, ANDREW C.
;  APPLICANT:  GONG, QIAN
;  APPLICANT:  MARTIN, FLAVIUS
;  TITLE OF INVENTION: Method for Augmenting B Cell Depletion
;  FILE REFERENCE: P2112R1
;  CURRENT APPLICATION NUMBER: US/11/107,028
;  CURRENT FILING DATE:  2005-04-15
;  PRIOR APPLICATION NUMBER: US 60/563,263
;  PRIOR FILING DATE: 2004-04-16
;  NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 40
;    LENGTH: 107
;    TYPE: PRT
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: sequence is synthesized
US-11-107-028-40

  Query Match             100.0%;  Score 112;  DB 7;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 8e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 8
US-11-107-028-42
; Sequence 42, Application US/11107028
; Publication No. US20050276803A1
; GENERAL INFORMATION:
;  APPLICANT: CHAN, ANDREW C.
;  APPLICANT:  GONG, QIAN
;  APPLICANT:  MARTIN, FLAVIUS
;  TITLE OF INVENTION: Method for Augmenting B Cell Depletion
;  FILE REFERENCE: P2112R1
;  CURRENT APPLICATION NUMBER: US/11/107,028
;  CURRENT FILING DATE:  2005-04-15
;  PRIOR APPLICATION NUMBER: US 60/563,263
;  PRIOR FILING DATE: 2004-04-16
;  NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 42
;    LENGTH: 107
;    TYPE: PRT
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: sequence is synthesized
US-11-107-028-42

  Query Match             100.0%;  Score 112;  DB 7;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 8e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 9
US-11-102-424-17
; Sequence 17, Application US/11102424
; Publication No. US20060018902A1
; GENERAL INFORMATION:
;  APPLICANT: Abbott Laboratories
;  APPLICANT:  Reilly, Edward B.
;  APPLICANT:  Lacy, Susan E.
;  APPLICANT:  Fung, Emma
;  APPLICANT:  Belk, Johathan P.
;  APPLICANT:  Roguska, Michael
;  TITLE OF INVENTION: Antibodies To Erythropoietin Receptor
;  TITLE OF INVENTION:  And Uses Thereof
;  FILE REFERENCE: 7349USO2
;  CURRENT APPLICATION NUMBER: US/11/102,424
;  CURRENT FILING DATE:  2005-04-08
;  PRIOR APPLICATION NUMBER: 60/561,084
;  PRIOR FILING DATE: 2004-04-09
;  PRIOR APPLICATION NUMBER: 60/561,313
;  PRIOR FILING DATE: 2004-04-12
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;    LENGTH: 107
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-11-102-424-17

  Query Match             100.0%;  Score 112;  DB 7;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 8e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 10
US-10-648-816-2
; Sequence 2, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
;  APPLICANT: Van Bruggen, Nicholas
;  APPLICANT:  Ferrara, Napoleone
;  TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
;  TITLE OF INVENTION:  and Uses Thereof
;  FILE REFERENCE: P1717D1
;  CURRENT APPLICATION NUMBER: US/10/648,816
;  CURRENT FILING DATE:  2003-08-26
;  PRIOR APPLICATION NUMBER: US/09/718,694
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: US 09/218,481
;  PRIOR FILING DATE: 1998-12-22
;  NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 2
;    LENGTH: 110
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;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-648-816-2

  Query Match             100.0%;  Score 112;  DB 6;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 11
US-10-648-816-3
; Sequence 3, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
;  APPLICANT: Van Bruggen, Nicholas
;  APPLICANT:  Ferrara, Napoleone
;  TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
;  TITLE OF INVENTION:  and Uses Thereof
;  FILE REFERENCE: P1717D1
;  CURRENT APPLICATION NUMBER: US/10/648,816
;  CURRENT FILING DATE:  2003-08-26
;  PRIOR APPLICATION NUMBER: US/09/718,694
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: US 09/218,481
;  PRIOR FILING DATE: 1998-12-22
;  NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 3
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-648-816-3

  Query Match             100.0%;  Score 112;  DB 6;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 12
US-10-648-816-4
; Sequence 4, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
;  APPLICANT: Van Bruggen, Nicholas
;  APPLICANT:  Ferrara, Napoleone
;  TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
;  TITLE OF INVENTION:  and Uses Thereof
;  FILE REFERENCE: P1717D1
;  CURRENT APPLICATION NUMBER: US/10/648,816
;  CURRENT FILING DATE:  2003-08-26
;  PRIOR APPLICATION NUMBER: US/09/718,694
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: US 09/218,481
;  PRIOR FILING DATE: 1998-12-22
;  NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 4
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-648-816-4

  Query Match             100.0%;  Score 112;  DB 6;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 13
US-10-648-816-5
; Sequence 5, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
;  APPLICANT: Van Bruggen, Nicholas
;  APPLICANT:  Ferrara, Napoleone
;  TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
;  TITLE OF INVENTION:  and Uses Thereof
;  FILE REFERENCE: P1717D1
;  CURRENT APPLICATION NUMBER: US/10/648,816
;  CURRENT FILING DATE:  2003-08-26
;  PRIOR APPLICATION NUMBER: US/09/718,694
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: US 09/218,481
;  PRIOR FILING DATE: 1998-12-22
;  NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 5
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-648-816-5

  Query Match             100.0%;  Score 112;  DB 6;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 14
US-10-648-816-6
; Sequence 6, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
;  APPLICANT: Van Bruggen, Nicholas
;  APPLICANT:  Ferrara, Napoleone
;  TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
;  TITLE OF INVENTION:  and Uses Thereof
;  FILE REFERENCE: P1717D1
;  CURRENT APPLICATION NUMBER: US/10/648,816
;  CURRENT FILING DATE:  2003-08-26
;  PRIOR APPLICATION NUMBER: US/09/718,694
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: US 09/218,481
;  PRIOR FILING DATE: 1998-12-22
;  NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 6
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-648-816-6

  Query Match             100.0%;  Score 112;  DB 6;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


RESULT 15
US-10-648-816-7
; Sequence 7, Application US/10648816
; Publication No. US20050244405A1
; GENERAL INFORMATION:
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;  APPLICANT: Van Bruggen, Nicholas
;  APPLICANT:  Ferrara, Napoleone
;  TITLE OF INVENTION: Vascular Endothelial Cell Growth Factor Antagonists
;  TITLE OF INVENTION:  and Uses Thereof
;  FILE REFERENCE: P1717D1
;  CURRENT APPLICATION NUMBER: US/10/648,816
;  CURRENT FILING DATE:  2003-08-26
;  PRIOR APPLICATION NUMBER: US/09/718,694
;  PRIOR FILING DATE: 2000-11-21
;  PRIOR APPLICATION NUMBER: US 09/218,481
;  PRIOR FILING DATE: 1998-12-22
;  NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 7
;   LENGTH: 110
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-648-816-7

  Query Match            100.0%;  Score 112;  DB 6;  Length 110;
  Best Local Similarity  100.0%;  Pred. No. 8.2e-09;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DIQLTQSPSSLSASVGDRVTITC 23
              |||||||||||||||||||||||
Db          1 DIQLTQSPSSLSASVGDRVTITC 23


Search completed: March 23, 2006, 01:17:45
Job time : 5.34884 secs
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:40:10 ; Search time 130.479 Seconds
(without alignments)
50.511 Million cell updates/sec

Title: US-10-755-382-27
Perfect score: 86
Sequence: 1 WYQQKPGKAPKLLIY 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	86	100.0	15	2	AAR27042	Aar27042 Human lig
2	86	100.0	15	2	AAR77205	Aar77205 Mouse ant
3	86	100.0	15	2	AAR97320	Aar97320 Humanised
4	86	100.0	15	2	AAR87042	Aar87042 Human gro
5	86	100.0	15	2	AAY52742	Aay52742 Humanised
6	86	100.0	15	4	AAB98279	Aab98279 Anti-A33
7	86	100.0	15	4	AAB98280	Aab98280 Anti-A33
8	86	100.0	15	4	AAB97660	Aab97660 A33 antig
9	86	100.0	15	4	AAB97659	Aab97659 A33 antig
10	86	100.0	15	5	AAE19670	Aae19670 Human gro
11	86	100.0	15	5	AAU70395	Aau70395 Human lig
12	86	100.0	15	8	ADO60478	Ado60478 Humanised
13	86	100.0	15	8	ADR38844	Adr38844 Mouse lig
14	86	100.0	15	8	ADU07265	Adu07265 IL-9 anti
15	86	100.0	15	8	ADT88332	Adt88332 Human IL-
16	86	100.0	15	8	ADU38487	Adu38487 Mouse ant
17	86	100.0	15	9	ADX27016	Adx27016 Human gro
18	86	100.0	15	9	ADY31248	Ady31248 Human ant
19	86	100.0	15	9	ADY31272	Ady31272 Human ant
20	86	100.0	15	9	ADY31299	Ady31299 Human ant
21	86	100.0	15	9	ADY31245	Ady31245 Human ant
22	86	100.0	15	9	ADY31233	Ady31233 Human ant
23	86	100.0	15	9	ADY31278	Ady31278 Human ant
24	86	100.0	15	9	ADY31230	Ady31230 Human ant
25	86	100.0	15	9	ADY31269	Ady31269 Human ant
26	86	100.0	15	9	ADY31290	Ady31290 Human ant
27	86	100.0	15	9	ADY31305	Ady31305 Human ant
28	86	100.0	15	9	ADY31296	Ady31296 Human ant
29	86	100.0	15	9	ADY31281	Ady31281 Human ant
30	86	100.0	15	9	AEA45521	Aea45521 Apolipopr
31	86	100.0	15	9	AEA22625	Aea22625 Synthetic
32	86	100.0	15	9	AEB00046	Aeb00046 Novel den
33	86	100.0	15	9	AEB00158	Aeb00158 Novel den
34	86	100.0	15	9	AEB00110	Aeb00110 Novel den
35	86	100.0	15	9	AEB00014	Aeb00014 Novel den
36	86	100.0	15	9	AEB00174	Aeb00174 Novel den
37	86	100.0	15	9	AEB24630	Aeb24630 Humanized
38	86	100.0	38	5	ABG98283	Abg98283 Human ant
39	86	100.0	40	3	AAB03708	Aab03708 Immunoglo
40	86	100.0	40	7	ADB72869	Adb72869 Human AAA
41	86	100.0	52	9	AEC20827	Aec20827 Human var
42	86	100.0	57	9	AEC20823	Aec20823 Human var
43	86	100.0	70	7	ABG75305	Abg75305 Human sub
44	86	100.0	70	8	ABM79517	Abm79517 Human DPK
45	86	100.0	71	8	ADU04182	Adu04182 Unidentif
46	86	100.0	72	8	ADU04131	Adu04131 Human imm
47	86	100.0	73	9	ADZ08785	Adz08785 Mammalian
48	86	100.0	73	9	AEA16517	Aea16517 Human MCP
49	86	100.0	73	9	AEB72752	Aeb72752 Anti-LTal
50	86	100.0	74	2	AAW62805	Aaw62805 Amino aci
51	86	100.0	75	2	AAW62802	Aaw62802 Amino aci
52	86	100.0	75	2	AAW62818	Aaw62818 Amino aci
53	86	100.0	76	2	AAW80981	Aaw80981 Variable
54	86	100.0	76	2	AAW80980	Aaw80980 Variable
55	86	100.0	76	6	ABO04825	Abo04825 Human epi
56	86	100.0	76	6	ABO04843	Abo04843 Human epi
57	86	100.0	76	9	AEA17738	Aea17738 Hybridoma
58	86	100.0	76	9	AEA17737	Aea17737 Hybridoma
59	86	100.0	79	8	ADL35149	Adl35149 CEA4-8A a
60	86	100.0	80	8	ADK51434	Adk51434 Human ant
61	86	100.0	80	8	ADK51399	Adk51399 Human ant
62	86	100.0	80	8	ADK51400	Adk51400 Human ant
63	86	100.0	80	8	ADK51401	Adk51401 Human ant
64	86	100.0	80	8	ADK51440	Adk51440 Human ant
65	86	100.0	80	8	ADK51441	Adk51441 Human ant
66	86	100.0	80	8	ADK51442	Adk51442 Human ant
67	86	100.0	80	8	ADL35157	Adl35157 Framework
68	86	100.0	80	8	ADU97910	Adu97910 Amino aci
69	86	100.0	80	9	AEA40691	Aea40691 Anti-VEGF
70	86	100.0	80	9	AEA40693	Aea40693 Anti-VEGF
71	86	100.0	80	9	AEA40688	Aea40688 Anti-VEGF
72	86	100.0	80	9	AEB26568	Aeb26568 Human ant
73	86	100.0	81	6	ABO27276	Abo27276 Human Hum
74	86	100.0	85	2	AAR06351	Aar06351 M13 VKPCR
75	86	100.0	86	2	AAY39533	Aay39533 Humanised
76	86	100.0	86	5	ABB83945	Abb83945 Humanised
77	86	100.0	86	6	ABG75598	Abg75598 REI frame
78	86	100.0	88	2	AAW59619	Aaw59619 Anti-RSV
79	86	100.0	88	3	AAY56654	Aay56654 Partial p
80	86	100.0	88	3	AAY56658	Aay56658 Partial p
81	86	100.0	88	3	AAY56672	Aay56672 Partial p
82	86	100.0	88	3	AAY56659	Aay56659 Partial p
83	86	100.0	88	3	AAY56652	Aay56652 Partial p
84	86	100.0	88	8	ADU04217	Adu04217 Human imm
85	86	100.0	88	9	ADY54719	Ady54719 Human V k
86	86	100.0	90	3	AAY71451	Aay71451 Human mod
87	86	100.0	90	3	AAB19753	Aab19753 Human lig
88	86	100.0	90	4	ABB19441	Abb19441 Protein #
89	86	100.0	90	4	AAM67153	Aam67153 Human bon
90	86	100.0	90	4	AAM54766	Aam54766 Human bra
91	86	100.0	90	4	ABG48819	Abg48819 Human liv
92	86	100.0	90	4	AAM02744	Aam02744 Peptide #
93	86	100.0	90	5	ABG36817	Abg36817 Human pep
94	86	100.0	91	8	ADL70194	Adl70194 Gonadotro
95	86	100.0	92	7	ADC99831	Adc99831 Anti-huma
96	86	100.0	92	7	ADD05435	Add05435 Anti-MUC1
97	86	100.0	92	7	ADF09873	Adf09873 Anti-MUC1

98	86	100.0	92	8	ADR72718	Adr72718 Human mon
99	86	100.0	93	7	ADC99815	Adc99815 Anti-huma
100	86	100.0	93	7	ADD05419	Add05419 Anti-MUC1
101	86	100.0	93	7	ADF09857	Adf09857 Anti-MUC1
102	86	100.0	93	9	ADW24717	Adw24717 Variable
103	86	100.0	93	9	ADZ44441	Adz44441 Human imm
104	86	100.0	95	2	AAR57478	Aar57478 Human K10
105	86	100.0	95	2	AAR72064	Aar72064 OF7K.17 V
106	86	100.0	95	2	AAR72065	Aar72065 S43434 VK
107	86	100.0	95	2	AAR72058	Aar72058 KL012 VK
108	86	100.0	95	2	AAR92081	Aar92081 Human K10
109	86	100.0	95	5	ABG31428	Abg31428 Amino aci
110	86	100.0	95	6	AAE35900	Aae35900 Human 012
111	86	100.0	95	6	ABJ18693	Abj18693 Antibody
112	86	100.0	95	6	ABO27123	Abo27123 Human ger
113	86	100.0	95	6	ABO27138	Abo27138 Human ger
114	86	100.0	95	6	ABO27134	Abo27134 Human ger
115	86	100.0	95	6	ABO27122	Abo27122 Human ger
116	86	100.0	95	6	ABO27130	Abo27130 Human ger
117	86	100.0	95	6	ABO27121	Abo27121 Human ger
118	86	100.0	95	6	ABO27132	Abo27132 Human ger
119	86	100.0	95	6	ABO27124	Abo27124 Human ger
120	86	100.0	95	6	ABO27131	Abo27131 Human ger
121	86	100.0	95	6	ABO27139	Abo27139 Human ger
122	86	100.0	95	6	ABO27136	Abo27136 Human ger
123	86	100.0	95	6	ABO27133	Abo27133 Human ger
124	86	100.0	95	7	ADB75645	Adb75645 Human pro
125	86	100.0	95	7	ADC99830	Adc99830 Germline
126	86	100.0	95	7	ADC99814	Adc99814 Germline
127	86	100.0	95	7	ADD05418	Add05418 Anti-MUC1
128	86	100.0	95	7	ADD05434	Add05434 Anti-MUC1
129	86	100.0	95	7	ADF09954	Adf09954 Antibody
130	86	100.0	95	7	ADF09955	Adf09955 Antibody
131	86	100.0	95	7	ADF10077	Adf10077 VEGF anti
132	86	100.0	95	7	ADF10161	Adf10161 Antibody
133	86	100.0	95	7	ADF10073	Adf10073 VEGF anti
134	86	100.0	95	7	ADF10162	Adf10162 Antibody
135	86	100.0	95	7	ADF09960	Adf09960 Antibody
136	86	100.0	95	7	ADF09961	Adf09961 Antibody
137	86	100.0	95	7	ADF09968	Adf09968 Antibody
138	86	100.0	95	7	ADF10163	Adf10163 Antibody
139	86	100.0	95	7	ADF10166	Adf10166 Antibody
140	86	100.0	95	7	ADF10176	Adf10176 Antibody
141	86	100.0	95	7	ADF09973	Adf09973 Antibody
142	86	100.0	95	7	ADF10059	Adf10059 VEGF anti
143	86	100.0	95	7	ADF10168	Adf10168 Antibody
144	86	100.0	95	7	ADF10179	Adf10179 Antibody
145	86	100.0	95	7	ADF09956	Adf09956 Antibody
146	86	100.0	95	7	ADF10064	Adf10064 VEGF anti
147	86	100.0	95	7	ADF10078	Adf10078 VEGF anti
148	86	100.0	95	7	ADF10165	Adf10165 Antibody
149	86	100.0	95	7	ADF09959	Adf09959 Antibody
150	86	100.0	95	7	ADF10061	Adf10061 VEGF anti
151	86	100.0	95	7	ADF10067	Adf10067 VEGF anti
152	86	100.0	95	7	ADF09962	Adf09962 Antibody
153	86	100.0	95	7	ADF10169	Adf10169 Antibody
154	86	100.0	95	7	ADF09972	Adf09972 Antibody
155	86	100.0	95	7	ADF10060	Adf10060 VEGF anti
156	86	100.0	95	7	ADF10066	Adf10066 VEGF anti
157	86	100.0	95	7	ADF10074	Adf10074 VEGF anti
158	86	100.0	95	7	ADF09958	Adf09958 Antibody
159	86	100.0	95	7	ADF10180	Adf10180 Antibody
160	86	100.0	95	7	ADF10065	Adf10065 VEGF anti
161	86	100.0	95	7	ADF10167	Adf10167 Antibody
162	86	100.0	95	7	ADF09969	Adf09969 Antibody
163	86	100.0	95	7	ADF10175	Adf10175 Antibody
164	86	100.0	95	7	ADF10063	Adf10063 VEGF anti
165	86	100.0	95	7	ADF09872	Adf09872 Anti-MUC1
166	86	100.0	95	7	ADF09856	Adf09856 Anti-MUC1
167	86	100.0	95	7	ADK18935	Adk18935 Anti-huma
168	86	100.0	95	7	ADK18583	Adk18583 Anti-huma
169	86	100.0	95	7	ADK18934	Adk18934 Anti-huma
170	86	100.0	95	7	ADJ80252	Adj80252 Vkappa ge
171	86	100.0	95	7	ADJ80242	Adj80242 Vkappa ge
172	86	100.0	95	7	ADJ80256	Adj80256 Vkappa ge
173	86	100.0	95	7	ADJ80258	Adj80258 Vkappa ge
174	86	100.0	95	7	ADJ80253	Adj80253 Vkappa ge
175	86	100.0	95	7	ADJ80244	Adj80244 Vkappa ge
176	86	100.0	95	7	ADJ80241	Adj80241 Vkappa ge
177	86	100.0	95	7	ADJ80251	Adj80251 Vkappa ge
178	86	100.0	95	7	ADJ80243	Adj80243 Vkappa ge
179	86	100.0	95	7	ADJ80250	Adj80250 Vkappa ge
180	86	100.0	95	7	ADJ80254	Adj80254 Vkappa ge
181	86	100.0	95	7	ADJ80259	Adj80259 Vkappa ge
182	86	100.0	95	7	ADP03925	Adp03925 Murine-ex
183	86	100.0	95	7	ADP03919	Adp03919 Murine-ex
184	86	100.0	95	8	ADO07313	Ado07313 Human ant
185	86	100.0	95	8	ADO07319	Ado07319 Human ant
186	86	100.0	95	8	ADO07321	Ado07321 Human ant
187	86	100.0	95	8	ADO07327	Ado07327 Human ant
188	86	100.0	95	8	ADO07323	Ado07323 Human ant
189	86	100.0	95	8	ADO07312	Ado07312 Human ant
190	86	100.0	95	8	ADO07322	Ado07322 Human ant
191	86	100.0	95	8	ADO07320	Ado07320 Human ant
192	86	100.0	95	8	ADO07325	Ado07325 Human ant
193	86	100.0	95	8	ADO07328	Ado07328 Human ant
194	86	100.0	95	8	ADO07310	Ado07310 Human ant
195	86	100.0	95	8	ADO07311	Ado07311 Human ant
196	86	100.0	95	8	ADO36510	Ado36510 Human ant
197	86	100.0	95	8	ADU86533	Adu86533 Immunoglo
198	86	100.0	95	8	ADU86534	Adu86534 Immunoglo
199	86	100.0	95	8	ADU86528	Adu86528 Immunoglo
200	86	100.0	95	8	ADU86532	Adu86532 Immunoglo
201	86	100.0	95	9	ADY54709	Ady54709 Human V k
202	86	100.0	95	9	ADY54710	Ady54710 Human V k
203	86	100.0	95	9	ADY54711	Ady54711 Human V k
204	86	100.0	95	9	ADY75433	Ady75433 Human ger
205	86	100.0	95	9	ADY75428	Ady75428 Human ger
206	86	100.0	95	9	ADY75416	Ady75416 Human ger
207	86	100.0	95	9	ADY75427	Ady75427 Human ger
208	86	100.0	95	9	ADY75418	Ady75418 Human ger
209	86	100.0	95	9	ADY75426	Ady75426 Human ger
210	86	100.0	95	9	ADY75424	Ady75424 Human ger
211	86	100.0	95	9	ADY75425	Ady75425 Human ger
212	86	100.0	95	9	ADY75430	Ady75430 Human ger
213	86	100.0	95	9	ADY75417	Ady75417 Human ger
214	86	100.0	95	9	ADY75432	Ady75432 Human ger
215	86	100.0	95	9	ADY75415	Ady75415 Human ger
216	86	100.0	95	9	ADZ47744	Adz47744 Human ger
217	86	100.0	95	9	AEA53913	Aea53913 Novel hum
218	86	100.0	95	9	AEA53904	Aea53904 Novel hum
219	86	100.0	95	9	AEA53925	Aea53925 Novel hum
220	86	100.0	95	9	AEA53979	Aea53979 Novel hum
221	86	100.0	95	9	AEA53988	Aea53988 Novel hum
222	86	100.0	95	9	AEA53916	Aea53916 Novel hum
223	86	100.0	95	9	AEA53961	Aea53961 Novel hum
224	86	100.0	95	9	AEA53973	Aea53973 Novel hum
225	86	100.0	95	9	AEB13615	Aeb13615 Human var
226	86	100.0	95	9	AEB13614	Aeb13614 Human var
227	86	100.0	95	9	AEB13616	Aeb13616 Human var
228	86	100.0	95	9	AEB13567	Aeb13567 Human var
229	86	100.0	95	9	AEB13628	Aeb13628 Human var
230	86	100.0	95	9	AEB13568	Aeb13568 Human var
231	86	100.0	95	9	AEB13621	Aeb13621 Human var
232	86	100.0	95	9	AEB13562	Aeb13562 Human var
233	86	100.0	95	9	AEB13618	Aeb13618 Human var
234	86	100.0	95	9	AEB13579	Aeb13579 Human var
235	86	100.0	95	9	AEB13619	Aeb13619 Human var
236	86	100.0	95	9	AEB13622	Aeb13622 Human var
237	86	100.0	95	9	AEB13576	Aeb13576 Human var
238	86	100.0	95	9	AEB13580	Aeb13580 Human var
239	86	100.0	95	9	AEB13569	Aeb13569 Human var
240	86	100.0	95	9	AEB13632	Aeb13632 Human var
241	86	100.0	95	9	AEB13633	Aeb13633 Human var
242	86	100.0	95	9	AEB13563	Aeb13563 Human var
243	86	100.0	95	9	AEB13565	Aeb13565 Human var

244	86	100.0	95	9	AEB13575	Aeb13575	Human var
245	86	100.0	95	9	AEB13620	Aeb13620	Human var
246	86	100.0	95	9	AEB13561	Aeb13561	Human var
247	86	100.0	95	9	AEB13566	Aeb13566	Human var
248	86	100.0	95	9	AEB13629	Aeb13629	Human var
249	86	100.0	95	9	AEC20816	Aec20816	Human var
250	86	100.0	96	5	ABG77155	Abg77155	Germline
251	86	100.0	96	8	ADR28576	Adr28576	Human ant
252	86	100.0	96	9	AEA53877	Aea53877	Novel hum
253	86	100.0	96	9	AEA53937	Aea53937	Novel hum
254	86	100.0	96	9	AEA53985	Aea53985	Novel hum
255	86	100.0	96	9	AEA53964	Aea53964	Novel hum
256	86	100.0	96	9	AEA53996	Aea53996	Novel hum
257	86	100.0	97	9	AEA53919	Aea53919	Novel hum
258	86	100.0	98	8	ADQ75211	Adq75211	Immunoglo
259	86	100.0	98	9	ADY31694	Ady31694	Anti-huma
260	86	100.0	100	8	ADR72751	Adr72751	Human mon
261	86	100.0	100	9	AEB01069	Aeb01069	Human lig
262	86	100.0	101	2	AAR22577	Aar22577	Light cha
263	86	100.0	101	7	ADL91311	Adl91311	VL chain
264	86	100.0	101	8	ADO36338	Ado36338	Intracell
265	86	100.0	102	3	AAY71446	Aay71446	Humanised
266	86	100.0	102	3	AAY71454	Aay71454	Humanised
267	86	100.0	102	4	AAB62264	Aab62264	Light cha
268	86	100.0	102	6	AAE38330	Aae38330	Human ant
269	86	100.0	102	9	ADY33965	Ady33965	Anti-Tie
270	86	100.0	103	7	ADF09997	Adf09997	Antibody
271	86	100.0	103	7	ADF10201	Adf10201	Antibody
272	86	100.0	103	7	ADF09994	Adf09994	Antibody
273	86	100.0	103	8	ADU04120	Adu04120	Human imm
274	86	100.0	104	2	AAR54318	Aar54318	Anti-HIV
275	86	100.0	104	2	AAW01285	Aaw01285	VL region
276	86	100.0	104	2	AAW52225	Aaw52225	Antibody
277	86	100.0	104	2	AAW62821	Aaw62821	Amino aci
278	86	100.0	104	3	AAY98246	Aay98246	Anti-gp12
279	86	100.0	104	3	AAY95137	Aay95137	Anti-gp12
280	86	100.0	104	5	AAO18425	Aao18425	Anti-GD2
281	86	100.0	104	6	ABR41821	Abr41821	Light cha
282	86	100.0	104	8	ADL11895	Adl11895	CDR trans
283	86	100.0	104	8	ADL11896	Adl11896	CDR trans
284	86	100.0	104	9	ADZ58537	Adz58537	VEGF rece
285	86	100.0	104	9	ADZ58541	Adz58541	VEGF rece
286	86	100.0	105	2	AAR88717	Aar88717	Human ant
287	86	100.0	105	2	AAW52239	Aaw52239	Antibody
288	86	100.0	105	2	AAW52237	Aaw52237	Antibody
289	86	100.0	105	2	AAW80978	Aaw80978	Kappa lig
290	86	100.0	105	2	AAW80968	Aaw80968	Kappa lig
291	86	100.0	105	3	AAY71455	Aay71455	Humanised
292	86	100.0	105	5	AAO18424	Aao18424	Anti-GD2
293	86	100.0	105	6	ABR54905	Abr54905	Light cha
294	86	100.0	105	6	ABO04842	Abo04842	Human epi
295	86	100.0	105	6	ABO04831	Abo04831	Human epi
296	86	100.0	105	7	ADP03985	Adp03985	Murine-ex
297	86	100.0	105	9	AEA17755	Aea17755	Hybridoma
298	86	100.0	105	9	AEA17745	Aea17745	Hybridoma
299	86	100.0	106	2	AAR25727	Aar25727	Humanised
300	86	100.0	106	2	AAR88847	Aar88847	Human ant
301	86	100.0	106	2	AAR97337	Aar97337	Humanised
302	86	100.0	106	2	AAR90686	Aar90686	Humanized
303	86	100.0	106	2	AAW58512	Aaw58512	Protein S
304	86	100.0	106	2	AAW52221	Aaw52221	Antibody
305	86	100.0	106	2	AAW52213	Aaw52213	Antibody
306	86	100.0	106	2	AAW37813	Aaw37813	Humanized
307	86	100.0	106	4	AAE10473	Aae10473	Humanised
308	86	100.0	106	4	AAE10507	Aae10507	Humanised
309	86	100.0	106	4	AAE10475	Aae10475	Humanised
310	86	100.0	106	4	AAB62754	Aab62754	Human HIV
311	86	100.0	106	4	AAG63262	Aag63262	Anti-RSV
312	86	100.0	106	4	AAG63258	Aag63258	Anti-RSV
313	86	100.0	106	4	AAG63264	Aag63264	Anti-RSV
314	86	100.0	106	4	AAG63266	Aag63266	Anti-RSV
315	86	100.0	106	4	AAG63260	Aag63260	Anti-RSV
316	86	100.0	106	4	AAG63242	Aag63242	Mouse ant
317	86	100.0	106	4	AAB69674	Aab69674	Humanised
318	86	100.0	106	4	AAB69658	Aab69658	Human Lay
319	86	100.0	106	4	AAB69647	Aab69647	Humanised
320	86	100.0	106	5	ABP66375	Abp66375	Human RSV
321	86	100.0	106	5	ABP66406	Abp66406	Human RSV
322	86	100.0	106	5	ABP66418	Abp66418	Human RSV
323	86	100.0	106	5	ABP66392	Abp66392	Human RSV
324	86	100.0	106	5	ABP66403	Abp66403	Human RSV
325	86	100.0	106	5	ABP66388	Abp66388	Human RSV
326	86	100.0	106	5	ABP66400	Abp66400	Human RSV
327	86	100.0	106	5	ABP66424	Abp66424	Human RSV
328	86	100.0	106	5	ABP66430	Abp66430	Human RSV
329	86	100.0	106	5	ABP66362	Abp66362	Human RSV
330	86	100.0	106	5	ABP66367	Abp66367	Human RSV
331	86	100.0	106	5	ABP66416	Abp66416	Human RSV
332	86	100.0	106	5	ABP66419	Abp66419	Human RSV
333	86	100.0	106	5	ABP66410	Abp66410	Human RSV
334	86	100.0	106	5	ABP66414	Abp66414	Human RSV
335	86	100.0	106	5	ABP66384	Abp66384	Human RSV
336	86	100.0	106	5	ABP66408	Abp66408	Human RSV
337	86	100.0	106	5	ABP66380	Abp66380	Human RSV
338	86	100.0	106	5	ABP66396	Abp66396	Human RSV
339	86	100.0	106	5	ABP66411	Abp66411	Human RSV
340	86	100.0	106	5	ABP66428	Abp66428	Human RSV
341	86	100.0	106	5	ABP66425	Abp66425	Human RSV
342	86	100.0	106	5	ABP66422	Abp66422	Human RSV
343	86	100.0	106	5	ABP66365	Abp66365	Human RSV
344	86	100.0	106	5	ABP66413	Abp66413	Human RSV
345	86	100.0	106	5	AAU99526	Aau99526	Humanised
346	86	100.0	106	5	AAU99519	Aau99519	Humanised
347	86	100.0	106	5	AAU99524	Aau99524	Humanised
348	86	100.0	106	5	AAU99523	Aau99523	Humanised
349	86	100.0	106	5	ABG30450	Abg30450	Human IgE
350	86	100.0	106	5	AAE28047	Aae28047	Human mod
351	86	100.0	106	5	AAE28071	Aae28071	Human mod
352	86	100.0	106	5	AAE28073	Aae28073	Human mod
353	86	100.0	106	5	AAE28065	Aae28065	Human mod
354	86	100.0	106	5	AAE28051	Aae28051	Human mod
355	86	100.0	106	5	AAE28074	Aae28074	Human mod
356	86	100.0	106	5	AAE28080	Aae28080	Human mod
357	86	100.0	106	5	AAE28017	Aae28017	Human mod
358	86	100.0	106	5	AAE28035	Aae28035	Human mod
359	86	100.0	106	5	AAE28055	Aae28055	Human mod
360	86	100.0	106	5	AAE28058	Aae28058	Human mod
361	86	100.0	106	5	AAE28061	Aae28061	Human mod
362	86	100.0	106	5	AAE28020	Aae28020	Human mod
363	86	100.0	106	5	AAE28077	Aae28077	Human mod
364	86	100.0	106	5	AAE28063	Aae28063	Human mod
365	86	100.0	106	5	AAE28083	Aae28083	Human mod
366	86	100.0	106	5	AAE28022	Aae28022	Human mod
367	86	100.0	106	5	AAE28043	Aae28043	Human mod
368	86	100.0	106	5	AAE28068	Aae28068	Human mod
369	86	100.0	106	5	AAE28069	Aae28069	Human mod
370	86	100.0	106	5	AAE28079	Aae28079	Human mod
371	86	100.0	106	5	AAE28030	Aae28030	Human mod
372	86	100.0	106	5	AAE28085	Aae28085	Human mod
373	86	100.0	106	5	AAE28039	Aae28039	Human mod
374	86	100.0	106	5	AAE28066	Aae28066	Human mod
375	86	100.0	106	6	ABU69247	Abu69247	Respirato
376	86	100.0	106	6	ABU69263	Abu69263	Respirato
377	86	100.0	106	6	ABU69288	Abu69288	Respirato
378	86	100.0	106	6	ABU69293	Abu69293	Respirato
379	86	100.0	106	6	ABU69228	Abu69228	Respirato
380	86	100.0	106	6	ABU69266	Abu69266	Respirato
381	86	100.0	106	6	ABU69277	Abu69277	Respirato
382	86	100.0	106	6	ABU69255	Abu69255	Respirato
383	86	100.0	106	6	ABU69282	Abu69282	Respirato
384	86	100.0	106	6	ABU69287	Abu69287	Respirato
385	86	100.0	106	6	ABU69238	Abu69238	Respirato
386	86	100.0	106	6	ABU69259	Abu69259	Respirato
387	86	100.0	106	6	ABU69279	Abu69279	Respirato
388	86	100.0	106	6	ABU69225	Abu69225	Respirato
389	86	100.0	106	6	ABU69274	Abu69274	Respirato

390	86	100.0	106	6	ABU69281	Abu69281 Respirato
391	86	100.0	106	6	ABU69251	Abu69251 Respirato
392	86	100.0	106	6	ABU69271	Abu69271 Respirato
393	86	100.0	106	6	ABU69230	Abu69230 Respirato
394	86	100.0	106	6	ABU69285	Abu69285 Respirato
395	86	100.0	106	6	ABU69291	Abu69291 Respirato
396	86	100.0	106	6	ABU69276	Abu69276 Respirato
397	86	100.0	106	6	ABU69243	Abu69243 Respirato
398	86	100.0	106	6	ABU69269	Abu69269 Respirato
399	86	100.0	106	6	ABU69273	Abu69273 Respirato
400	86	100.0	106	6	AAE33532	Aae33532 Human AQC
401	86	100.0	106	7	ABR61522	Abr61522 Human SA-
402	86	100.0	106	7	ADE35738	Ade35738 SYNAGIS a
403	86	100.0	106	7	ADE35742	Ade35742 SYNAGIS a
404	86	100.0	106	7	ADE35758	Ade35758 SYNAGIS a
405	86	100.0	106	7	ADE35733	Ade35733 SYNAGIS a
406	86	100.0	106	7	ADE35750	Ade35750 SYNAGIS a
407	86	100.0	106	7	ADE35782	Ade35782 SYNAGIS a
408	86	100.0	106	7	ADE35772	Ade35772 SYNAGIS a
409	86	100.0	106	7	ADE35774	Ade35774 SYNAGIS a
410	86	100.0	106	7	ADE35777	Ade35777 SYNAGIS a
411	86	100.0	106	7	ADE35764	Ade35764 SYNAGIS a
412	86	100.0	106	7	ADE35769	Ade35769 SYNAGIS a
413	86	100.0	106	7	ADE35746	Ade35746 SYNAGIS a
414	86	100.0	106	7	ADE35783	Ade35783 SYNAGIS a
415	86	100.0	106	7	ADE35776	Ade35776 SYNAGIS a
416	86	100.0	106	7	ADE35754	Ade35754 SYNAGIS a
417	86	100.0	106	7	ADE35761	Ade35761 SYNAGIS a
418	86	100.0	106	7	ADE35720	Ade35720 SYNAGIS a
419	86	100.0	106	7	ADE35766	Ade35766 SYNAGIS a
420	86	100.0	106	7	ADE35723	Ade35723 SYNAGIS a
421	86	100.0	106	7	ADE35780	Ade35780 SYNAGIS a
422	86	100.0	106	7	ADE35725	Ade35725 SYNAGIS a
423	86	100.0	106	7	ADE35768	Ade35768 SYNAGIS a
424	86	100.0	106	7	ADE35771	Ade35771 SYNAGIS a
425	86	100.0	106	7	ADE35786	Ade35786 SYNAGIS a
426	86	100.0	106	7	ADE35788	Ade35788 SYNAGIS a
427	86	100.0	106	7	ADP03944	Adp03944 Murine-ex
428	86	100.0	106	8	ADG34368	Adg34368 Humanised
429	86	100.0	106	8	ADG64763	Adg64763 C1 mouse
430	86	100.0	106	8	ADI01225	Adi01225 Murine an
431	86	100.0	106	8	ADI22107	Adi22107 Anti-plat
432	86	100.0	106	8	ADI22139	Adi22139 Anti-plat
433	86	100.0	106	8	ADI56908	Adi56908 RSV antib
434	86	100.0	106	8	ADI56923	Adi56923 RSV antib
435	86	100.0	106	8	ADI56920	Adi56920 RSV antib
436	86	100.0	106	8	ADI56934	Adi56934 RSV antib
437	86	100.0	106	8	ADI56939	Adi56939 RSV antib
438	86	100.0	106	8	ADI56938	Adi56938 RSV antib
439	86	100.0	106	8	ADI56945	Adi56945 RSV antib
440	86	100.0	106	8	ADI56912	Adi56912 RSV antib
441	86	100.0	106	8	ADI56926	Adi56926 RSV antib
442	86	100.0	106	8	ADI56904	Adi56904 RSV antib
443	86	100.0	106	8	ADI56882	Adi56882 RSV antib
444	86	100.0	106	8	ADI56887	Adi56887 RSV antib
445	86	100.0	106	8	ADI56950	Adi56950 RSV antib
446	86	100.0	106	8	ADI56885	Adi56885 RSV antib
447	86	100.0	106	8	ADI56895	Adi56895 RSV antib
448	86	100.0	106	8	ADI56948	Adi56948 RSV antib
449	86	100.0	106	8	ADI56933	Adi56933 RSV antib
450	86	100.0	106	8	ADI56936	Adi56936 RSV antib
451	86	100.0	106	8	ADI56930	Adi56930 RSV antib
452	86	100.0	106	8	ADI56900	Adi56900 RSV antib
453	86	100.0	106	8	ADI56928	Adi56928 RSV antib
454	86	100.0	106	8	ADI56942	Adi56942 RSV antib
455	86	100.0	106	8	ADI56931	Adi56931 RSV antib
456	86	100.0	106	8	ADI56916	Adi56916 RSV antib
457	86	100.0	106	8	ADI56944	Adi56944 RSV antib
458	86	100.0	106	8	ADL11891	Adl11891 CDR trans
459	86	100.0	106	8	ADJ97213	Adj97213 Human pro
460	86	100.0	106	8	ADO47730	Ado47730 PDL-only
461	86	100.0	106	8	ADO47721	Ado47721 Humanised
462	86	100.0	106	8	ADO47751	Ado47751 Human LAY
463	86	100.0	106	8	ADM95100	Adm95100 Humanised
464	86	100.0	106	8	ADM98322	Adm98322 Humanised
465	86	100.0	106	8	ADP22224	Adp22224 Human ant
466	86	100.0	106	8	ADR47411	Adr47411 Human ger
467	86	100.0	106	8	ADS64657	Ads64657 Human 9C1
468	86	100.0	106	8	ADT89231	Adt89231 Humanised
469	86	100.0	106	8	ADT89253	Adt89253 Humanised
470	86	100.0	106	8	ADT89273	Adt89273 Humanised
471	86	100.0	106	8	ADT89262	Adt89262 Humanised
472	86	100.0	106	8	ADT89261	Adt89261 Humanised
473	86	100.0	106	8	ADT89205	Adt89205 Humanised
474	86	100.0	106	8	ADT89246	Adt89246 Humanised
475	86	100.0	106	8	ADT89239	Adt89239 Humanised
476	86	100.0	106	8	ADT89223	Adt89223 Humanised
477	86	100.0	106	8	ADT89235	Adt89235 Humanised
478	86	100.0	106	8	ADT89243	Adt89243 Humanised
479	86	100.0	106	8	ADT89265	Adt89265 Humanised
480	86	100.0	106	8	ADT89227	Adt89227 Humanised
481	86	100.0	106	8	ADT89249	Adt89249 Humanised
482	86	100.0	106	8	ADT89267	Adt89267 Humanised
483	86	100.0	106	8	ADT89271	Adt89271 Humanised
484	86	100.0	106	8	ADT89218	Adt89218 Humanised
485	86	100.0	106	8	ADT89256	Adt89256 Humanised
486	86	100.0	106	8	ADT89251	Adt89251 Humanised
487	86	100.0	106	8	ADT89257	Adt89257 Humanised
488	86	100.0	106	8	ADT89259	Adt89259 Humanised
489	86	100.0	106	8	ADT89208	Adt89208 Humanised
490	86	100.0	106	8	ADT89210	Adt89210 Humanised
491	86	100.0	106	8	ADT89268	Adt89268 Humanised
492	86	100.0	106	8	ADT89254	Adt89254 Humanised
493	86	100.0	106	8	ADY72815	Ady72815 Anti-hepa
494	86	100.0	106	9	ADW19903	Adw19903 RSV antig
495	86	100.0	106	9	ADW19906	Adw19906 RSV antig
496	86	100.0	106	9	ADW19875	Adw19875 RSV antig
497	86	100.0	106	9	ADW19896	Adw19896 RSV antig
498	86	100.0	106	9	ADW19910	Adw19910 RSV antig
499	86	100.0	106	9	ADW19914	Adw19914 RSV antig
500	86	100.0	106	9	ADW19918	Adw19918 RSV antig
501	86	100.0	106	9	ADW19924	Adw19924 RSV antig
502	86	100.0	106	9	ADW19865	Adw19865 RSV antig
503	86	100.0	106	9	ADW19867	Adw19867 RSV antig
504	86	100.0	106	9	ADW19862	Adw19862 RSV antig
505	86	100.0	106	9	ADW19928	Adw19928 RSV antig
506	86	100.0	106	9	ADW19911	Adw19911 RSV antig
507	86	100.0	106	9	ADW19900	Adw19900 RSV antig
508	86	100.0	106	9	ADW19908	Adw19908 RSV antig
509	86	100.0	106	9	ADW19919	Adw19919 RSV antig
510	86	100.0	106	9	ADW19922	Adw19922 RSV antig
511	86	100.0	106	9	ADW19888	Adw19888 RSV antig
512	86	100.0	106	9	ADW19884	Adw19884 RSV antig
513	86	100.0	106	9	ADW19880	Adw19880 RSV antig
514	86	100.0	106	9	ADW19913	Adw19913 RSV antig
515	86	100.0	106	9	ADW19925	Adw19925 RSV antig
516	86	100.0	106	9	ADW19930	Adw19930 RSV antig
517	86	100.0	106	9	ADW19892	Adw19892 RSV antig
518	86	100.0	106	9	ADW19916	Adw19916 RSV antig
519	86	100.0	106	9	ADX01785	Adx01785 SARS coro
520	86	100.0	106	9	ADY70206	Ady70206 Human mon
521	86	100.0	106	9	ADZ08202	Adz08202 IGF-speci
522	86	100.0	106	9	ADZ58538	Adz58538 VEGF rece
523	86	100.0	106	9	AEB00155	Aeb00155 Novel den
524	86	100.0	106	9	AEB06901	Aeb06901 RSV-speci
525	86	100.0	106	9	AEB06857	Aeb06857 RSV-speci
526	86	100.0	106	9	AEB07114	Aeb07114 RSV-speci
527	86	100.0	106	9	AEB06882	Aeb06882 RSV-speci
528	86	100.0	106	9	AEB06844	Aeb06844 RSV-speci
529	86	100.0	106	9	AEB06906	Aeb06906 RSV-speci
530	86	100.0	106	9	AEB06907	Aeb06907 RSV-speci
531	86	100.0	106	9	AEB07116	Aeb07116 RSV-speci
532	86	100.0	106	9	AEB06866	Aeb06866 RSV-speci
533	86	100.0	106	9	AEB06870	Aeb06870 RSV-speci
534	86	100.0	106	9	AEB06890	Aeb06890 RSV-speci
535	86	100.0	106	9	AEB06893	Aeb06893 RSV-speci

536	86	100.0	106	9	AEB06878	Aeb06878 RSV-speci
537	86	100.0	106	9	AEB06888	Aeb06888 RSV-speci
538	86	100.0	106	9	AEB06895	Aeb06895 RSV-speci
539	86	100.0	106	9	AEB06896	Aeb06896 RSV-speci
540	86	100.0	106	9	AEB06912	Aeb06912 RSV-speci
541	86	100.0	106	9	AEB06849	Aeb06849 RSV-speci
542	86	100.0	106	9	AEB06885	Aeb06885 RSV-speci
543	86	100.0	106	9	AEB06862	Aeb06862 RSV-speci
544	86	100.0	106	9	AEB06892	Aeb06892 RSV-speci
545	86	100.0	106	9	AEB06898	Aeb06898 RSV-speci
546	86	100.0	106	9	AEB06904	Aeb06904 RSV-speci
547	86	100.0	106	9	AEB06874	Aeb06874 RSV-speci
548	86	100.0	106	9	AEB06900	Aeb06900 RSV-speci
549	86	100.0	106	9	AEB06847	Aeb06847 RSV-speci
550	86	100.0	106	9	AEB06910	Aeb06910 RSV-speci
551	86	100.0	106	9	AEB45972	Aeb45972 Human mon
552	86	100.0	107	2	AAR11987	Aar11987 Human ant
553	86	100.0	107	2	AAR25731	Aar25731 Humanised
554	86	100.0	107	2	AAR30770	Aar30770 Consensus
555	86	100.0	107	2	AAR30769	Aar30769 huxCD3v9,
556	86	100.0	107	2	AAR38592	Aar38592 Human lam
557	86	100.0	107	2	AAR40950	Aar40950 Humanised
558	86	100.0	107	2	AAR54319	Aar54319 Anti-HIV
559	86	100.0	107	2	AAR54262	Aar54262 Anti-HIV
560	86	100.0	107	2	AAR54261	Aar54261 Anti-HIV
561	86	100.0	107	2	AAR54260	Aar54260 Anti-HIV
562	86	100.0	107	2	AAR92082	Aar92082 Murine 13
563	86	100.0	107	2	AAR92090	Aar92090 Human K10
564	86	100.0	107	2	AAW01283	Aaw01283 VL region
565	86	100.0	107	2	AAW01286	Aaw01286 VL region
566	86	100.0	107	2	AAW01287	Aaw01287 VL region
567	86	100.0	107	2	AAW01284	Aaw01284 VL region
568	86	100.0	107	2	AAW27568	Aaw27568 Anti-TNF-
569	86	100.0	107	2	AAW16649	Aaw16649 Anti-canc
570	86	100.0	107	2	AAW41401	Aaw41401 Humanised
571	86	100.0	107	2	AAW41400	Aaw41400 Humanised
572	86	100.0	107	2	AAW41397	Aaw41397 Anti-CEA
573	86	100.0	107	2	AAW58492	Aaw58492 Human kap
574	86	100.0	107	2	AAW86804	Aaw86804 Variable
575	86	100.0	107	2	AAW86805	Aaw86805 Variable
576	86	100.0	107	2	AAW49811	Aaw49811 Amino aci
577	86	100.0	107	2	AAW70623	Aaw70623 Humanised
578	86	100.0	107	2	AAW70625	Aaw70625 Humanised
579	86	100.0	107	2	AAW78434	Aaw78434 Antibody
580	86	100.0	107	2	AAW87455	Aaw87455 Humanised
581	86	100.0	107	2	AAY52722	Aay52722 Humanised
582	86	100.0	107	2	AAY52721	Aay52721 Humanised
583	86	100.0	107	2	AAY52723	Aay52723 Humanised
584	86	100.0	107	2	AAW80972	Aaw80972 Kappa lig
585	86	100.0	107	3	AAY98245	Aay98245 Anti-gp12
586	86	100.0	107	3	AAY98244	Aay98244 Anti-gp12
587	86	100.0	107	3	AAY98247	Aay98247 Anti-gp12
588	86	100.0	107	3	AAY98248	Aay98248 Anti-gp12
589	86	100.0	107	3	AAY95136	Aay95136 Anti-gp12
590	86	100.0	107	3	AAY95135	Aay95135 Anti-gp12
591	86	100.0	107	3	AAY95138	Aay95138 Anti-gp12
592	86	100.0	107	3	AAY95139	Aay95139 Anti-gp12
593	86	100.0	107	3	AAY96062	Aay96062 Human ant
594	86	100.0	107	4	AAB62085	Aab62085 Humanised
595	86	100.0	107	4	AAB62087	Aab62087 Human Vl
596	86	100.0	107	4	AAB60398	Aab60398 Humanised
597	86	100.0	107	4	AAB60400	Aab60400 Consensus
598	86	100.0	107	4	AAG65567	Aag65567 Amino aci
599	86	100.0	107	4	AAG65571	Aag65571 Amino aci
600	86	100.0	107	4	AAG93646	Aag93646 Human ant
601	86	100.0	107	4	AAG93596	Aag93596 Human ant
602	86	100.0	107	4	AAG93597	Aag93597 Human ant
603	86	100.0	107	4	AAG93663	Aag93663 Human ant
604	86	100.0	107	4	AAG93591	Aag93591 Human ant
605	86	100.0	107	4	AAG93592	Aag93592 Human ant
606	86	100.0	107	4	AAG93644	Aag93644 Human ant
607	86	100.0	107	4	AAG93664	Aag93664 Human ant
608	86	100.0	107	4	AAG93667	Aag93667 Human ant
609	86	100.0	107	4	AAG93594	Aag93594 Human ant
610	86	100.0	107	4	AAG93595	Aag93595 Human ant
611	86	100.0	107	4	AAG93590	Aag93590 Human ant
612	86	100.0	107	4	AAG93601	Aag93601 Human ant
613	86	100.0	107	4	AAB61585	Aab61585 Human var
614	86	100.0	107	4	AAB61583	Aab61583 Humanised
615	86	100.0	107	4	AAB69696	Aab69696 Human Eu
616	86	100.0	107	4	AAB74982	Aab74982 Humanised
617	86	100.0	107	4	AAB74984	Aab74984 Humanised
618	86	100.0	107	4	AAB74983	Aab74983 Humanised
619	86	100.0	107	5	AAE28884	Aae28884 Human KDR
620	86	100.0	107	5	AAE28874	Aae28874 Human KDR
621	86	100.0	107	5	AAE28876	Aae28876 Human KDR
622	86	100.0	107	5	AAE19665	Aae19665 Human TNF
623	86	100.0	107	5	AAO18394	Aao18394 Humanised
624	86	100.0	107	5	ABG31429	Abg31429 Humanised
625	86	100.0	107	5	AAM47643	Aam47643 Human G1C
626	86	100.0	107	5	ABG97821	Abg97821 Human MPL
627	86	100.0	107	5	ABG35324	Abg35324 Thrombopo
628	86	100.0	107	5	ABB07239	Abb07239 Anti-IL-4
629	86	100.0	107	5	ABB07557	Abb07557 HCV-AB 68
630	86	100.0	107	5	ABB97977	Abb97977 Light cha
631	86	100.0	107	5	ABP61192	Abp61192 Humanised
632	86	100.0	107	5	ABP61194	Abp61194 Humanised
633	86	100.0	107	5	ABG32512	Abg32512 Human VK
634	86	100.0	107	6	ABP96012	Abp96012 HSA antib
635	86	100.0	107	6	ABR55856	Abr55856 Anti-Her-
636	86	100.0	107	6	ABR55866	Abr55866 Human imm
637	86	100.0	107	6	ABJ26767	Abj26767 VEGF bind
638	86	100.0	107	6	ABJ26769	Abj26769 VEGF bind
639	86	100.0	107	6	ABJ26777	Abj26777 VEGF bind
640	86	100.0	107	6	ABR54904	Abr54904 Light cha
641	86	100.0	107	6	ABO04835	Abo04835 Human epi
642	86	100.0	107	6	AAO16459	Aao16459 Human ant
643	86	100.0	107	6	AAO27194	Aao27194 Chimeric
644	86	100.0	107	6	ABP59951	Abp59951 Monoclona
645	86	100.0	107	6	ABJ18721	Abj18721 Antibody
646	86	100.0	107	6	ABB82945	Abb82945 Anti-EGFR
647	86	100.0	107	6	ABR40160	Abr40160 Humanised
648	86	100.0	107	6	ABR40159	Abr40159 Humanised
649	86	100.0	107	6	AAO16821	Aao16821 Blood flo
650	86	100.0	107	6	ABR63606	Abr63606 Human gly
651	86	100.0	107	6	ABO27399	Abo27399 Anti-Rh(D
652	86	100.0	107	6	ABO27451	Abo27451 Anti-Rh(D
653	86	100.0	107	6	ABO27474	Abo27474 Anti-Rh(D
654	86	100.0	107	6	ABO27401	Abo27401 Anti-Rh(D
655	86	100.0	107	6	ABO27453	Abo27453 Anti-Rh(D
656	86	100.0	107	6	ABO27471	Abo27471 Anti-Rh(D
657	86	100.0	107	6	ABO27403	Abo27403 Anti-Rh(D
658	86	100.0	107	6	ABO27398	Abo27398 Anti-Rh(D
659	86	100.0	107	6	ABO27402	Abo27402 Anti-Rh(D
660	86	100.0	107	6	ABO27408	Abo27408 Anti-Rh(D
661	86	100.0	107	6	ABO27397	Abo27397 Anti-Rh(D
662	86	100.0	107	6	ABO27470	Abo27470 Anti-Rh(D
663	86	100.0	107	6	ABO27404	Abo27404 Anti-Rh(D
664	86	100.0	107	7	ADC99797	Adc99797 Anti-huma
665	86	100.0	107	7	ADD05401	Add05401 Anti-MUC1
666	86	100.0	107	7	ADD24426	Add24426 Human lig
667	86	100.0	107	7	ADD24446	Add24446 Human lig
668	86	100.0	107	7	ADD24430	Add24430 Human lig
669	86	100.0	107	7	ADE28417	Ade28417 Human ant
670	86	100.0	107	7	ADD80807	Add80807 Human KDR
671	86	100.0	107	7	ADD80823	Add80823 Human KDR
672	86	100.0	107	7	ADD80803	Add80803 Human clo
673	86	100.0	107	7	ADF69656	Adf69656 Humanised
674	86	100.0	107	7	ADF09839	Adf09839 Human ant
675	86	100.0	107	7	ADG75564	Adg75564 Humanised
676	86	100.0	107	7	ADG75565	Adg75565 Humanised
677	86	100.0	107	7	ADG88415	Adg88415 VL chain
678	86	100.0	107	7	ADK18619	Adk18619 Anti-huma
679	86	100.0	107	7	ADK18794	Adk18794 Anti-huma
680	86	100.0	107	7	ADO51596	Ado51596 Human TAG
681	86	100.0	107	7	ADO51598	Ado51598 Human TAG

682	86	100.0	107	7	ADP03929	Adp03929	Murine-ex
683	86	100.0	107	7	ADP03948	Adp03948	Murine-ex
684	86	100.0	107	7	ADP03949	Adp03949	Murine-ex
685	86	100.0	107	7	ADP03922	Adp03922	Murine-ex
686	86	100.0	107	7	ADP03989	Adp03989	Murine-ex
687	86	100.0	107	7	ADP03920	Adp03920	Murine-ex
688	86	100.0	107	7	ADP03994	Adp03994	Murine-ex
689	86	100.0	107	7	ADP03926	Adp03926	Murine-ex
690	86	100.0	107	7	ADP03923	Adp03923	Murine-ex
691	86	100.0	107	8	ADE71452	Ade71452	Humanise
692	86	100.0	107	8	ADE71454	Ade71454	Human ant
693	86	100.0	107	8	ADG34381	Adg34381	Humanised
694	86	100.0	107	8	ADG64762	Adg64762	C1 mouse
695	86	100.0	107	8	ABM79492	Abm79492	Human KM3
696	86	100.0	107	8	ABG75335	Abg75335	Antibody
697	86	100.0	107	8	ADI01154	Adi01154	Human kap
698	86	100.0	107	8	ADI22109	Adi22109	Anti-plat
699	86	100.0	107	8	ADJ88008	Adj88008	Human var
700	86	100.0	107	8	ADJ88006	Adj88006	Humanised
701	86	100.0	107	8	ADJ57622	Adj57622	TNFalpha
702	86	100.0	107	8	ADJ57614	Adj57614	TNFalpha
703	86	100.0	107	8	ADK18299	Adk18299	KDR bindi
704	86	100.0	107	8	ADK18279	Adk18279	KDR bindi
705	86	100.0	107	8	ADK18283	Adk18283	KDR bindi
706	86	100.0	107	8	ADJ58745	Adj58745	Human D2E
707	86	100.0	107	8	ADJ58753	Adj58753	Human 2SD
708	86	100.0	107	8	ADN12054	Adn12054	Variable
709	86	100.0	107	8	ADN12052	Adn12052	Variable
710	86	100.0	107	8	ADL25454	Adl25454	Human mAb
711	86	100.0	107	8	ADL93584	Adl93584	Human CD4
712	86	100.0	107	8	ADN49404	Adn49404	Human ant
713	86	100.0	107	8	ADO47807	Ado47807	Humanised
714	86	100.0	107	8	ADN49723	Adn49723	Variable
715	86	100.0	107	8	ADN49707	Adn49707	Light cha
716	86	100.0	107	8	ADO06815	Ado06815	Virucidal
717	86	100.0	107	8	ADO06843	Ado06843	Virucidal
718	86	100.0	107	8	ADO36506	Ado36506	Human ant
719	86	100.0	107	8	ADO36498	Ado36498	Human ant
720	86	100.0	107	8	ADP43328	Adp43328	Human mon
721	86	100.0	107	8	ADP43326	Adp43326	Humanised
722	86	100.0	107	8	ADP22406	Adp22406	Human ant
723	86	100.0	107	8	ADP22402	Adp22402	Human ant
724	86	100.0	107	8	ADP22412	Adp22412	Human ant
725	86	100.0	107	8	ADP22216	Adp22216	Human ant
726	86	100.0	107	8	ADQ26400	Adq26400	Anti-EGFR
727	86	100.0	107	8	ADQ77018	Adq77018	TAR1-27d2
728	86	100.0	107	8	ADQ77010	Adq77010	TAR1-5d2
729	86	100.0	107	8	ADQ77032	Adq77032	TAR1-27d3
730	86	100.0	107	8	ADQ77016	Adq77016	TAR1-27d1
731	86	100.0	107	8	ADQ77024	Adq77024	TAR1-27d1
732	86	100.0	107	8	ADQ77020	Adq77020	TAR1-27d7
733	86	100.0	107	8	ADQ77022	Adq77022	TAR1-27d8
734	86	100.0	107	8	ADQ77034	Adq77034	TAR1-27d3
735	86	100.0	107	8	ADQ77030	Adq77030	TAR1-27d3
736	86	100.0	107	8	ADQ77028	Adq77028	TAR1-27d2
737	86	100.0	107	8	ADQ90913	Adq90913	Vk/Ck pro
738	86	100.0	107	8	ADU07233	Adu07233	Human 4D4
739	86	100.0	107	8	ADU07241	Adu07241	Human 4D4
740	86	100.0	107	8	ADU07253	Adu07253	Human 7F3
741	86	100.0	107	8	ADU07249	Adu07249	Human 71A
742	86	100.0	107	8	ADU07250	Adu07250	Human 7F3
743	86	100.0	107	8	ADU07257	Adu07257	Human 7F3
744	86	100.0	107	8	ADU07290	Adu07290	Human 7F3
745	86	100.0	107	8	ADT88317	Adt88317	Human IL-
746	86	100.0	107	8	ADT88308	Adt88308	Human IL-
747	86	100.0	107	8	ADT88316	Adt88316	Human IL-
748	86	100.0	107	8	ADT88320	Adt88320	Human IL-
749	86	100.0	107	8	ADT88300	Adt88300	Human IL-
750	86	100.0	107	8	ADT88324	Adt88324	Human IL-
751	86	100.0	107	8	ADU74399	Adu74399	Human imm
752	86	100.0	107	8	ADU74383	Adu74383	Herceptin
753	86	100.0	107	8	ADU67060	Adu67060	Human LPS
754	86	100.0	107	8	ADW75668	Adw75668	Novel mod
755	86	100.0	107	9	ADV21397	Adv21397	Human ant
756	86	100.0	107	9	ADV21349	Adv21349	Human ant
757	86	100.0	107	9	ADX15508	Adx15508	Human ant
758	86	100.0	107	9	ADX45251	Adx45251	Anti-inte
759	86	100.0	107	9	ADX27048	Adx27048	Human gro
760	86	100.0	107	9	ADX80643	Adx80643	Humanized
761	86	100.0	107	9	ADY26697	Ady26697	Anti-NGF-
762	86	100.0	107	9	ADZ23015	Adz23015	Human CXC
763	86	100.0	107	9	ADZ22999	Adz22999	Human CXC
764	86	100.0	107	9	ADZ69224	Adz69224	IL-5R alp
765	86	100.0	107	9	AEA12439	Aea12439	Rat anti-
766	86	100.0	107	9	AEA12440	Aea12440	Rat anti-
767	86	100.0	107	9	AEA12454	Aea12454	Rat anti-
768	86	100.0	107	9	AEA12455	Aea12455	Rat anti-
769	86	100.0	107	9	AEA12435	Aea12435	Rat anti-
770	86	100.0	107	9	AEA12401	Aea12401	Rat anti-
771	86	100.0	107	9	AEA12434	Aea12434	Rat anti-
772	86	100.0	107	9	AEA12445	Aea12445	Rat anti-
773	86	100.0	107	9	AEA12444	Aea12444	Rat anti-
774	86	100.0	107	9	AEA12402	Aea12402	Rat anti-
775	86	100.0	107	9	AEA17749	Aea17749	Hybridoma
776	86	100.0	107	9	AEA41073	Aea41073	Germline
777	86	100.0	107	9	AEA08944	Aea08944	Antibody
778	86	100.0	107	9	AEA40481	Aea40481	Anti-VEGF
779	86	100.0	107	9	AEA40482	Aea40482	Anti-VEGF
780	86	100.0	107	9	AEA40478	Aea40478	Anti-VEGF
781	86	100.0	107	9	AEB03875	Aeb03875	B-CLL pha
782	86	100.0	107	9	AEB19280	Aeb19280	IgG kappa
783	86	100.0	107	9	AEB19281	Aeb19281	IgG kappa
784	86	100.0	107	9	AEB12538	Aeb12538	Humanized
785	86	100.0	107	9	AEB01059	Aeb01059	Human IP1
786	86	100.0	107	9	AEB45976	Aeb45976	Human mon
787	86	100.0	108	2	AAR28747	Aar28747	Light cha
788	86	100.0	108	2	AAR54320	Aar54320	Anti-HIV
789	86	100.0	108	2	AAR54258	Aar54258	Anti-HIV
790	86	100.0	108	2	AAW01281	Aaw01281	VL region
791	86	100.0	108	2	AAW01288	Aaw01288	VL region
792	86	100.0	108	2	AAW19891	Aaw19891	CEA-speci
793	86	100.0	108	2	AAW19892	Aaw19892	CEA-speci
794	86	100.0	108	2	AAW19885	Aaw19885	CEA-speci
795	86	100.0	108	2	AAW19895	Aaw19895	CEA-speci
796	86	100.0	108	2	AAW19890	Aaw19890	CEA-speci
797	86	100.0	108	2	AAW10231	Aaw10231	CDR-graft
798	86	100.0	108	2	AAW27529	Aaw27529	Light cha
799	86	100.0	108	2	AAW15524	Aaw15524	Anti-TGF
800	86	100.0	108	2	AAW62017	Aaw62017	Light cha
801	86	100.0	108	2	AAW70622	Aaw70622	Human con
802	86	100.0	108	2	AAW63529	Aaw63529	Humanised
803	86	100.0	108	3	AAY82343	Aay82343	Humanised
804	86	100.0	108	3	AAY82345	Aay82345	Human con
805	86	100.0	108	3	AAY71450	Aay71450	Humanised
806	86	100.0	108	3	AAY98249	Aay98249	Anti-gp12
807	86	100.0	108	3	AAY98242	Aay98242	Anti-gp12
808	86	100.0	108	3	AAY95140	Aay95140	Anti-gp12
809	86	100.0	108	3	AAY95133	Aay95133	Anti-gp12
810	86	100.0	108	3	AAY56678	Aay56678	Anti-inte
811	86	100.0	108	3	AAY56675	Aay56675	Anti-IL5
812	86	100.0	108	3	AAB52192	Aab52192	Human ant
813	86	100.0	108	4	AAB62785	Aab62785	Human HIV
814	86	100.0	108	4	AAG62951	Aag62951	Amino aci
815	86	100.0	108	4	AAG62953	Aag62953	Amino aci
816	86	100.0	108	4	AAG62965	Aag62965	Amino aci
817	86	100.0	108	4	AAG62959	Aag62959	Amino aci
818	86	100.0	108	4	AAE12062	Aae12062	Human ant
819	86	100.0	108	4	AAU02534	Aau02534	Anti-adip
820	86	100.0	108	4	AAG93589	Aag93589	Human ant
821	86	100.0	108	4	AAG93600	Aag93600	Human ant
822	86	100.0	108	4	AAG93655	Aag93655	Human ant
823	86	100.0	108	4	AAG93665	Aag93665	Human ant
824	86	100.0	108	4	AAG93588	Aag93588	Human ant
825	86	100.0	108	4	AAG93598	Aag93598	Human ant
826	86	100.0	108	4	AAG93669	Aag93669	Human ant
827	86	100.0	108	4	AAG93649	Aag93649	Human ant

828	86	100.0	108	4	AAG93651	Aag93651 Human ant
829	86	100.0	108	5	ABP61191	Abp61191 Human ant
830	86	100.0	108	6	ABP96009	Abp96009 HSA antib
831	86	100.0	108	6	ABP96010	Abp96010 HSA antib
832	86	100.0	108	6	ABP96011	Abp96011 HSA antib
833	86	100.0	108	6	AAO16704	Aao16704 Human ant
834	86	100.0	108	6	AAO16706	Aao16706 Human ant
835	86	100.0	108	6	AAE35210	Aae35210 Human IgE
836	86	100.0	108	6	ABO27262	Abo27262 ICAM-1 bi
837	86	100.0	108	6	ABO27266	Abo27266 ICAM-1 bi
838	86	100.0	108	6	ABO27278	Abo27278 Humanised
839	86	100.0	108	6	ABO27260	Abo27260 ICAM-1 bi
840	86	100.0	108	6	ABO27258	Abo27258 ICAM-1 bi
841	86	100.0	108	6	ABO27256	Abo27256 ICAM-1 bi
842	86	100.0	108	6	ABO27264	Abo27264 ICAM-1 bi
843	86	100.0	108	6	ABJ18679	Abj18679 Antibody
844	86	100.0	108	6	ABO10817	Abo10817 Human ger
845	86	100.0	108	6	ABO27462	Abo27462 Anti-Rh(D
846	86	100.0	108	6	ABO27472	Abo27472 Anti-Rh(D
847	86	100.0	108	6	ABO27476	Abo27476 Anti-Rh(D
848	86	100.0	108	6	ABO27395	Abo27395 Anti-Rh(D
849	86	100.0	108	6	ABO27456	Abo27456 Anti-Rh(D
850	86	100.0	108	6	ABO27407	Abo27407 Anti-Rh(D
851	86	100.0	108	6	ABO27396	Abo27396 Anti-Rh(D
852	86	100.0	108	6	ABO27458	Abo27458 Anti-Rh(D
853	86	100.0	108	6	ABO27405	Abo27405 Anti-Rh(D
854	86	100.0	108	7	ADC27465	Adc27465 Humanised
855	86	100.0	108	7	ABR61524	Abr61524 Humanised
856	86	100.0	108	7	ADK18933	Adk18933 Anti-huma
857	86	100.0	108	7	ADL91345	Adl91345 VL chain
858	86	100.0	108	7	ADL91347	Adl91347 VL chain
859	86	100.0	108	7	ADL91344	Adl91344 VL chain
860	86	100.0	108	7	ADL91353	Adl91353 VL chain
861	86	100.0	108	7	ADL91334	Adl91334 VL chain
862	86	100.0	108	7	ADL91313	Adl91313 Consenus
863	86	100.0	108	7	ADL91354	Adl91354 VL chain
864	86	100.0	108	7	ADL91337	Adl91337 VL chain
865	86	100.0	108	8	ADG38990	Adg38990 Humanised
866	86	100.0	108	8	ADG38991	Adg38991 Human con
867	86	100.0	108	8	ABG75343	Abg75343 Antibody
868	86	100.0	108	8	ADL92423	Adl92423 Partner d
869	86	100.0	108	8	ADL92461	Adl92461 Single do
870	86	100.0	108	8	ADL92411	Adl92411 Partner d
871	86	100.0	108	8	ADL92462	Adl92462 Single do
872	86	100.0	108	8	ADL92386	Adl92386 Anti-HSA
873	86	100.0	108	8	ADL92388	Adl92388 Anti-MSA
874	86	100.0	108	8	ADL92393	Adl92393 Single do
875	86	100.0	108	8	ADL92407	Adl92407 Single do
876	86	100.0	108	8	ADL92399	Adl92399 Single do
877	86	100.0	108	8	ADL92415	Adl92415 Partner d
878	86	100.0	108	8	ADL92427	Adl92427 Partner d
879	86	100.0	108	8	ADL92397	Adl92397 Single do
880	86	100.0	108	8	ADL92405	Adl92405 Partner d
881	86	100.0	108	8	ADL92401	Adl92401 Partner d
882	86	100.0	108	8	ADL92425	Adl92425 Partner d
883	86	100.0	108	8	ADL92409	Adl92409 Partner d
884	86	100.0	108	8	ADL92429	Adl92429 Partner d
885	86	100.0	108	8	ADL92465	Adl92465 Anti-MSA
886	86	100.0	108	8	ADL92403	Adl92403 Partner d
887	86	100.0	108	8	ADL92417	Adl92417 Partner d
888	86	100.0	108	8	ADL92421	Adl92421 Partner d
889	86	100.0	108	8	ADL92413	Adl92413 Partner d
890	86	100.0	108	8	ADL92431	Adl92431 Partner d
891	86	100.0	108	8	ADL92419	Adl92419 Partner d
892	86	100.0	108	8	ADL92463	Adl92463 Single do
893	86	100.0	108	8	ADO01441	Ado01441 Human mut
894	86	100.0	108	8	ADN41877	Adn41877 Humanised
895	86	100.0	108	8	ADO60445	Ado60445 Humanised
896	86	100.0	108	8	ADO36340	Ado36340 Intracell
897	86	100.0	108	8	ADO36371	Ado36371 Intracell
898	86	100.0	108	8	ADO36361	Ado36361 Intracell
899	86	100.0	108	8	ADO36372	Ado36372 Intracell
900	86	100.0	108	8	ADO36364	Ado36364 Intracell
901	86	100.0	108	8	ADO36374	Ado36374 Intracell
902	86	100.0	108	8	ADO36411	Ado36411 Intracell
903	86	100.0	108	8	ADO36412	Ado36412 Intracell
904	86	100.0	108	8	ADO36397	Ado36397 Intracell
905	86	100.0	108	8	ADP66616	Adp66616 Anti-RAS
906	86	100.0	108	8	ADP66615	Adp66615 Anti-RAS
907	86	100.0	108	8	ADP66614	Adp66614 Anti-RAS
908	86	100.0	108	8	ADP66622	Adp66622 Anti-RAS
909	86	100.0	108	8	ADQ75245	Adq75245 Immunoglo
910	86	100.0	108	8	ADQ75247	Adq75247 Immunoglo
911	86	100.0	108	8	ADQ75237	Adq75237 Immunoglo
912	86	100.0	108	8	ADQ75213	Adq75213 Immunoglo
913	86	100.0	108	8	ADP47103	Adp47103 Human pho
914	86	100.0	108	8	ADP47299	Adp47299 Human pho
915	86	100.0	108	8	ADP47294	Adp47294 Human pho
916	86	100.0	108	8	ADP47113	Adp47113 Human pho
917	86	100.0	108	8	ADQ14601	Adq14601 Single-do
918	86	100.0	108	8	ADQ14602	Adq14602 Single-do
919	86	100.0	108	8	ADQ77004	Adq77004 TAR1-5-19
920	86	100.0	108	8	ADQ77026	Adq77026 TAR1-27d1
921	86	100.0	108	8	ADQ77184	Adq77184 VK C3 seq
922	86	100.0	108	8	ADQ77038	Adq77038 TAR1-27d3
923	86	100.0	108	8	ADQ77012	Adq77012 TAR1-5d4
924	86	100.0	108	8	ADQ77191	Adq77191 Dummy VK
925	86	100.0	108	8	ADQ77193	Adq77193 Anti muri
926	86	100.0	108	8	ADQ77001	Adq77001 TAR1-5-19
927	86	100.0	108	8	ADQ77036	Adq77036 TAR1-27d3
928	86	100.0	108	8	ADQ77008	Adq77008 TAR1-5d1
929	86	100.0	108	8	ADQ77014	Adq77014 TAR1-27 p
930	86	100.0	108	8	ADQ77183	Adq77183 VK E5sd s
931	86	100.0	108	8	ADQ77006	Adq77006 TAR1-5 pr
932	86	100.0	108	8	ADQ77181	Adq77181 VK dummy
933	86	100.0	108	8	ADQ77182	Adq77182 VK K8 seq
934	86	100.0	108	8	ADQ77195	Adq77195 Anti muri
935	86	100.0	108	8	ADQ90912	Adq90912 Vk/Ck pro
936	86	100.0	108	8	ADR03365	Adr03365 Humanised
937	86	100.0	108	8	ADR03366	Adr03366 Human sub
938	86	100.0	108	8	ADP79572	Adp79572 Human kap
939	86	100.0	108	8	ADO79338	Ado79338 Anti-RAS
940	86	100.0	108	8	ADO79340	Ado79340 Anti-RAS
941	86	100.0	108	8	ADO79346	Ado79346 Anti-RAS
942	86	100.0	108	8	ADO79339	Ado79339 Anti-RAS
943	86	100.0	108	8	ADR72710	Adr72710 Human mon
944	86	100.0	108	8	ADR72714	Adr72714 Human mon
945	86	100.0	108	8	ADR72712	Adr72712 Human mon
946	86	100.0	108	8	ADR72708	Adr72708 Human mon
947	86	100.0	108	8	ADR72706	Adr72706 Human mon
948	86	100.0	108	8	ADS78333	Ads78333 Vkappa du
949	86	100.0	108	8	ADS78331	Ads78331 DPkappa9-
950	86	100.0	108	8	ADS16523	Ads16523 Human ant
951	86	100.0	108	8	ADS16567	Ads16567 Human ant
952	86	100.0	108	8	ADT88240	Adt88240 Human ant
953	86	100.0	108	8	ADT88242	Adt88242 Human BSA
954	86	100.0	108	8	ADU86517	Adu86517 Immunoglo
955	86	100.0	108	8	ADU86722	Adu86722 TNFR1 bin
956	86	100.0	108	8	ADU77872	Adu77872 Humanized
957	86	100.0	108	8	ADU77865	Adu77865 Humanized
958	86	100.0	108	8	ADU77880	Adu77880 Humanized
959	86	100.0	108	8	ADW38457	Adw38457 CD11a lig
960	86	100.0	108	9	ADW04801	Adw04801 PAPP-A im
961	86	100.0	108	9	ADX80645	Adx80645 Humanized
962	86	100.0	108	9	ADZ42051	Adz42051 Ig L chai
963	86	100.0	108	9	ADZ42046	Adz42046 Ig L chai
964	86	100.0	108	9	ADZ42049	Adz42049 Ig L chai
965	86	100.0	108	9	ADZ42053	Adz42053 Ig L chai
966	86	100.0	108	9	ADZ42054	Adz42054 Ig L chai
967	86	100.0	108	9	ADZ42050	Adz42050 Ig L chai
968	86	100.0	108	9	ADZ42056	Adz42056 Ig L chai
969	86	100.0	108	9	ADZ42052	Adz42052 Ig L chai
970	86	100.0	108	9	ADZ42055	Adz42055 Ig L chai
971	86	100.0	108	9	ADZ42048	Adz42048 Ig L chai
972	86	100.0	108	9	ADZ42057	Adz42057 Ig L chai
973	86	100.0	108	9	ADZ41145	Adz41145 Dummy Vka

974	86	100.0	108	9	ADZ41149	Adz41149 Anti-mous
975	86	100.0	108	9	ADZ41157	Adz41157 Domain an
976	86	100.0	108	9	ADZ41173	Adz41173 Domain an
977	86	100.0	108	9	ADZ41189	Adz41189 Domain an
978	86	100.0	108	9	ADZ41167	Adz41167 Domain an
979	86	100.0	108	9	ADZ41179	Adz41179 Domain an
980	86	100.0	108	9	ADZ41185	Adz41185 Domain an
981	86	100.0	108	9	ADZ41177	Adz41177 Domain an
982	86	100.0	108	9	ADZ41183	Adz41183 Domain an
983	86	100.0	108	9	ADZ41187	Adz41187 Domain an
984	86	100.0	108	9	ADZ41155	Adz41155 Domain an
985	86	100.0	108	9	ADZ41175	Adz41175 Domain an
986	86	100.0	108	9	ADZ41181	Adz41181 Domain an
987	86	100.0	108	9	ADZ41147	Adz41147 Anti-mous
988	86	100.0	108	9	ADZ41159	Adz41159 Domain an
989	86	100.0	108	9	ADZ41161	Adz41161 Domain an
990	86	100.0	108	9	ADZ41169	Adz41169 Domain an
991	86	100.0	108	9	ADZ41171	Adz41171 Domain an
992	86	100.0	108	9	ADZ41165	Adz41165 Domain an
993	86	100.0	108	9	ADZ41191	Adz41191 Domain an
994	86	100.0	108	9	ADZ41225	Adz41225 Anti-CD40
995	86	100.0	108	9	ADZ41163	Adz41163 Domain an
996	86	100.0	108	9	ADZ52590	Adz52590 Antibody
997	86	100.0	108	9	ADZ52589	Adz52589 Antibody
998	86	100.0	108	9	ADZ57819	Adz57819 Gangliosi
999	86	100.0	108	9	ADZ99428	Adz99428 Rat anti-
1000	86	100.0	108	9	AEA41087	Aea41087 Germline

ALIGNMENTS

RESULT 1
AAR27042
ID AAR27042 standard; peptide; 15 AA.
XX
AC AAR27042;
XX
DT 25-MAR-2003 (revised)
DT 01-MAR-1993 (first entry)
XX
DE Human light chain framework 2 used in humanised MAb.
XX
KW Monoclonal antibody; complementarity determining region; CDR; antigens;
KW tumour; melanoma; carcinoma; glioma.
XX
OS Homo sapiens.
XX
PN WO9215683-A1.
XX
PD 17-SEP-1992.
XX
PF 04-MAR-1992; 92WO-EP000480.
XX
PR 06-MAR-1991; 91EP-00103389.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Bendig MM, Kettleborough CA, Saldanha J;
XX
DR WPI; 1992-331729/40.
XX
PT Human monoclonal antibodies binding to human receptors - for treatment
PT and diagnosis of tumours, e.g. melanoma and carcinoma.
XX
PS Claim 5; Page 62; 89pp; English.
XX
CC The human framework sequence FR2 was used in the prodn. of humanised
CC monoclonal antibodies comprising antigen binding sites (CDRs) of non
CC human origen based on consensus sequence of CDRs. The sequence is a light
CC chain framework region. The humanised antibodies or their chimeric
CC variants may be used as therapeutic or diagnostic agents in order to
CC combat e.g. glioma, melanoma or carcinoma. See also AAR27299-300 and
CC AAR27037-51. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 2
AAR77205
ID AAR77205 standard; peptide; 15 AA.
XX
AC AAR77205;
XX
DT 25-MAR-2003 (revised)
DT 23-AUG-1995 (first entry)
XX
DE Mouse anti-human IL-6 Ab L chain V region framework region 2.
XX
KW Primer; PCR; amplify; kappa; light chain; variable region; mouse; human;
KW interleukin; antibody; hybridoma; CDR; framework; constant region;
KW heavy chain; disorder; antigenicity.
XX
OS Synthetic.
XX
PN WO9428159-A1.
XX
PD 08-DEC-1994.
XX
PF 30-MAY-1994; 94WO-JP000859.
XX
PR 31-MAY-1993; 93JP-00129787.
XX
PA (CHUS) CHUGAI SEIYAKU KK.
XX
PI Tsuchiya M, Sato K, Hirata Y;
XX
DR WPI; 1995-022828/03.
XX
PT Antibody against IL-6 - useful for the therapy and treatment of IL-6
PT related disorders.
XX
PS Claim 6; Page 64; 82pp; Japanese.
XX
CC The sequence of the mouse anti-human interleukin-6 (IL-6) antibody light
CC chain variable region framework region (FR) 2. The sequences of FR1-4
CC (AAR77204-7) were used in conjunction with the complementarity
CC determining regions 1-3 (AAR77201-3) to construct a chimaeric antibody
CC against human interleukin-6 (IL-6). The vectors AAQ75914-7 express
CC constructs encoding fragments of a chimaeric antibody to the human IL-6
CC comprising (a) a light chain with (i) a variable region containing 3 CDR
CC (AAR77201-3) inserted into several framework regions (FR) (AAR77204-7)
CC and (ii) a human light chain constant region and (b) a heavy chain with
CC (i) a variable region containing 3 CDR (AAR77212-4) inserted into FR
CC (AAR77215-8) and (ii) a human light chain constant region. The FR of the
CC light chain may be mouse derived (AAQ75888) or from the human antibody
CC REI. The heavy chain FR may also be mouse derived (AAQ75889) or from the
CC human antibody DAW. The antibodies can be used in the treatment of IL-6
CC related disorders. The antibodies are useful as they have low
CC antigenicity due to the use of human derived sequences and low
CC antigenicity mouse derived sequences. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 3
AAR97320
ID   AAR97320 standard; peptide; 15 AA.
XX
AC   AAR97320;
XX
DT   15-OCT-1996  (first entry)
XX
DE   Humanised monoclonal antibody light chain framework region.
XX
KW   Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
KW   complementary determining region; anti-carcinoembryonic antigen; CEA;
KW   diagnosis; imaging; therapy; immune response.
XX
OS   Homo sapiens.
XX
PN   WO9611013-A1.
XX
PD   18-APR-1996.
XX
PF   28-SEP-1995;   95WO-US011964.
XX
PR   05-OCT-1994;   94US-00318157.
XX
PA   (IMMU-) IMMUNOMEDICS INC.
XX
PI   Hansen HJ,  Armour KL;
XX
DR   WPI; 1996-209653/21.
XX
PT   New humanised anti-CEA monoclonal antibody - having engrafted murine
PT   CDRs, used for diagnosis, imaging and therapy of CEA-producing cancers.
XX
PS   Claim 7; Page 39; 62pp; English.
XX
CC   New humanised monoclonal antibodies (MAbs) comprising the complementary
CC   determining regions (CDRs) of a parental murine class III anti-
CC   carcinoembryonic (CEA) MAb engrafted to the framework regions (FRs) of a
CC   heterologous antibody which can be derived from any species including
CC   human, retain the anti-CEA binding specificity of the parental murine MAb
CC   but are less immunogenic in a human subject than the parental MAb. The
CC   humanised antibodies can be used in diagnosis, imaging and therapy of CEA
CC   -producing cancers and patients receiving the humanised antibodies and
CC   conjugates show improved therapeutic results, decreased immune responses
CC   and decreased immune-mediated adverse effects compared to the parent
CC   antibody. This sequence corresponds to the second framework region of the
CC   light chain of the humanised MAb. See AAR97313-97333
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 86;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 4
AAR87042
ID   AAR87042 standard; peptide; 15 AA.
XX
AC   AAR87042;
XX
DT   25-JUN-1996  (first entry)
XX
DE   Human group I light chain framework 2.
XX
KW   Humanised antibody; interleukin-5; IL-5; recombinant antibody;
KW   antibody engineering; monoclonal antibody; MAb; 39D10; CDR;
KW   complementarity determining region; light chain; framework; eosinophilia;
KW   allergy; asthma.
XX
OS   Homo sapiens.
XX
PN   WO9535375-A1.
XX
PD   28-DEC-1995.
XX
PF   16-JUN-1995;   95WO-GB001411.
XX
PR   17-JUN-1994;   94GB-00012230.
XX
PA   (CLLT ) CELLTECH THERAPEUTICS LTD.
XX
PI   Emtage JS,  Bodmer MW,  Athwal DS;
XX
DR   WPI; 1996-058412/06.
XX
PT   Anti-human IL-5 recombinant antibody - useful for preventing or reducing
PT   eosinophilia and for treating certain allergic diseases, esp. asthma.
XX
PS   Example 3; Fig 3; 69pp; English.
XX
CC   Framework regions (AAR87041-44) of human group I (gp1) germ line antibody
CC   light chain showed homology to corresponding regions (AAR87045-48,
CC   respectively) of the rat anti-human interleukin-5 monoclonal antibody
CC   39D10 light chain (see AAR87040). This homology was utilised in the
CC   prodn. of a humanised 39D10 VL (AAR87057) in which rat 39D10 VL
CC   complementarity determining regions were grafted into the human gp1
CC   framework
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 86;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 5
AAY52742
ID   AAY52742 standard; peptide; 15 AA.
XX
AC   AAY52742;
XX
DT   26-JAN-2000  (first entry)
XX
DE   Humanised ATR-5 L chain V region FR2 for a, b and c.
XX
KW   Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
KW   ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
KW   disseminated intravascular coagulation; immunogenicity; chimeric.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9951743-A1.
XX
PD   14-OCT-1999.
XX
PF   02-APR-1999;   99WO-JP001768.
XX
PR   03-APR-1998;   98JP-00091850.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
```

XX
PI Sato K, Adachi H, Yabuta N;
XX
DR WPI; 1999-620204/53.
XX
PT Humanised antibody recognizing human tissue factor, used for treatment of
PT disseminated intravascular coagulation.
XX
PS Claim 17; Page 269; 291pp; Japanese.
XX
CC The present invention describes chimeric antibody (Ab) heavy (H) chains
CC containing the variable region of the H chain of a mouse monoclonal Ab
CC recognising human tissue factor (hTF) and the constant region of the H
CC chain of a human Ab. The variable region is one of six specified
CC sequences (which are the H chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) chains
CC containing the variable region of the L chain of a mouse monoclonal Ab
CC recognising human tissue factor (hTF) and the constant region of the L
CC chain of a human Ab, the variable region being one of six specified
CC sequences (which are the L chain variable regions from mouse monoclonal
CC Ab's ATR-2,3,4,5,7 or 8). The chimeric Ab's can be used for the treatment
CC and prevention of thrombotic disease, especially of disseminated
CC intravascular coagulation (DIC). The humanised antibody has the high hTF
CC binding activity of the mouse monoclonal antibody but greatly reduced
CC immunogenicity. AAZ33001 to AAZ33091 and Y527007 to AAY52767 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 6
AAB98279
ID AAB98279 standard; peptide; 15 AA.
XX
AC AAB98279;
XX
DT 20-AUG-2001 (first entry)
XX
DE Anti-A33 antigen immunoglobulin VL FR2 SEQ ID NO:85.
XX
KW Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
KW immunoglobulin; complementarity determining region; CDR; cancer;
KW cytostatic; anticancer; colon cancer; stomach cancer.
XX
OS Homo sapiens.
XX
PN WO200130393-A2.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US029289.
XX
PR 22-OCT-1999; 99US-00425638.
PR 04-APR-2000; 2000US-00543004.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (SCRI) SCRIPPS RES INST.
XX
PI Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
XX
DR WPI; 2001-328613/34.
XX
PT Treating cancers, particularly of stomach and colon, that express A33
PT antigen by administering conjugate of anticancer agent with specific
PT immunoglobulin product.
XX
PS Claim 15; Page 39; 85pp; English.
XX
CC The present invention describes a method for treating cancers that
CC express the A33 antigen. The method comprises administering an anticancer
CC agent (I) conjugated to an immunoglobulin product (II) that binds
CC specifically to A33 and contains one or more of 13 specified
CC complementarity determining regions (CDRs), given in AAB98262 to
CC AAB98274. (I) has cytostatic activity. The method can be used for
CC treating colon and stomach cancers. (II), or the nucleic acid encoding
CC it, can be used directly, in unconjugated form, for immunotherapy of
CC cancer, and, when labeled, for detection or diagnosis of diseases
CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
CC AAB98321 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 7
AAB98280
ID AAB98280 standard; peptide; 15 AA.
XX
AC AAB98280;
XX
DT 20-AUG-2001 (first entry)
XX
DE Anti-A33 antigen immunoglobulin VL FR2 SEQ ID NO:86.
XX
KW Human; rabbit; humanised; A33 antigen; anti-A33 antigen antibody;
KW immunoglobulin; complementarity determining region; CDR; cancer;
KW cytostatic; anticancer; colon cancer; stomach cancer.
XX
OS Homo sapiens.
XX
PN WO200130393-A2.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US029289.
XX
PR 22-OCT-1999; 99US-00425638.
PR 04-APR-2000; 2000US-00543004.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
PA (SCRI) SCRIPPS RES INST.
XX
PI Barbas CF, Rader C, Ritter G, Welt S, Old LJ;
XX
DR WPI; 2001-328613/34.
XX
PT Treating cancers, particularly of stomach and colon, that express A33
PT antigen by administering conjugate of anticancer agent with specific
PT immunoglobulin product.
XX
PS Claim 15; Page 39; 85pp; English.
XX
CC The present invention describes a method for treating cancers that
CC express the A33 antigen. The method comprises administering an anticancer
CC agent (I) conjugated to an immunoglobulin product (II) that binds
CC specifically to A33 and contains one or more of 13 specified
CC complementarity determining regions (CDRs), given in AAB98262 to
CC AAB98274. (I) has cytostatic activity. The method can be used for

CC treating colon and stomach cancers. (II), or the nucleic acid encoding
CC it, can be used directly, in unconjugated form, for immunotherapy of
CC cancer, and, when labeled, for detection or diagnosis of diseases
CC associated with A33 expression. AAH22218 to AAH22254 and AAB98230 to
CC AAB98321 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 8
AAB97660
ID AAB97660 standard; peptide; 15 AA.
XX
AC AAB97660;
XX
DT 08-AUG-2001 (first entry)
XX
DE A33 antigen binding immunoglobulin product VLFR2 peptide SEQ ID NO:86.
XX
KW Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
KW immunoreact; anti A33 antigen antibody; immunoglobulin.
XX
OS Homo sapiens.
XX
PN WO200131065-A1.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US029026.
XX
PR 22-OCT-1999; 99US-00425638.
PR 04-APR-2000; 2000US-00543004.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Barbas CF, Rader C;
XX
DR WPI; 2001-328657/34.
XX
PT Preparing humanized rabbit antibodies that specifically immunoreact with
PT a particular antigen using display technology for expressing libraries of
PT antibody domains and fine tuning variable domain regions.
XX
PS Example 9; Page 39; 62pp; English.
XX
CC The present invention describes a method for preparing a humanised rabbit
CC antibody that specifically immunoreacts with a particular antigen. The
CC method comprises expressing a library of antibodies comprising one or
CC more complementarity determining region (CDR) from the variable domain
CC sequences that specifically immunoreact with the antigen grafted into
CC framework regions from humans, and selecting the antibodies that react
CC with the antigen. The method is useful for humanising non-human mammalian
CC antibodies, which can be used for the treatment of a variety of diseases.
CC The present sequence represents an A33 antigen binding immunoglobulin
CC product VLFR2 peptide which is given in an example from the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 9
AAB97659
ID AAB97659 standard; peptide; 15 AA.
XX
AC AAB97659;
XX
DT 08-AUG-2001 (first entry)
XX
DE A33 antigen binding immunoglobulin product VLFR2 peptide SEQ ID NO:85.
XX
KW Chimeric antibody; humanised; humanisation; mammalian antibody; antigen;
KW immunoreact; anti A33 antigen antibody; immunoglobulin.
XX
OS Homo sapiens.
XX
PN WO200131065-A1.
XX
PD 03-MAY-2001.
XX
PF 20-OCT-2000; 2000WO-US029026.
XX
PR 22-OCT-1999; 99US-00425638.
PR 04-APR-2000; 2000US-00543004.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Barbas CF, Rader C;
XX
DR WPI; 2001-328657/34.
XX
PT Preparing humanized rabbit antibodies that specifically immunoreact with
PT a particular antigen using display technology for expressing libraries of
PT antibody domains and fine tuning variable domain regions.
XX
PS Example 9; Page 39; 62pp; English.
XX
CC The present invention describes a method for preparing a humanised rabbit
CC antibody that specifically immunoreacts with a particular antigen. The
CC method comprises expressing a library of antibodies comprising one or
CC more complementarity determining region (CDR) from the variable domain
CC sequences that specifically immunoreact with the antigen grafted into
CC framework regions from humans, and selecting the antibodies that react
CC with the antigen. The method is useful for humanising non-human mammalian
CC antibodies, which can be used for the treatment of a variety of diseases.
CC The present sequence represents an A33 antigen binding immunoglobulin
CC product VLFR2 peptide which is given in an example from the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 10
AAE19670
ID AAE19670 standard; peptide; 15 AA.
XX
AC AAE19670;
XX
DT 31-MAY-2002 (first entry)
XX
DE Human group 1 consensus peptide #2.
XX

KW Human; tumour necrosis factor 40; TNF40; osteopathic; cardiant; CDR;
KW complementarity determining region; rheumatoid; osteo-arthritis; sepsis;
KW congestive heart failure; shock; tissue transplant; tuberculosis; AIDS;
KW Acquired Immune Deficiency Syndrome; adult respiratory distress syndrome;
KW cachexia; allergy; psoriasis; blood coagulation disorder; thyroiditis;
KW inflammatory bone disorder; Crohn's disease; autoimmune disease; burn;
KW neoplasty therapy; immunomodulator; vulnerary; graft rejection.
XX
OS Homo sapiens.
XX
PN WO200194585-A1.
XX
PD 13-DEC-2001.
XX
PF 05-JUN-2001; 2001WO-GB002477.
XX
PR 06-JUN-2000; 2000GB-00013810.
XX
PA (CELL-) CELLTECH R & D LTD.
XX
PI Athwal DS, Brown DT, Weir ANC, Popplewell AG, Chapman AP;
PI King DJ;
XX
DR WPI; 2002-216732/27.
XX
PT New antibody specific for human tumor necrosis factor (TNF)-alpha, useful
PT for treating TNF-alpha-mediated diseases, e.g. congestive heart failure,
PT septic or endotoxic shock, cachexia, adult respiratory distress syndrome.
XX
PS Example 1; Fig 1; 119pp; English.
XX
CC The invention relates to an antibody molecule having specificity for
CC human tumour necrosis factor-alpha (TNFalpha) comprising a heavy or light
CC chain. The antibody or the compound comprising the antibody is useful for
CC treating or manufacturing a medicament for treating a pathology mediated
CC by TNFalpha, such as rheumatoid or osteo-arthritis. TNFalpha mediated
CC diseases which can be treated by the antibody include sepsis, congestive
CC heart failure, septic or endotoxic shock, cachexia, adult respiratory
CC distress syndrome, acquired immunodeficiency syndrome (AIDS), allergies,
CC psoriasis, tuberculosis, inflammatory bone disorders, blood coagulation
CC disorders, burns, rejection episodes following organ or tissue
CC transplant, Crohn's disease and autoimmune diseases, such as thyroiditis.
CC The antibodies may also be used to reduce the side effects associated
CC with TNFalpha generation during neoplasty therapy, to eliminate or reduce
CC shock-related symptoms associated with the treatment or prevention of
CC graft rejection by use of an anti-lymphocyte antibody, for treating multi
CC -organ failure, or in the diagnosis and imaging of disease states
CC involving elevated levels of TNF alpha. The present sequence is human
CC group 1 consensus peptide used in the exemplification of the invention
XX
SQ Sequence 15 AA;

```
  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15
```

RESULT 11
AAU70395
ID AAU70395 standard; peptide; 15 AA.
XX
AC AAU70395;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human light chain immunoglobulin framework region 2 #1.
XX
KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IgBP;
KW transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
KW IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
XX
OS Homo sapiens.
XX
PN WO200183806-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US014349.
XX
PR 02-MAY-2000; 2000US-00563222.
XX
PA (EPIC-) EPICYTE PHARM INC.
XX
PI Hiatt AC, Hein MB;
XX
DR WPI; 2002-055482/07.
XX
PT Preparing immunoglobulin binding protein array in plant cells by
PT transforming the cells with different polynucleotides encoding binding
PT protein polypeptides specific to ligand, selecting plant cells for
PT preparing array.
XX
PS Disclosure; Fig 1A; 129pp; English.
XX
CC The invention relates to transforming a population of cells (e.g. plant
CC cells), comprising using a library of two different polynucleotides
CC encoding different immunoglobulin binding protein (IgBP) polypeptides
CC that specifically bind to a ligand or form one or more disulphide bonds
CC with polypeptides in transfected cells, to generate an IgBP that binds to
CC a ligand, and transformed plant cells are selected, and preparing an IgBP
CC array in plant cells. At least one peptide sequence has at least 75%
CC sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
CC IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
CC useful for preparing an immunoglobulin binding protein array, preferably
CC heavy chain binding protein (CHBP) array in eukaryotic cells especially
CC plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
CC cells (e.g. insect cells or mammalian cells). The CHBP is useful for
CC discovery of e.g. screening assays of IgBPs having desired
CC characteristics. The present sequence is a mammalian immunoglobulin
CC derived peptide that may be incorporated into an IgBP of the invention
XX
SQ Sequence 15 AA;

```
  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15
```

RESULT 12
ADO60478
ID ADO60478 standard; peptide; 15 AA.
XX
AC ADO60478;
XX
DT 12-AUG-2004 (first entry)
XX
DE Humanised mouse 83-14 antibody light chain framework 2.
XX
KW neuroprotective; targeted therapy; humanised antibody;
KW human insulin receptor; HIR; heavy chain; constant region;
KW variable region; complementarity determining region; CDR; framework;
KW neuropharmaceutical agent; blood brain barrier; avidin-biotin linkage;
KW mouse; antibody 83-14; Mab 83-14; light chain variable region; framework;
KW FR2.
XX
OS Mus sp.
OS Homo sapiens.

OS Synthetic.
XX
PN US2004101904-A1.
XX
PD 27-MAY-2004.
XX
PF 27-NOV-2002; 2002US-00307276.
XX
PR 27-NOV-2002; 2002US-00307276.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Pardridge WM, Boado RJ;
XX
DR WPI; 2004-459888/43.
XX
PT Humanized murine antibody that bind to human insulin receptor useful to
PT transport neuropharmaceutical agents, has heavy and light amino acid
PT chain having complementarity determining regions interspersed between
PT humanized framework regions.
XX
PS Claim 6; SEQ ID NO 39; 34pp; English.
XX
CC The invention describes a humanised antibody (I) that binds with the
CC human insulin receptor (HIR. The humanised antibody comprises a heavy
CC chain of amino acids comprising a constant region and a variable region
CC where the variable region has an amino end and a carboxyl end and
CC comprises complementarity determining regions (CDR) interspersed between
CC framework regions, the CDR comprises a first CDR located at the amino end
CC of the variable region, a third CDR located at the carboxyl end of the
CC variable region and a second CDR located between the first and third
CC CDRs. The framework regions comprise a first frame work region located
CC adjacent to the amino end of the first CDR, a second framework region
CC located between the first and second CDR, a third frame work region
CC located between the second and third CDR and a fourth frame work region
CC located adjacent to the carboxyl end of the third CDRs, where the
CC framework regions have been humanized, and a light chain of aminoacids
CC compatible with the heavy chain. (I) is useful for increasing the ability
CC of neuropharmaceutical agent to cross the human blood brain barrier which
CC involves linking the neuropharmaceutical agent to (I) by an avidin-biotin
CC linkage or by genetic fusion. (I) is useful for targeting a
CC pharmaceutical agent to the HIR in vivo which involves linking the
CC pharmaceutical agent to (I). A preparation (II) comprising (I) is useful
CC for intravenously administering a pharmaceutical agent to a human patient
CC which involves injecting (II) into blood stream of the human patient. (I)
CC is useful in combination with drug and diagnostic agent to treat human
CC beings in vivo. (I) is useful as Trojan horse to transport
CC neuropharmaceutical agents across blood brain barrier. This is the amino
CC acid sequence of the preferred sequence of framework region 2 (FR2) in
CC the humanised mouse antibody 83-14 light chain.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 13
ADR38844
ID ADR38844 standard; peptide; 15 AA.
XX
AC ADR38844;
XX
DT 02-DEC-2004 (first entry)
XX
DE Mouse light chain anti-BoNT-antibody framework 2 seqid 246.
XX
KW antibacterial; antibody; botulinum neurotoxin type A; BoNT/A;
KW BoNT/A neutralising epitope; anti-botulinum neurotoxin antibody;
KW toxin neutralisation; botulinum neurotoxin poisoning; mouse; light chain;
KW framework 2.
XX
OS Mus sp.
XX
PN US2004175385-A1.
XX
PD 09-SEP-2004.
XX
PF 01-AUG-2003; 2003US-00632706.
XX
PR 31-AUG-1998; 98US-00144886.
PR 01-AUG-2002; 2002US-0400721P.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Marks JD, Amersdorfer P;
XX
DR WPI; 2004-652009/63.
XX
PT New isolated antibody that neutralizes botulinum neurotoxin type A,
PT useful for diagnosing botulism or for treating pathologies associated
PT with botulinum neurotoxin poisoning.
XX
PS Example 4; SEQ ID NO 246; 110pp; English.
XX
CC The invention describes an isolated antibody (I) that specifically binds
CC to an epitope specifically bound by an antibody expressed by a specific
CC clone where (I) binds to and neutralises botulinum neurotoxin type A
CC (BoNT/A). An isolated antibody (I) that specifically binds to an epitope
CC specifically bound by an antibody expressed by a clone chosen from clone
CC S25, C25, C39, 1C6, 3D12, B4, 1F3, huC25, Ar1, Ar2, WR1(V), WR1(T), 3-1,
CC 3-8, 3-10 and ING1, where (I) binds to and neutralizes botulinum
CC neurotoxin type A (BoNT/A). Also described are: a polypeptide (II)
CC comprising BoNT/A neutralising epitope having an epitope that is
CC specifically bound by an antibody expressed by clones as mentioned in (I)
CC ; producing (I); and a composition (III) comprising several anti-
CC botulinum neurotoxin antibodies, where each antibody is specific for a
CC different epitope of a botulinum neurotoxin and the combination of
CC antibodies shows greater toxin neutralisation than the single antibodies
CC in surplus. The following are disclosed: a pharmaceutical composition
CC comprising (I); and a kit comprising (I). (I) is useful for neutralising
CC BoNT/A antibody and for neutralising a botulinum neurotoxin which
CC involves contacting neurotoxin with (I) in surplus, where each of (I) is
CC specific for a different epitope of the botulinum neurotoxin and the
CC combination of antibodies shows greater toxin neutralisation than the
CC single antibodies in surplus. (I) is useful for diagnosing the botulism
CC or for treating pathologies associated with botulinum neurotoxin
CC poisoning. (I) exhibits specificity and affinity towards BoNT/A. (I)
CC enables rapid detection or diagnosis of botulism. This is the amino acid
CC sequence of mouse light chain anti-BoNT-antibody framework region 2.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 14
ADU07265
ID ADU07265 standard; peptide; 15 AA.
XX
AC ADU07265;
XX
DT 13-JAN-2005 (first entry)
XX
DE IL-9 antibody variable light chain (VL) framework region 2.

XX
KW Respiratory infection; human; interleukin-9 antagonist; IL-9;
KW respiratory syncytial virus; anti-RSV antigen antibody;
KW leukotriene modifier; asthma-like symptom; wheezing; allergy;
KW immunomodulatory; anti-inflammatory; anti-viral; antibiotic; antifungal;
KW mast cell modulator; virucide; antibacterial; fungicide; antiasthmatic;
KW antiallergic; IL-9 antibody; variable light chain; VL; framework region.
XX
OS Homo sapiens.
XX
PN WO2004091519-A2.
XX
PD 28-OCT-2004.
XX
PF 12-APR-2004; 2004WO-US011329.
XX
PR 11-APR-2003; 2003US-0462307P.
PR 10-JUN-2003; 2003US-0477801P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Reed JL;
XX
DR WPI; 2004-775524/76.
XX
PT Managing, treating or ameliorating in a human subject a respiratory
PT infection or its symptoms caused by bacteria, fungi or respiratory
PT syncytial virus by administering an IL-9 antagonist.
XX
PS Disclosure; SEQ ID NO 40; 276pp; English.
XX
CC The invention relates to a method of managing, treating or ameliorating a
CC respiratory infection or its symptom in a human subject by administering
CC an interleukin-9 (IL-9) antagonist. The method further comprises
CC administering to the subject an anti-respiratory syncytial virus (anti-
CC RSV) antigen antibody. The anti-RSV antigen antibody is palivizumab. The
CC method further comprises administering a leukotriene modifier, which is
CC montelukast, zafirlukast, pranlukast or zileuton. Also disclosed are: a
CC method of preventing the development, onset or progression of asthma or
CC one or more asthma-like symptoms in a child, a method of preventing,
CC managing, treating or ameliorating wheezing in a pre-term infant, infant
CC or child, a method of preventing, managing, treating or ameliorating
CC wheezing in a human subject, and a method of preventing, managing,
CC treating or ameliorating asthma or an allergy or its symptoms in a human
CC subject. Preventing the development, onset or progression of asthma or
CC one or more asthma-like symptoms in a child having or previously having a
CC respiratory infection comprises administering an IL-9 antagonist.
CC Preventing, managing, treating or ameliorating wheezing in a pre-term
CC infant, infant or child comprises administering an IL-9 antagonist. The
CC method further comprises administering at least one other therapy that is
CC not administration of an IL-9 antagonist. Preventing, managing, treating
CC or ameliorating wheezing in a human subject comprises administering an IL
CC -9 antagonist and at least one other therapy that is not administration
CC of an IL-9 antagonist. The therapy is an immunomodulatory agent, an anti-
CC inflammatory agent, an anti-viral agent, an antibiotic, an antifungal
CC agent or a mast cell modulator. The method further comprises
CC administering to the subject a leukotriene modifier, an anti-histamine,
CC an anti-immunoglobulin E (IgE) antibody, an anti-IL-4 antibody or a mast
CC cell protease inhibitor. Preventing, managing, treating or ameliorating
CC asthma or an allergy or its symptoms in a human subject comprises
CC administering an IL-9 antagonist and at least one other asthma or allergy
CC therapy. The IL-9 antagonist is an antibody that immunospecifically binds
CC to an IL-9 receptor (IL-9R) or its subunit or to an IL-9 polypeptide. The
CC methods are useful in managing, treating or ameliorating in a human
CC subject a respiratory infection or its symptoms caused by bacteria, fungi
CC or RSV. This sequence represents a framework region from an antibody
CC against IL-9.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 15
ADT88332
ID ADT88332 standard; peptide; 15 AA.
XX
AC ADT88332;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human IL-19 antibody VL framework region 2 seqid 40.
XX
KW respiratory; antiinflammatory; immunosuppressive; antiasthmatic;
KW antiallergic; antiarthritic; neuroprotective; antirheumatic; immunotoxin;
KW angiogenesis inhibitor; TNF alpha antagonist; IL-9 antagonist; IL-9;
KW IL-9 antibody; 4D4; 4D4 H2-1 D11; 4D4com-XF9; 4D4com-2F9; 7F3; 71A10;
KW 22D3; 7F3com-2H2; 7F3com-3H5; 7F3com-3D4; IL-9 associated disorder;
KW respiratory infection; respiratory syncytial virus; parainfluenza virus;
KW human metapneumovirus; inflammatory disorder; asthma; allergy; arthritis;
KW autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
KW framework region 2; variable light chain.
XX
OS Homo sapiens.
XX
PN WO2004091510-A2.
XX
PD 28-OCT-2004.
XX
PF 12-APR-2004; 2004WO-US011172.
XX
PR 11-APR-2003; 2003US-0462259P.
PR 10-JUN-2003; 2003US-0477797P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Reed JL;
XX
DR WPI; 2004-775520/76.
XX
PT New IL-9 antibody comprising a variable heavy or light domain or a
PT complementarity determining region having an amino acid sequence of e.g.,
PT 4D4, useful in treating or preventing e.g., respiratory infection or
PT inflammatory disorder.
XX
PS Disclosure; SEQ ID NO 40; 291pp; English.
XX
CC The invention describes a new IL-9 antibody comprising: a variable heavy
CC (VH) or variable light (VL) domain having an amino acid sequence of the
CC VH or VL domain of 4D4, 4D4 H2-1 D11, 4D4com-XF9, 4D4com-2F9, 7F3, 71A10,
CC 22D3, 7F3com-2H2, 7F3com-3H5 or 7F3com-3D4; or a complementarity
CC determining region (CDR) having an amino acid sequence of a CDR of 4D4,
CC 4D4 H2-1 D11, 4D4com-XF9, 4D4com-2F9, 7F3, 71A10, 22D3, 7F3com-2H2,
CC 7F3com-3H5 or 7F3com-3D4. The antibody immunospecifically binds to a
CC human IL-9 polypeptide. Also described are: a pharmaceutical composition
CC comprising the IL-9 antibody and a carrier; a method for preventing,
CC treating, managing or ameliorating a disease or disorder characterised by
CC aberrant expression or activity of an IL-9 polypeptide or an IL-9R; a
CC method of diagnosing, prognosing, or monitoring a disorder or disease
CC characterised by aberrant expression or activity of an IL-9 polypeptide
CC or aberrant expression or activity of an IL-9R; a kit comprising the
CC antibody and instructions for use, in one or more containers; and an
CC article of manufacture comprising a packaging material and a
CC pharmaceutical agent contained within the packaging material, where the
CC pharmaceutical agent comprises the IL-9 antibody and a carrier. The IL-9
CC antibody is useful in preparing a composition for diagnosing, treating or
CC preventing a disease or disorder characterised by aberrant expression or
CC activity of an IL-9 polypeptide or an IL-9R, e.g., respiratory infection
CC caused by bacteria or respiratory syncytial virus, parainfluenza virus or
CC human metapneumovirus, inflammatory disorder such as asthma, allergy or

```
CC   arthritis or autoimmune disorder such as rheumatoid arthritis and
CC   multiple sclerosis. This is the amino acid sequence of a human IL-19
CC   antibody variable light chain framework region 2.
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 86;  DB 8;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 16
ADU38487
ID   ADU38487 standard; peptide; 15 AA.
XX
AC   ADU38487;
XX
DT   27-JAN-2005  (first entry)
XX
DE   Mouse antibody 14F7-derived single chain antibody #3 framework region 2.
XX
KW   cytostatic; angiogenesis inhibitor; antibody engineering; antibody;
KW   hybridoma; framework region; ganglioside; angiogenesis; melanoma;
KW   neoplasm.
XX
OS   Mus sp.
OS   Synthetic.
XX
PN   WO2004094477-A1.
XX
PD   04-NOV-2004.
XX
PF   22-APR-2004; 2004WO-CU000006.
XX
PR   23-APR-2003; 2003CU-00000092.
XX
PA   (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
XX
PI   Roque Navarro LT,  Mateo De Acosta Del Rio CM,  Rodriguez Gonzalez M;
PI   Rojas Dorantes G,  Talavera Perez A,  Moreno Frias E;
XX
DR   WPI; 2004-775911/76.
XX
PT   New recombinant antibody derived from murine antibody 14F7, useful for
PT   treatment and detection of malignant tumors, is specific for the
PT   ganglioside N-glycolyl-GM3, has reduced immunogenicity.
XX
PS   Claim 14; Page 26; 54pp; Spanish.
XX
CC   The invention relates to a recombinant antibody (rAb), derived from the
CC   murine monoclonal antibody 14F7 (produced by hybridoma ECACC 98101901),
CC   in which the complementarity determining regions (CDR) have the following
CC   sequences: heavy chain: CDR1, Ser-Tyr-Trp-Ile-His; CDR2, Tyr-Ile-Asp-Pro-
CC   Ala-Thr-Ala-Tyr-Thr-Glu-Ser-Asn-Gln-Lys-Phe-Lys-Asp; CDR3, Glu-Ser-Pro-
CC   Arg-Leu-Arg-Arg-Gly-Ile(Tyr) 3 Ala-Met-Asp-Tyr; light chain: CDR1, Arg-
CC   Ala-Ser-Gln-Ser-Ile-Ser-Asn-Asn-Leu-His; CDR2, Tyr-Ala-Ser-Gln-Ser-Ile-
CC   Ser; CDR3, Gln-Gln-Ser-Asn-Arg-Trp-Pro-Leu-Thr. The rAb and its
CC   derivatives recognize specifically the ganglioside N-glycoly-GM3, so
CC   inhibit angiogenesis. The rAb, and derived single-chain Fv fragments, are
CC   used, when labelled with a radioisotope, for treatment of malignant
CC   tumors (especially of the breast, or melanomas), including metastases and
CC   relapses; also when appropriately labelled, they are useful for in vivo
CC   localization and detection of tumors. The rAb and its derivatives are
CC   less immunogenic in humans than 14F7 itself. This sequence corresponds to
CC   the mutated framework region 2 derived from the mouse antibody 14F7 and
CC   used to generate the antibody of the invention.
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 86;  DB 8;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 17
ADX27016
ID   ADX27016 standard; peptide; 15 AA.
XX
AC   ADX27016;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Human group 1 consensus light chain framework region peptide - SEQ ID 85.
XX
KW   antibody; antiarthritic; antirheumatic; gastrointestinal-gen.;
KW   antiinflammatory; rheumatoid arthritis; musculoskeletal disease;
KW   inflammatory bowel disease; gastrointestinal disease; inflammation;
KW   Crohns disease; immune disorder; light chain.
XX
OS   Homo sapiens.
XX
PN   WO2005014649-A2.
XX
PD   17-FEB-2005.
XX
PF   29-JUL-2004; 2004WO-IB002529.
XX
PR   08-AUG-2003; 2003US-0493740P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Banerjee A,  Gustafson M,  Ho SV,  Mclaughlin J,  Thomas K;
XX
DR   WPI; 2005-152548/16.
XX
PT   Preparing a tumor necrosis factor-alpha antibody having a heavy and light
PT   chain comprises fermenting a cell mixture, forming a cell pellet and
PT   allowing the pellet to stand for a hold time.
XX
PS   Example 4; SEQ ID NO 85; 125pp; English.
XX
CC   The invention relates to a novel method for preparing an antibody with a
CC   heavy and light chain comprising fermenting a cell mixture, where the
CC   cells are capable of expressing the light and heavy chain, separating the
CC   cells from the supernatant to form a cell pellet, allowing the pellet to
CC   stand for a hold time, extracting the cell pellet and producing the TNF
CC   (tumor necrosis factor)-alpha antibody fragment or its dimer or adduct.
CC   The antibody of the invention demonstrates antiarthritic, antirheumatic,
CC   gastrointestinal-gen. and antiinflammatory activities and may be useful
CC   for treatment of rheumatoid arthritis or an inflammatory bowel disease,
CC   such as Crohn's disease. Currently used anti-TNF-alpha monoclonal
CC   antibodies, such as infliximab and etanercept, have limited success in
CC   the treatment of disease since they must be administered frequently or
CC   intravenously. Furthermore, both of these molecules comprise large
CC   proteins and as such are difficult and expensive to manufacture. The
CC   current sequence is that of a human group 1 consensus light chain
CC   framework region peptide of the invention which may be used to construct
CC   a chimeric antibody targeted to TNF-alpha.
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 86;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15
```

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RESULT 18
ADY31248
ID   ADY31248 standard; peptide; 15 AA.
XX
AC   ADY31248;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Human antibody kappa chain framework peptide - SEQ ID 80.
XX
KW   DNA library; humanized antibody; antibody engineering;
KW   kappa chain framework.
XX
OS   Homo sapiens.
XX
PN   US2005042664-A1.
XX
PD   24-FEB-2005.
XX
PF   20-AUG-2004; 2004US-00923068.
XX
PR   22-AUG-2003; 2003US-0497213P.
PR   13-OCT-2003; 2003US-0510741P.
XX
PA   (MEDI-) MEDIMMUNE INC.
XX
PI   Wu H,  Dall-Acqua W,  Damschroder M;
XX
DR   WPI; 2005-180802/19.
XX
PT   New library of nucleic acid sequences comprises nucleotide sequences
PT   encoding humanized heavy chain variable regions and humanized light chain
PT   variable regions, useful for producing humanized antibodies.
XX
PS   Disclosure; SEQ ID NO 80; 179pp; English.
XX
CC   The invention comprises a library of nucleotide sequences encoding
CC   humanized antibody heavy chain variable regions and humanized antibody
CC   light chain variable regions. The library of the invention is useful for
CC   producing humanized antibodies, or for re-engineering or reshaping an
CC   antibody from a first species for use in a second species. The present
CC   amino acid sequence represents a human germline kappa chain framework
CC   peptide.
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 86;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 19
ADY31272
ID   ADY31272 standard; peptide; 15 AA.
XX
AC   ADY31272;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Human antibody kappa chain framework peptide - SEQ ID 104.
XX
KW   DNA library; humanized antibody; antibody engineering;
KW   kappa chain framework.
XX
OS   Homo sapiens.
XX
PN   US2005042664-A1.
XX
PD   24-FEB-2005.
XX
PF   20-AUG-2004; 2004US-00923068.
XX
PR   22-AUG-2003; 2003US-0497213P.
PR   13-OCT-2003; 2003US-0510741P.
XX
PA   (MEDI-) MEDIMMUNE INC.
XX
PI   Wu H,  Dall-Acqua W,  Damschroder M;
XX
DR   WPI; 2005-180802/19.
XX
PT   New library of nucleic acid sequences comprises nucleotide sequences
PT   encoding humanized heavy chain variable regions and humanized light chain
PT   variable regions, useful for producing humanized antibodies.
XX
PS   Disclosure; SEQ ID NO 104; 179pp; English.
XX
CC   The invention comprises a library of nucleotide sequences encoding
CC   humanized antibody heavy chain variable regions and humanized antibody
CC   light chain variable regions. The library of the invention is useful for
CC   producing humanized antibodies, or for re-engineering or reshaping an
CC   antibody from a first species for use in a second species. The present
CC   amino acid sequence represents a human germline kappa chain framework
CC   peptide.
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 86;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 20
ADY31299
ID   ADY31299 standard; peptide; 15 AA.
XX
AC   ADY31299;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Human antibody kappa chain framework peptide - SEQ ID 131.
XX
KW   DNA library; humanized antibody; antibody engineering;
KW   kappa chain framework.
XX
OS   Homo sapiens.
XX
PN   US2005042664-A1.
XX
PD   24-FEB-2005.
XX
PF   20-AUG-2004; 2004US-00923068.
XX
PR   22-AUG-2003; 2003US-0497213P.
PR   13-OCT-2003; 2003US-0510741P.
XX
PA   (MEDI-) MEDIMMUNE INC.
XX
PI   Wu H,  Dall-Acqua W,  Damschroder M;
XX
DR   WPI; 2005-180802/19.
XX
PT   New library of nucleic acid sequences comprises nucleotide sequences
PT   encoding humanized heavy chain variable regions and humanized light chain
PT   variable regions, useful for producing humanized antibodies.
XX
```

PS Disclosure; SEQ ID NO 131; 179pp; English.
XX
CC The invention comprises a library of nucleotide sequences encoding
CC humanized antibody heavy chain variable regions and humanized antibody
CC light chain variable regions. The library of the invention is useful for
CC producing humanized antibodies, or for re-engineering or reshaping an
CC antibody from a first species for use in a second species. The present
CC amino acid sequence represents a human germline kappa chain framework
CC peptide.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 21
ADY31245
ID ADY31245 standard; peptide; 15 AA.
XX
AC ADY31245;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody kappa chain framework peptide - SEQ ID 77.
XX
KW DNA library; humanized antibody; antibody engineering;
KW kappa chain framework.
XX
OS Homo sapiens.
XX
PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
PF 20-AUG-2004; 2004US-00923068.
XX
PR 22-AUG-2003; 2003US-0497213P.
PR 13-OCT-2003; 2003US-0510741P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Wu H, Dall-Acqua W, Damschroder M;
XX
DR WPI; 2005-180802/19.
XX
PT New library of nucleic acid sequences comprises nucleotide sequences
PT encoding humanized heavy chain variable regions and humanized light chain
PT variable regions, useful for producing humanized antibodies.
XX
PS Disclosure; SEQ ID NO 77; 179pp; English.
XX
CC The invention comprises a library of nucleotide sequences encoding
CC humanized antibody heavy chain variable regions and humanized antibody
CC light chain variable regions. The library of the invention is useful for
CC producing humanized antibodies, or for re-engineering or reshaping an
CC antibody from a first species for use in a second species. The present
CC amino acid sequence represents a human germline kappa chain framework
CC peptide.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 22
ADY31233
ID ADY31233 standard; peptide; 15 AA.
XX
AC ADY31233;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody kappa chain framework peptide - SEQ ID 65.
XX
KW DNA library; humanized antibody; antibody engineering;
KW kappa chain framework.
XX
OS Homo sapiens.
XX
PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
PF 20-AUG-2004; 2004US-00923068.
XX
PR 22-AUG-2003; 2003US-0497213P.
PR 13-OCT-2003; 2003US-0510741P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Wu H, Dall-Acqua W, Damschroder M;
XX
DR WPI; 2005-180802/19.
XX
PT New library of nucleic acid sequences comprises nucleotide sequences
PT encoding humanized heavy chain variable regions and humanized light chain
PT variable regions, useful for producing humanized antibodies.
XX
PS Disclosure; SEQ ID NO 65; 179pp; English.
XX
CC The invention comprises a library of nucleotide sequences encoding
CC humanized antibody heavy chain variable regions and humanized antibody
CC light chain variable regions. The library of the invention is useful for
CC producing humanized antibodies, or for re-engineering or reshaping an
CC antibody from a first species for use in a second species. The present
CC amino acid sequence represents a human germline kappa chain framework
CC peptide.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 23
ADY31278
ID ADY31278 standard; peptide; 15 AA.
XX
AC ADY31278;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody kappa chain framework peptide - SEQ ID 110.
XX
KW DNA library; humanized antibody; antibody engineering;
KW kappa chain framework.
XX
OS Homo sapiens.
XX

PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
PF 20-AUG-2004; 2004US-00923068.
XX
PR 22-AUG-2003; 2003US-0497213P.
PR 13-OCT-2003; 2003US-0510741P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Wu H, Dall-Acqua W, Damschroder M;
XX
DR WPI; 2005-180802/19.
XX
PT New library of nucleic acid sequences comprises nucleotide sequences
PT encoding humanized heavy chain variable regions and humanized light chain
PT variable regions, useful for producing humanized antibodies.
XX
PS Disclosure; SEQ ID NO 110; 179pp; English.
XX
CC The invention comprises a library of nucleotide sequences encoding
CC humanized antibody heavy chain variable regions and humanized antibody
CC light chain variable regions. The library of the invention is useful for
CC producing humanized antibodies, or for re-engineering or reshaping an
CC antibody from a first species for use in a second species. The present
CC amino acid sequence represents a human germline kappa chain framework
CC peptide.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 24
ADY31230
ID ADY31230 standard; peptide; 15 AA.
XX
AC ADY31230;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody kappa chain framework peptide - SEQ ID 62.
XX
KW DNA library; humanized antibody; antibody engineering;
KW kappa chain framework.
XX
OS Homo sapiens.
XX
PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
PF 20-AUG-2004; 2004US-00923068.
XX
PR 22-AUG-2003; 2003US-0497213P.
PR 13-OCT-2003; 2003US-0510741P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Wu H, Dall-Acqua W, Damschroder M;
XX
DR WPI; 2005-180802/19.
XX
PT New library of nucleic acid sequences comprises nucleotide sequences
PT encoding humanized heavy chain variable regions and humanized light chain
PT variable regions, useful for producing humanized antibodies.
XX
PS Disclosure; SEQ ID NO 62; 179pp; English.
XX
CC The invention comprises a library of nucleotide sequences encoding
CC humanized antibody heavy chain variable regions and humanized antibody
CC light chain variable regions. The library of the invention is useful for
CC producing humanized antibodies, or for re-engineering or reshaping an
CC antibody from a first species for use in a second species. The present
CC amino acid sequence represents a human germline kappa chain framework
CC peptide.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 25
ADY31269
ID ADY31269 standard; peptide; 15 AA.
XX
AC ADY31269;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody kappa chain framework peptide - SEQ ID 101.
XX
KW DNA library; humanized antibody; antibody engineering;
KW kappa chain framework.
XX
OS Homo sapiens.
XX
PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
PF 20-AUG-2004; 2004US-00923068.
XX
PR 22-AUG-2003; 2003US-0497213P.
PR 13-OCT-2003; 2003US-0510741P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Wu H, Dall-Acqua W, Damschroder M;
XX
DR WPI; 2005-180802/19.
XX
PT New library of nucleic acid sequences comprises nucleotide sequences
PT encoding humanized heavy chain variable regions and humanized light chain
PT variable regions, useful for producing humanized antibodies.
XX
PS Disclosure; SEQ ID NO 101; 179pp; English.
XX
CC The invention comprises a library of nucleotide sequences encoding
CC humanized antibody heavy chain variable regions and humanized antibody
CC light chain variable regions. The library of the invention is useful for
CC producing humanized antibodies, or for re-engineering or reshaping an
CC antibody from a first species for use in a second species. The present
CC amino acid sequence represents a human germline kappa chain framework
CC peptide.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15

```
              ||||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 26
ADY31290
ID   ADY31290 standard; peptide; 15 AA.
XX
AC   ADY31290;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Human antibody kappa chain framework peptide - SEQ ID 122.
XX
KW   DNA library; humanized antibody; antibody engineering;
KW   kappa chain framework.
XX
OS   Homo sapiens.
XX
PN   US2005042664-A1.
XX
PD   24-FEB-2005.
XX
PF   20-AUG-2004; 2004US-00923068.
XX
PR   22-AUG-2003; 2003US-0497213P.
PR   13-OCT-2003; 2003US-0510741P.
XX
PA   (MEDI-) MEDIMMUNE INC.
XX
PI   Wu H,  Dall-Acqua W,  Damschroder M;
XX
DR   WPI; 2005-180802/19.
XX
PT   New library of nucleic acid sequences comprises nucleotide sequences
PT   encoding humanized heavy chain variable regions and humanized light chain
PT   variable regions, useful for producing humanized antibodies.
XX
PS   Disclosure; SEQ ID NO 122; 179pp; English.
XX
CC   The invention comprises a library of nucleotide sequences encoding
CC   humanized antibody heavy chain variable regions and humanized antibody
CC   light chain variable regions. The library of the invention is useful for
CC   producing humanized antibodies, or for re-engineering or reshaping an
CC   antibody from a first species for use in a second species. The present
CC   amino acid sequence represents a human germline kappa chain framework
CC   peptide.
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 86;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 27
ADY31305
ID   ADY31305 standard; peptide; 15 AA.
XX
AC   ADY31305;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Human antibody kappa chain framework peptide - SEQ ID 137.
XX
KW   DNA library; humanized antibody; antibody engineering;
KW   kappa chain framework.
XX
OS   Homo sapiens.
XX
PN   US2005042664-A1.
XX
PD   24-FEB-2005.
XX
PF   20-AUG-2004; 2004US-00923068.
XX
PR   22-AUG-2003; 2003US-0497213P.
PR   13-OCT-2003; 2003US-0510741P.
XX
PA   (MEDI-) MEDIMMUNE INC.
XX
PI   Wu H,  Dall-Acqua W,  Damschroder M;
XX
DR   WPI; 2005-180802/19.
XX
PT   New library of nucleic acid sequences comprises nucleotide sequences
PT   encoding humanized heavy chain variable regions and humanized light chain
PT   variable regions, useful for producing humanized antibodies.
XX
PS   Disclosure; SEQ ID NO 137; 179pp; English.
XX
CC   The invention comprises a library of nucleotide sequences encoding
CC   humanized antibody heavy chain variable regions and humanized antibody
CC   light chain variable regions. The library of the invention is useful for
CC   producing humanized antibodies, or for re-engineering or reshaping an
CC   antibody from a first species for use in a second species. The present
CC   amino acid sequence represents a human germline kappa chain framework
CC   peptide.
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 86;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 28
ADY31296
ID   ADY31296 standard; peptide; 15 AA.
XX
AC   ADY31296;
XX
DT   05-MAY-2005  (first entry)
XX
DE   Human antibody kappa chain framework peptide - SEQ ID 128.
XX
KW   DNA library; humanized antibody; antibody engineering;
KW   kappa chain framework.
XX
OS   Homo sapiens.
XX
PN   US2005042664-A1.
XX
PD   24-FEB-2005.
XX
PF   20-AUG-2004; 2004US-00923068.
XX
PR   22-AUG-2003; 2003US-0497213P.
PR   13-OCT-2003; 2003US-0510741P.
XX
PA   (MEDI-) MEDIMMUNE INC.
XX
PI   Wu H,  Dall-Acqua W,  Damschroder M;
XX
DR   WPI; 2005-180802/19.
XX
PT   New library of nucleic acid sequences comprises nucleotide sequences
PT   encoding humanized heavy chain variable regions and humanized light chain
```

PT variable regions, useful for producing humanized antibodies.
XX
PS Disclosure; SEQ ID NO 128; 179pp; English.
XX
CC The invention comprises a library of nucleotide sequences encoding
CC humanized antibody heavy chain variable regions and humanized antibody
CC light chain variable regions. The library of the invention is useful for
CC producing humanized antibodies, or for re-engineering or reshaping an
CC antibody from a first species for use in a second species. The present
CC amino acid sequence represents a human germline kappa chain framework
CC peptide.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 29
ADY31281
ID ADY31281 standard; peptide; 15 AA.
XX
AC ADY31281;
XX
DT 05-MAY-2005 (first entry)
XX
DE Human antibody kappa chain framework peptide - SEQ ID 113.
XX
KW DNA library; humanized antibody; antibody engineering;
KW kappa chain framework.
XX
OS Homo sapiens.
XX
PN US2005042664-A1.
XX
PD 24-FEB-2005.
XX
PF 20-AUG-2004; 2004US-00923068.
XX
PR 22-AUG-2003; 2003US-0497213P.
PR 13-OCT-2003; 2003US-0510741P.
XX
PA (MEDI-) MEDIMMUNE INC.
XX
PI Wu H, Dall-Acqua W, Damschroder M;
XX
DR WPI; 2005-180802/19.
XX
PT New library of nucleic acid sequences comprises nucleotide sequences
PT encoding humanized heavy chain variable regions and humanized light chain
PT variable regions, useful for producing humanized antibodies.
XX
PS Disclosure; SEQ ID NO 113; 179pp; English.
XX
CC The invention comprises a library of nucleotide sequences encoding
CC humanized antibody heavy chain variable regions and humanized antibody
CC light chain variable regions. The library of the invention is useful for
CC producing humanized antibodies, or for re-engineering or reshaping an
CC antibody from a first species for use in a second species. The present
CC amino acid sequence represents a human germline kappa chain framework
CC peptide.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 30
AEA45521
ID AEA45521 standard; peptide; 15 AA.
XX
AC AEA45521;
XX
DT 11-AUG-2005 (first entry)
XX
DE Apolipoprotein E C-terminal domain antibody VL-FR2 peptide #18.
XX
KW Neuroprotective; Nootropic; Antidiabetic; Endocrine-Gen.; Nephrotropic;
KW Antiparkinsonian; Anticonvulsant; Respiratory-Gen; Apolipoprotein E;
KW Alzheimers disease; amyloidosis; Parkinsons disease; Huntingtons chorea;
KW Kuru; Dementia; non-insulin dependent diabetes; Down syndrome;
KW Spongiform encephalopathy; Creutzfeldt Jakob disease;
KW motor neurone disease; chronic obstructive pulmonary disease.
XX
OS Homo sapiens.
XX
PN GB2408508-A.
XX
PD 01-JUN-2005.
XX
PF 26-NOV-2004; 2004GB-00026043.
XX
PR 28-NOV-2003; 2003US-0525174P.
XX
PA (ASTR) ASTRAZENECA AB.
PA (DYAX-) DYAX CORP.
XX
PI Nordstedt C, Goldschmidt T, Henderikx M, Hoet R, Hoogenboom H;
PI Hufton S, Andersson CV, Lindquist J, Sunnemark D, Leonov S;
XX
DR WPI; 2005-408785/42.
XX
PT New human antibody or antibody fragment which binds to a sequence of the
PT C-terminal domain of Apolipoprotein E (ApoE-CTD), useful for
PT manufacturing a medicament for treating or preventing an amyloid disorder
PT e.g. Alzheimers disease.
XX
PS Example 8; Page 97; 392pp; English.
XX
CC The present invention relates to a human antibody or antibody fragment,
CC which binds to the C-terminal domain of Apolipoprotein E (ApoE-CTD;
CC AEA44803) and also to human plaques. The antibody or its fragment is
CC useful for manufacturing a medicament for treating or preventing an
CC amyloid disorder such as Alzheimers disease, primary systemic
CC amyloidosis, secondary systemic amyloidosis, senile systemic amyloidosis,
CC familial amyloid polyneuropathy I, familial amyloid polyneuropathy III,
CC familial non-neuropathic amyloidosis, hereditary cerebral amyloid
CC angiopathy, Familial British Dementia, Hemodialysis-related amyloidosis,
CC Familial amyloidosis (Finnish type), Familial subepithelial corneal
CC amyloid, type II diabetes, Hereditary renal amyloidosis, Pituitary-gland
CC amyloidosis, injection localized amyloidosis, Medullary carcinoma of the
CC thyroid, Atrial amyloidosis, Familial Danish dementia (FDD), Downs
CC syndrome, Spongiform encephalopathies, Sporadic Creutzfeldt-Jakob
CC disease, Gerstmann-Straussler-Scheinker Disease (GSS), Kuru, Parkinsons
CC disease, Huntingtons disease, Familial amyotrophic lateral sclerosis, and
CC chronic obstructive pulmonary disease. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15

```
                  ||||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 31
AEA22625
ID   AEA22625 standard; peptide; 15 AA.
XX
AC   AEA22625;
XX
DT   11-AUG-2005  (first entry)
XX
DE   Synthetic antibody framework peptide SEQ ID NO 28.
XX
KW   antibody engineering.
XX
OS   Synthetic.
XX
PN   WO2005049652-A2.
XX
PD   02-JUN-2005.
XX
PF   17-NOV-2004; 2004WO-US038488.
XX
PR   17-NOV-2003; 2003US-0520881P.
PR   17-JUN-2004; 2004US-0581072P.
XX
PA   (ROTH-) ROTHBERG INST CHILDHOOD DISEASES.
XX
PI   Weiner MP,  Rothberg JM;
XX
DR   WPI; 2005-396085/40.
DR   N-PSDB; AEA22624.
XX
PT   Making a double-stranded nucleic acid encoding a single-chain antibody
PT   comprises combining the primed oligonucleotide complexes with a
PT   polymerase, one or more nucleotides, and optionally a ligase.
XX
PS   Example 4; SEQ ID NO 28; 118pp; English.
XX
CC   The invention relates to a method of making a double-stranded nucleic
CC   acid encoding a single-chain antibody which comprises combining the
CC   primed oligonucleotide complexes with a polymerase, one or more
CC   nucleotides, and optionally a ligase. The method is useful for making a
CC   double-stranded nucleic acid encoding a single-chain antibody. The
CC   present sequence represents the amino acid sequence of a synthetic
CC   antibody framework peptide.
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 86;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 32
AEB00046
ID   AEB00046 standard; peptide; 15 AA.
XX
AC   AEB00046;
XX
DT   25-AUG-2005  (first entry)
XX
DE   Novel dengue virus antibody-related 3C1 light chain FR2 peptide SeqID44.
XX
KW   antibody engineering; flavivirus infection; diagnostic; pharmaceutical;
KW   virucide; antiviral; 3C1.
XX
OS   Pan troglodytes.
OS   Synthetic.
XX
PN   WO2005056600-A2.
XX
PD   23-JUN-2005.
XX
PF   03-DEC-2004; 2004WO-US040674.
XX
PR   08-DEC-2003; 2003US-0528161P.
PR   04-FEB-2004; 2004US-0541676P.
PR   12-MAR-2004; 2004US-0552528P.
PR   26-MAY-2004; 2004US-0574492P.
PR   01-NOV-2004; 2004US-0624261P.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Lai C,  Purcell RH;
XX
DR   WPI; 2005-458565/46.
XX
PT   Novel polypeptide comprising fully human or humanized chimpanzee
PT   monoclonal antibody that binds or neutralizes dengue type 1, 2, 3, and/or
PT   4 virus, useful for treatment and diagnosis of dengue.
XX
PS   Disclosure; SEQ ID NO 44; 121pp; English.
XX
CC   This invention relates to novel substantially pure polypeptide comprising
CC   a fully human or humanized chimpanzee monoclonal antibody that binds or
CC   neutralizes dengue type 1, 2, 3, and/or 4 virus, a monoclonal antibody
CC   that binds the antigen to which monoclonal antibody 5H2 (ATCC Accession
CC   No. PTA-5662) binds, or a monoclonal antibody that binds the antigen to
CC   which monoclonal antibody 1A5 (ATCC Accession No. PTA-6265) binds. The
CC   invention may be useful for the development of compounds with a virucide
CC   activity acting by viral neutralization. The invention is useful as
CC   pharmaceutical preparation and a diagnostic preparation for treatment and
CC   diagnosis of dengue virus disease. The present sequence is that of a 3C1
CC   light chain peptide which was used during the development of the novel
CC   anitbodies of the invention.
XX
SQ   Sequence 15 AA;

  Query Match             100.0%;  Score 86;  DB 9;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 33
AEB00158
ID   AEB00158 standard; peptide; 15 AA.
XX
AC   AEB00158;
XX
DT   25-AUG-2005  (first entry)
XX
DE   Novel dengue virus antibody-related 3A2 light chain FR2 peptide SeqID156.
XX
KW   antibody engineering; flavivirus infection; diagnostic; pharmaceutical;
KW   virucide; antiviral; 3A2.
XX
OS   Pan troglodytes.
OS   Synthetic.
XX
PN   WO2005056600-A2.
XX
PD   23-JUN-2005.
XX
PF   03-DEC-2004; 2004WO-US040674.
XX
PR   08-DEC-2003; 2003US-0528161P.
```

PR 04-FEB-2004; 2004US-0541676P.
PR 12-MAR-2004; 2004US-0552528P.
PR 26-MAY-2004; 2004US-0574492P.
PR 01-NOV-2004; 2004US-0624261P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Lai C, Purcell RH;
XX
DR WPI; 2005-458565/46.
XX
PT Novel polypeptide comprising fully human or humanized chimpanzee
PT monoclonal antibody that binds or neutralizes dengue type 1, 2, 3, and/or
PT 4 virus, useful for treatment and diagnosis of dengue.
XX
PS Disclosure; SEQ ID NO 156; 121pp; English.
XX
CC This invention relates to novel substantially pure polypeptide comprising
CC a fully human or humanized chimpanzee monoclonal antibody that binds or
CC neutralizes dengue type 1, 2, 3, and/or 4 virus, a monoclonal antibody
CC that binds the antigen to which monoclonal antibody 5H2 (ATCC Accession
CC No. PTA-5662) binds, or a monoclonal antibody that binds the antigen to
CC which monoclonal antibody 1A5 (ATCC Accession No. PTA-6265) binds. The
CC invention may be useful for the development of compounds with a virucide
CC activity acting by viral neutralization. The invention is useful as
CC pharmaceutical preparation and a diagnostic preparation for treatment and
CC diagnosis of dengue virus disease. The present sequence is that of a 3A2
CC light chain peptide which was used during the development of the novel
CC anitbodies of the invention.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||| |
Db 1 WYQQKPGKAPKLLIY 15

RESULT 34
AEB00110
ID AEB00110 standard; peptide; 15 AA.
XX
AC AEB00110;
XX
DT 25-AUG-2005 (first entry)
XX
DE Novel dengue virus antibody-related 1A5 light chain FR2 peptide SeqID108.
XX
KW antibody engineering; flavivirus infection; diagnostic; pharmaceutical;
KW virucide; antiviral; 1A5.
XX
OS Pan troglodytes.
OS Synthetic.
XX
PN WO2005056600-A2.
XX
PD 23-JUN-2005.
XX
PF 03-DEC-2004; 2004WO-US040674.
XX
PR 08-DEC-2003; 2003US-0528161P.
PR 04-FEB-2004; 2004US-0541676P.
PR 12-MAR-2004; 2004US-0552528P.
PR 26-MAY-2004; 2004US-0574492P.
PR 01-NOV-2004; 2004US-0624261P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Lai C, Purcell RH;
XX
DR WPI; 2005-458565/46.
XX
PT Novel polypeptide comprising fully human or humanized chimpanzee
PT monoclonal antibody that binds or neutralizes dengue type 1, 2, 3, and/or
PT 4 virus, useful for treatment and diagnosis of dengue.
XX
PS Disclosure; SEQ ID NO 108; 121pp; English.
XX
CC This invention relates to novel substantially pure polypeptide comprising
CC a fully human or humanized chimpanzee monoclonal antibody that binds or
CC neutralizes dengue type 1, 2, 3, and/or 4 virus, a monoclonal antibody
CC that binds the antigen to which monoclonal antibody 5H2 (ATCC Accession
CC No. PTA-5662) binds, or a monoclonal antibody that binds the antigen to
CC which monoclonal antibody 1A5 (ATCC Accession No. PTA-6265) binds. The
CC invention may be useful for the development of compounds with a virucide
CC activity acting by viral neutralization. The invention is useful as
CC pharmaceutical preparation and a diagnostic preparation for treatment and
CC diagnosis of dengue virus disease. The present sequence is that of a 1A5
CC light chain peptide which was used during the development of the novel
CC anitbodies of the invention.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||| |
Db 1 WYQQKPGKAPKLLIY 15

RESULT 35
AEB00014
ID AEB00014 standard; peptide; 15 AA.
XX
AC AEB00014;
XX
DT 25-AUG-2005 (first entry)
XX
DE Novel dengue virus antibody-related 5H2 light chain FR2 peptide SeqID12.
XX
KW antibody engineering; flavivirus infection; diagnostic; pharmaceutical;
KW virucide; antiviral; 5H2.
XX
OS Pan troglodytes.
OS Synthetic.
XX
PN WO2005056600-A2.
XX
PD 23-JUN-2005.
XX
PF 03-DEC-2004; 2004WO-US040674.
XX
PR 08-DEC-2003; 2003US-0528161P.
PR 04-FEB-2004; 2004US-0541676P.
PR 12-MAR-2004; 2004US-0552528P.
PR 26-MAY-2004; 2004US-0574492P.
PR 01-NOV-2004; 2004US-0624261P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Lai C, Purcell RH;
XX
DR WPI; 2005-458565/46.
XX
PT Novel polypeptide comprising fully human or humanized chimpanzee
PT monoclonal antibody that binds or neutralizes dengue type 1, 2, 3, and/or
PT 4 virus, useful for treatment and diagnosis of dengue.
XX
PS Disclosure; SEQ ID NO 12; 121pp; English.
XX
CC This invention relates to novel substantially pure polypeptide comprising

CC a fully human or humanized chimpanzee monoclonal antibody that binds or
CC neutralizes dengue type 1, 2, 3, and/or 4 virus, a monoclonal antibody
CC that binds the antigen to which monoclonal antibody 5H2 (ATCC Accession
CC No. PTA-5662) binds, or a monoclonal antibody that binds the antigen to
CC which monoclonal antibody 1A5 (ATCC Accession No. PTA-6265) binds. The
CC invention may be useful for the development of compounds with a virucide
CC activity acting by viral neutralization. The invention is useful as
CC pharmaceutical preparation and a diagnostic preparation for treatment and
CC diagnosis of dengue virus disease. The present sequence is that of a 5H2
CC light chain peptide which was used during the development of the novel
CC anitbodies of the invention.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 36
AEB00174
ID AEB00174 standard; peptide; 15 AA.
XX
AC AEB00174;
XX
DT 25-AUG-2005 (first entry)
XX
DE Novel dengue virus antibody-related 1B2 light chain FR2 peptide SeqID172.
XX
KW antibody engineering; flavivirus infection; diagnostic; pharmaceutical;
KW virucide; antiviral; 1B2.
XX
OS Pan troglodytes.
OS Synthetic.
XX
PN WO2005056600-A2.
XX
PD 23-JUN-2005.
XX
PF 03-DEC-2004; 2004WO-US040674.
XX
PR 08-DEC-2003; 2003US-0528161P.
PR 04-FEB-2004; 2004US-0541676P.
PR 12-MAR-2004; 2004US-0552528P.
PR 26-MAY-2004; 2004US-0574492P.
PR 01-NOV-2004; 2004US-0624261P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Lai C, Purcell RH;
XX
DR WPI; 2005-458565/46.
XX
PT Novel polypeptide comprising fully human or humanized chimpanzee
PT monoclonal antibody that binds or neutralizes dengue type 1, 2, 3, and/or
PT 4 virus, useful for treatment and diagnosis of dengue.
XX
PS Disclosure; SEQ ID NO 172; 121pp; English.
XX
CC This invention relates to novel substantially pure polypeptide comprising
CC a fully human or humanized chimpanzee monoclonal antibody that binds or
CC neutralizes dengue type 1, 2, 3, and/or 4 virus, a monoclonal antibody
CC that binds the antigen to which monoclonal antibody 5H2 (ATCC Accession
CC No. PTA-5662) binds, or a monoclonal antibody that binds the antigen to
CC which monoclonal antibody 1A5 (ATCC Accession No. PTA-6265) binds. The
CC invention may be useful for the development of compounds with a virucide
CC activity acting by viral neutralization. The invention is useful as
CC pharmaceutical preparation and a diagnostic preparation for treatment and
CC diagnosis of dengue virus disease. The present sequence is that of a 1B2
CC light chain peptide which was used during the development of the novel
CC anitbodies of the invention.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 37
AEB24630
ID AEB24630 standard; peptide; 15 AA.
XX
AC AEB24630;
XX
DT 08-SEP-2005 (first entry)
XX
DE Humanized murine MAb 83-14 VL FR2, SEQ ID 39.
XX
KW Metabolic; delivery mechanism; blood-brain barrier; monoclonal antibody;
KW insulin receptor; lysosome storage disease; light chain variable region;
KW humanized antibody.
XX
OS Mus sp.
OS Homo sapiens.
XX
PN US2005142141-A1.
XX
PD 30-JUN-2005.
XX
PF 17-FEB-2005; 2005US-00061956.
XX
PR 27-NOV-2002; 2002US-00307276.
XX
PA (PARD/) PARDRIDGE W M.
XX
PI Pardridge WM;
XX
DR WPI; 2005-519715/53.
XX
PT New composition comprising a large enzyme and a blood-brain barrier
PT targeting agent, useful for treating lysosomal storage disorders.
XX
PS Disclosure; SEQ ID NO 39; 48pp; English.
XX
CC The present invention relates to a composition, which is capable of
CC delivering a large enzyme, such as a lysosomal enzyme, across the blood
CC brain barrier. The composition comprises a large enzyme and a blood-brain
CC barrier targeting agent, where the blood brain barrier targeting agent is
CC linked to the large enzyme. The blood brain barrier targeting agent can
CC be a monoclonal antibody (MAb) to the insulin receptor such as murine MAb
CC 83-14, which binds to the human insulin receptor (HIR). The composition
CC is useful for treating lysosomal storage disorders and other conditions
CC where the enzyme being delivered is missing from the brain cell. The
CC present sequence is a framework region (FR) of the murine light chain
CC variable region (VL) of MAb 83-14.
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 86; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

```
RESULT 38
ABG98283
ID   ABG98283 standard; peptide; 38 AA.
XX
AC   ABG98283;
XX
DT   08-JAN-2003  (first entry)
XX
DE   Human antibody 012/V3b germline kappa chain variable region FR1/FR2 #1.
XX
KW   Antibody; variable region; light chain; heavy chain; VH; VL; gp39; CD40;
KW   T-cell activation; B-cell differentiation; framework region;
KW   cellular immune response; gene therapy; graft rejection; human; FR;
KW   autoimmune disease; rheumatoid arthritis; multiple sclerosis; diabetes;
KW   asthma; multiple sclerosis; allergy; diabetes mellitus;
KW   systemic lupus erythematosus; graft-versus-host disease.
XX
OS   Homo sapiens.
XX
PN   WO200194586-A2.
XX
PD   13-DEC-2001.
XX
PF   06-JUN-2001; 2001WO-US018098.
XX
PR   06-JUN-2000; 2000US-0209584P.
XX
PA   (IDEC-) IDEC PHARM CORP.
XX
PI   Anderson DR,  Pan LZ,  Hanna N,  Rastetter WH,  Kloetzer WS;
XX
DR   WPI; 2002-188261/24.
XX
PT   New antibodies binding to an epitope on gp39, useful for preventing graft
PT   rejection, or for treating autoimmune diseases (e.g. diabetes, asthma or
PT   multiple sclerosis), and non-autoimmune diseases (e.g. graft-versus-host
PT   disease).
XX
PS   Disclosure; Page 46; 130pp; English.
XX
CC   The invention relates to an antibody which binds to an epitope on gp39,
CC   is new, where the epitope is distinct from the epitope bound by IDEC-131,
CC   and the antibody has a non-agonistic effect on T-cell activation and
CC   inhibits gp39/CD40 interaction. Also included are: (1) an improved method
CC   of treating a disease by modulating gp39 expression or inhibiting the
CC   gp39/CD40 interaction comprising administering an antibody specific for
CC   gp39 that inhibits the gp39/CD40 interaction and is non-agonistic of T-
CC   cell activation; (2) an antibody which antagonises B-cell differentiation
CC   and antibody production, and is non- agonistic of T-cell activation; (3)
CC   a DNA sequence which encodes an antibody defined above; (4) an expression
CC   vector, which contains a DNA sequence of (3); (5) a method of suppressing
CC   humoral and/or cellular immune responses against cells or vectors
CC   administered during cell or gene therapy comprising further administering
CC   prior, during or after gene therapy, an antibody defined above; and (6)
CC   an improved method of treatment which involves the transplantation of
CC   cells, tissues or organs of the same or different species into a subject,
CC   where the improvement comprises administering an antibody defined above
CC   prior, during or after transplantation, to suppress immune responses
CC   against the transplanted cell, tissue or organ, or to suppress immune
CC   responses elicited by the transplanted cell, tissue or organ against the
CC   host. The antibody is useful for preventing graft rejection, and for
CC   treating autoimmune diseases, e.g., rheumatoid arthritis, multiple
CC   sclerosis, diabetes, asthma, multiple sclerosis, allergic conditions,
CC   diabetes mellitus, or systemic lupus erythematosus, as well as non-
CC   autoimmune diseases such as graft-versus-host disease (many other
CC   diseases and conditions are given in the specification). The antibodies
CC   are also useful in gene or cellular therapy, and to inhibit humoral and
CC   cellular immune responses against viral vectors. The present sequence is
CC   a framework region (FR) fragment of a human anti-gp39 antibody used to
CC   determine which amino acids should be humanised in a mouse anti-gp39
CC   molecule
XX
SQ   Sequence 38 AA;

  Query Match             100.0%;  Score 86;  DB 5;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 39
AAB03708
ID   AAB03708 standard; protein; 40 AA.
XX
AC   AAB03708;
XX
DT   04-OCT-2000  (first entry)
XX
DE   Immunoglobulin kappa amino acid sequence fragment.
XX
KW   Aortic aneurysm-associated antigen protein; AAAP; microfibrillar protein;
KW   abdominal aortic aneurysm disease; treatment; detect; tolerance;
KW   immunoglobulin kappa; IgK.
XX
OS   Unidentified.
XX
PN   US6048704-A.
XX
PD   11-APR-2000.
XX
PF   07-MAR-1997;   97US-00812586.
XX
PR   07-MAR-1996;   96US-0012976P.
XX
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI   Tilson MD;
XX
DR   WPI; 2000-316895/27.
XX
PT   Isolated microfibrillar protein for alleviating abdominal aortic aneurysm
PT   disease is purified from human aortic tissue and binds immunoreactively
PT   with immunoglobulin.
XX
PS   Example 3; Col 30; 70pp; English.
XX
CC   The present invention relates to an isolated microfibrillar protein of
CC   approximately 40kD. The protein is isolated from human aortic tissue and
CC   binds immunoreactively with immunoglobulin purified from human abdominal
CC   aortic aneurysm (AAA) tissue. The protein is referred to as aortic
CC   aneurysm-associated antigenic protein (AAAP). The protein is capable of
CC   forming a disulphide bonded dimer. The protein is immunoreactive with
CC   human kappa immunoglobulin. Also included in the invention are
CC   recombinantly produced human AAA proteins. AAAP shows regions of homology
CC   with the bovine microfibril associated glycoprotein MFAP-4 and also with
CC   fibrinogen and vitronectin. The isolated microfibrillar protein is useful
CC   for alleviating abdominal aortic aneurysm (AAA) disease and detecting the
CC   presence of AAA-associated immunoglobulin bound to the human aortic
CC   tissue. Antibodies directed against AAAP can be used to detect AAA
CC   disease. The recombinant protein can be used to induce tolerance to
CC   antigenic AAA protein in the subject e.g. human. This sequence represents
CC   an immunoglobulin kappa amino acid sequence. The sequence shares homology
CC   with the AAAP of the invention, it was used to identify and characterise
CC   AAAP
XX
SQ   Sequence 40 AA;

  Query Match             100.0%;  Score 86;  DB 3;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
```

```
Db          1 WYQQKPGKAPKLLIY 15


RESULT 40
ADB72869
ID   ADB72869 standard; protein; 40 AA.
XX
AC   ADB72869;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human AAA-associated immunoglobulin related polypeptide, SEQ ID No:37.
XX
KW   Aortic tissue; immunoreactive; abdominal aortic aneurysm;
KW   AAA-associated immunoglobulin 40kDa protein.
XX
OS   Unidentified.
XX
PN   US6537769-B1.
XX
PD   25-MAR-2003.
XX
PF   28-MAR-2000; 2000US-00535832.
XX
PR   07-MAR-1996;   96US-0012976P.
PR   07-MAR-1997;   97US-00812586.
XX
PA   (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI   Tilson MD;
XX
DR   WPI; 2003-687181/65.
XX
PT   Purified protein useful in diagnosing abdominal aortic aneurysm disease
PT   in subject, e.g. human, contains specified amino acids.
XX
PS   Disclosure; Col 71-72; 67pp; English.
XX
CC   The present invention relates to the isolation of a protein approximately
CC   40kDa which is purified from human aortic tissue. The protein is
CC   immunoreactive with abdominal aortic aneurysms(AAA)-associated
CC   immunoglobulin. The protein is useful for diagnosing AAA disease in a
CC   subject, e.g. human, by administering the protein or a composition
CC   comprising the protein. The inventive protein is capable of forming a
CC   disulphide-bonded dimer of 80 kDa. The present sequence of unknown
CC   function is given in the Sequence Listing but is not mentioned elsewhere
CC   in the specification.
XX
SQ   Sequence 40 AA;

  Query Match             100.0%;  Score 86;  DB 7;  Length 40;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 41
AEC20827
ID   AEC20827 standard; protein; 52 AA.
XX
AC   AEC20827;
XX
DT   20-OCT-2005  (first entry)
XX
DE   Human variable light chain (hVK1) consensus SEQ ID NO 66.
XX
KW   endocrine-gen.; antiarthritic; antibacterial; antiinflammatory;
KW   antirheumatic; antithyroid; bone metastases; calcium antagonist; cancer;
KW   cardiovascular-gen.; degeneration; eating-disorders-gen.;
KW   endocrine disease; endocrine-gen.; endocrine-gen.; gastrointestinal-gen.;
KW   genetic disorder; hepatotropic; hypercalcemia; immune disorder;
KW   immunotherapy; inflammation; monoclonal antibody; mouth disease;
KW   musculoskeletal disease; neoplasm; nephrotropic; osteopathic;
KW   osteopetrosis; osteoporosis; pagets disease; periodontal disease;
KW   pharmaceutical; rheumatoid arthritis; variable light chain region.
XX
OS   Synthetic.
XX
PN   WO2005068503-A2.
XX
PD   28-JUL-2005.
XX
PF   06-JAN-2005; 2005WO-US000546.
XX
PR   07-JAN-2004; 2004US-0535181P.
PR   02-JUN-2004; 2004US-0576417P.
XX
PA   (CHIR ) CHIRON CORP.
PA   (XOMA ) XOMA TECHNOLOGY LTD.
XX
PI   Liu C,  Zimmerman DL,  Harrowe GM,  Koths K,  Kavanaugh WM,  Long L;
PI   Calderon-Cacia M,  Horwitz AH;
XX
DR   WPI; 2005-597707/61.
XX
PT   Novel non-murine antibody that competes with monoclonal antibody RX1 for
PT   binding to macrophage colony stimulating factor, useful for treating
PT   hypogonadism, hypercalcemia, rickets, scurvy, homocystinuria, cancer,
PT   osteoporosis.
XX
PS   Disclosure; SEQ ID NO 66; 269pp; English.
XX
CC   The invention describes a non-murine antibody (I) that competes with
CC   monoclonal antibody RX1 for binding to macrophage colony stimulating
CC   factor (M-CSF) by more than 75%, where the monoclonal antibody RXI has
CC   the heavy chain and light chain amino acid sequences having a fully
CC   defined 447 amino acids (SEQ ID No. 2) and 214 amino acids (SEQ ID No. 4)
CC   sequences given in the specification, respectively. (I) is useful for
CC   preventing a subject afflicted with a disease that causes or contributes
CC   to osteolysis, where the antibody effectively reduces the severity of
CC   bone loss associated with the disease. The disease is chosen from
CC   metabolic bone diseases associated with relatively increased osteoclast
CC   activity, including endocrinopathies, hypercalcemia, deficiency states,
CC   chronic diseases, and hereditary diseases, cancer, osteoporosis,
CC   osteopetrosis, inflammation of bone associated with arthritis and
CC   rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or
CC   Paget's disease. (I) is useful for preventing or treating metastatic
CC   cancer. Antibodies of the invention are useful for preventing or reducing
CC   bone loss; osteolysis; metastatic cancer to bone and cancer. (I) is
CC   useful for manufacturing a medicament for preventing or reducing bone
CC   loss in a patient exhibiting osteolysis, manufacturing a medicament for
CC   treating a patient afflicted with a disease that causes or contributes to
CC   osteolysis, and metastatic cancer to bone in a patient suffering from
CC   metastatic cancer, for manufacturing a medicament for treating a patient
CC   having cancer. (I) in synergistic combination, is useful for preparing a
CC   medicament for treating a patient exhibiting osteolysis. This is the
CC   amino acid sequence of human variable light chain region (hVK1) used in a
CC   comparison with macrophage colony stimulating factor (M-CSF) specific
CC   murine antibody RX1 light chain.
XX
SQ   Sequence 52 AA;

  Query Match             100.0%;  Score 86;  DB 9;  Length 52;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 42
AEC20823
```

ID AEC20823 standard; protein; 57 AA.
XX
AC AEC20823;
XX
DT 20-OCT-2005 (first entry)
XX
DE Human variable light chain (HK1) consensus SEQ ID NO 62.
XX
KW endocrine-gen.; antiarthritic; antibacterial; antiinflammatory;
KW antirheumatic; antithyroid; bone metastases; calcium antagonist; cancer;
KW cardiovascular-gen.; degeneration; eating-disorders-gen.;
KW endocrine disease; endocrine-gen.; endocrine-gen.; gastrointestinal-gen.;
KW genetic disorder; hepatotropic; hypercalcemia; immune disorder;
KW immunotherapy; inflammation; monoclonal antibody; mouth disease;
KW musculoskeletal disease; neoplasm; nephrotropic; osteopathic;
KW osteopetrosis; osteoporosis; pagets disease; periodontal disease;
KW pharmaceutical; rheumatoid arthritis; variable light chain region.
XX
OS Synthetic.
XX
PN WO2005068503-A2.
XX
PD 28-JUL-2005.
XX
PF 06-JAN-2005; 2005WO-US000546.
XX
PR 07-JAN-2004; 2004US-0535181P.
PR 02-JUN-2004; 2004US-0576417P.
XX
PA (CHIR) CHIRON CORP.
PA (XOMA) XOMA TECHNOLOGY LTD.
XX
PI Liu C, Zimmerman DL, Harrowe GM, Koths K, Kavanaugh WM, Long L;
PI Calderon-Cacia M, Horwitz AH;
XX
DR WPI; 2005-597707/61.
XX
PT Novel non-murine antibody that competes with monoclonal antibody RX1 for
PT binding to macrophage colony stimulating factor, useful for treating
PT hypogonadism, hypercalcemia, rickets, scurvy, homocystinuria, cancer,
PT osteoporosis.
XX
PS Disclosure; SEQ ID NO 62; 269pp; English.
XX
CC The invention describes a non-murine antibody (I) that competes with
CC monoclonal antibody RX1 for binding to macrophage colony stimulating
CC factor (M-CSF) by more than 75%, where the monoclonal antibody RXI has
CC the heavy chain and light chain amino acid sequences having a fully
CC defined 447 amino acids (SEQ ID No. 2) and 214 amino acids (SEQ ID No. 4)
CC sequences given in the specification, respectively. (I) is useful for
CC preventing a subject afflicted with a disease that causes or contributes
CC to osteolysis, where the antibody effectively reduces the severity of
CC bone loss associated with the disease. The disease is chosen from
CC metabolic bone diseases associated with relatively increased osteoclast
CC activity, including endocrinopathies, hypercalcemia, deficiency states,
CC chronic diseases, and hereditary diseases, cancer, osteoporosis,
CC osteopetrosis, inflammation of bone associated with arthritis and
CC rheumatoid arthritis, periodontal disease, fibrous dysplasia, and/or
CC Paget's disease. (I) is useful for preventing or treating metastatic
CC cancer. Antibodies of the invention are useful for preventing or reducing
CC bone loss; osteolysis; metastatic cancer to bone and cancer. (I) is
CC useful for manufacturing a medicament for preventing or reducing bone
CC loss in a patient exhibiting osteolysis, manufacturing a medicament for
CC treating a patient afflicted with a disease that causes or contributes to
CC osteolysis, and metastatic cancer to bone in a patient suffering from
CC metastatic cancer, for manufacturing a medicament for treating a patient
CC having cancer. (I) in synergistic combination, is useful for preparing a
CC medicament for treating a patient exhibiting osteolysis. This is the
CC amino acid sequence of human variable light chain region (HK1) used in a
CC comparison with macrophage colony stimulating factor (M-CSF) specific
CC murine antibody RX1 light chain.
XX
SQ Sequence 57 AA;

Query Match 100.0%; Score 86; DB 9; Length 57;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 40 WYQQKPGKAPKLLIY 54

RESULT 43
ABG75305
ID ABG75305 standard; protein; 70 AA.
XX
AC ABG75305;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human sub-group DPK9+JK1 acceptor light chain protein.
XX
KW Antibody; CD22; human; mouse; cytostatic; gene therapy; lymphoma.
XX
OS Homo sapiens.
XX
PN WO2003093320-A2.
XX
PD 13-NOV-2003.
XX
PF 02-MAY-2003; 2003WO-GB001934.
XX
PR 02-MAY-2002; 2002GB-00010121.
XX
PA (CELL-) CELLTECH R & D LTD.
XX
PI Popplewell AG, Tickle SP, Ladyman HM;
XX
DR WPI; 2003-877512/81.
XX
PT New antibody molecule having specificity for human CD22 comprising a
PT complementary determining region, useful for treating a pathology e.g.
PT malignant lymphoma, specifically, Non-Hodgkin's lymphoma.
XX
PS Disclosure; Page 56; 0pp; English.
XX
CC The present invention relates to an antibody molecule having specificity
CC for human CD22 which comprises a heavy and a light chain, where the
CC variable domain comprises a complementary determining region (CDR). The
CC antibody molecule or its DNA sequence is useful in manufacture of a
CC medicament for treating a pathology mediated by cells expressing CD22 or
CC use in therapy. The pathology is malignant lymphoma, specifically, Non-
CC Hodgkin's lymphoma. The present sequence is a fragment of an antibody of
CC the invention
XX
SQ Sequence 70 AA;

Query Match 100.0%; Score 86; DB 7; Length 70;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 24 WYQQKPGKAPKLLIY 38

RESULT 44
ABM79517
ID ABM79517 standard; protein; 70 AA.
XX
AC ABM79517;
XX
DT 22-APR-2004 (first entry)
XX
DE Human DPK9 protein.

XX
KW Drug/carrier conjugate; cytotoxic; calicheamicin; CD22; human; mouse;
KW antibody; cancer.
XX
OS Homo sapiens.
XX
PN WO2003092623-A2.
XX
PD 13-NOV-2003.
XX
PF 02-MAY-2003; 2003WO-US013910.
XX
PR 02-MAY-2002; 2002US-0377440P.
XX
PA (AMHP) WYETH HOLDINGS CORP.
XX
PI Kunz A, Moran JK, Rubino JT, Jain N, Vidunas EJ, Simpson JM;
PI Robbins PD, Merchant N, Dijoseph JF, Ruppen ME, Damle NK;
PI Popplewell AG;
XX
DR WPI; 2004-053034/05.
XX
PT Preparing monomeric cytotoxic drug/carrier conjugates for treating
PT cancer, comprises incubating a cytotoxic drug derivative with a
PT proteinaceous carrier in a non-nucleophilic, protein-compatible buffered
PT solution.
XX
PS Disclosure; Page 161; 0pp; English.
XX
CC The present invention relates to a method of preparing monomeric
CC cytotoxic drug/carrier conjugates with reduced low conjugated fraction,
CC which comprises incubating a mixture of a cytotoxic drug derivative and a
CC proteinaceous carrier in a non-nucleophilic, protein-compatible buffered
CC solution to produce a monomeric cytotoxic drug/carrier conjugate. The
CC method is useful for producing monomeric cytotoxic drug/carrier
CC conjugates having reduced low conjugated fraction. The conjugates or
CC compositions comprising the monomeric cytotoxic drug derivative/carrier
CC conjugates are useful for treating a proliferative disorder, particularly
CC cancer (e.g. carcinoma or sarcoma) or a B-cell malignancy, such as
CC leukaemia expressing cell surface antigen CD22, lymphoma expressing cell
CC surface antigen CD22, Non-Hodgkin's lymphoma. The present sequence is a
CC polypeptide used in the exemplification of the invention
XX
SQ Sequence 70 AA;

Query Match 100.0%; Score 86; DB 8; Length 70;
Best Local Similarity 100.0%; Pred. No. 8.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 24 WYQQKPGKAPKLLIY 38

RESULT 45
ADU04182
ID ADU04182 standard; protein; 71 AA.
XX
AC ADU04182;
XX
DT 13-JAN-2005 (first entry)
XX
DE Unidentified immunoglobulin light chain variable region L3 protein.
XX
KW viral infection; virucide; autoimmune disease;
KW lymphoproliferative disorder; vaccine; gene therapy; immunoglobulin;
KW antibody; light chain variable region.
XX
OS Unidentified.
XX
PN WO2004090544-A2.
XX
PD 21-OCT-2004.
XX
PF 13-APR-2004; 2004WO-CA000544.
XX
PR 09-APR-2003; 2003US-0461137P.
PR 30-SEP-2003; 2003US-0506779P.
XX
PA (CABL-) CANADIAN BLOOD SERVICES.
XX
PI Hu Y, Brown E;
XX
DR WPI; 2004-766498/75.
XX
PT Characterizing a viral infection in a host, for developing treatment for
PT severe acute respiratory syndrome-coronavirus (SARS-CoV), by determining
PT homology profile of a viral-based sequence element with an endogenous
PT host element.
XX
PS Example 1; Fig 10; 166pp; English.
XX
CC The invention relates to a novel method for characterising a viral
CC infection in a host. The method comprises identifying at least one viral-
CC based sequence element in a biological sample obtained from the host,
CC determining a homology profile of the viral-based sequence element with
CC at least one endogenous host element and characterising the viral
CC infection based on the homology profile, where the homology profile is
CC indicative of a viral behaviour of the viral infection in the host. The
CC method of the invention demonstrates virucide applications and may be
CC useful for preparing a medicament for detecting and/or treating a viral
CC infection or related condition, such as an autoimmune disease e.g. type
CC II cryoglobulinaemia, or lymphoproliferative disorder. The viral
CC infection may be due to HCV (Hepatitis C virus), HIV or a member of a
CC Retroviridae, Flaviviridae, Herpesviridae, Papillomaviridae or
CC Coronaviridae virus family. Treatment of the infection may utilise
CC vaccine or gene therapy. The target compound of the invention may be
CC useful for detecting the presence of a virus in a biological sample or
CC for manufacturing a medicament for treating SARS coronavirus (SARS-CoV)
CC and/or Human T-lymphotropic virus 1 (HTLV-I) infection. The methods are
CC further useful for developing treatment regimes to target genotype-
CC specific viral variants. The current sequence is that of an unidentified
CC immunoglobulin light chain variable region protein of the invention.
XX
SQ Sequence 71 AA;

Query Match 100.0%; Score 86; DB 8; Length 71;
Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 34 WYQQKPGKAPKLLIY 48

RESULT 46
ADU04131
ID ADU04131 standard; protein; 72 AA.
XX
AC ADU04131;
XX
DT 13-JAN-2005 (first entry)
XX
DE Human immunoglobulin light chain kappa (IgVLk) vda protein.
XX
KW viral infection; virucide; autoimmune disease;
KW lymphoproliferative disorder; vaccine; gene therapy; immunoglobulin;
KW antibody.
XX
OS Homo sapiens.
XX
PN WO2004090544-A2.
XX
PD 21-OCT-2004.
XX
PF 13-APR-2004; 2004WO-CA000544.

XX
PR 09-APR-2003; 2003US-0461137P.
PR 30-SEP-2003; 2003US-0506779P.
XX
PA (CABL-) CANADIAN BLOOD SERVICES.
XX
PI Hu Y, Brown E;
XX
DR WPI; 2004-766498/75.
XX
PT Characterizing a viral infection in a host, for developing treatment for
PT severe acute respiratory syndrome-coronavirus (SARS-CoV), by determining
PT homology profile of a viral-based sequence element with an endogenous
PT host element.
XX
PS Example 1; Fig 1B; 166pp; English.
XX
CC The invention relates to a novel method for characterising a viral
CC infection in a host. The method comprises identifying at least one viral-
CC based sequence element in a biological sample obtained from the host,
CC determining a homology profile of the viral-based sequence element with
CC at least one endogenous host element and characterising the viral
CC infection based on the homology profile, where the homology profile is
CC indicative of a viral behaviour of the viral infection in the host. The
CC method of the invention demonstrates virucide applications and may be
CC useful for preparing a medicament for detecting and/or treating a viral
CC infection or related condition, such as an autoimmune disease e.g. type
CC II cryoglobulinaemia, or lymphoproliferative disorder. The viral
CC infection may be due to HCV (Hepatitis C virus), HIV or a member of a
CC Retroviridae, Flaviviridae, Herpesviridae, Papillomaviridae or
CC Coronaviridae virus family. Treatment of the infection may utilise
CC vaccine or gene therapy. The target compound of the invention may be
CC useful for detecting the presence of a virus in a biological sample or
CC for manufacturing a medicament for treating SARS coronavirus (SARS-CoV)
CC and/or Human T-lymphotropic virus 1 (HTLV-I) infection. The methods are
CC further useful for developing treatment regimes to target genotype-
CC specific viral variants. The current sequence is that of the human
CC immunoglobulin light chain kappa (IgVLk) vda protein of the invention.
XX
SQ Sequence 72 AA;

Query Match 100.0%; Score 86; DB 8; Length 72;
Best Local Similarity 100.0%; Pred. No. 8.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 35 WYQQKPGKAPKLLIY 49

RESULT 47
ADZ08785
ID ADZ08785 standard; protein; 73 AA.
XX
AC ADZ08785;
XX
DT 16-JUN-2005 (first entry)
XX
DE Mammalian amyloid antibody, light chain variable region SEQ ID No:10.
XX
KW amyloid; antibody engineering; antibody production;
KW amyloid-associated disorder; Alzheimers disease; cancer; allergy;
KW autoimmune disease; Parkinsons disease;
KW acquired immune deficiency syndrome; multiple sclerosis; migraine;
KW dementia; infection; nootropic; neuroprotective; cytostatic;
KW antiallergic; Immunosuppressive; antiparkinsonian; antimigraine;
KW antimicrobial; anti-HIV; light chain variable region.
XX
OS Mammalia.
XX
PN WO2005028511-A2.
XX
PD 31-MAR-2005.
XX
PF 26-MAR-2004; 2004WO-US009522.
XX
PR 28-MAR-2003; 2003US-0458469P.
PR 28-MAR-2003; 2003US-0458474P.
PR 28-MAR-2003; 2003US-0458509P.
PR 28-MAR-2003; 2003US-0458510P.
XX
PA (CENZ) CENTOCOR INC.
PA (MERC/) MERCKEN M.
PA (BENS/) BENSON J M.
XX
PI Mercken M, Benson JM;
XX
DR WPI; 2005-242565/25.
XX
PT New isolated mammalian anti-amyloid antibodies useful for treating
PT amyloid-associated disorders, such as Alzheimer's disease, cancer,
PT allergies, autoimmune disease, Parkinson's disease, multiple sclerosis,
PT migraine and dementia.
XX
PS Disclosure; SEQ ID NO 10; 306pp; English.
XX
CC The invention relates to at least one isolated mammalian amyloid antibody
CC comprising at least one variable region comprising at least one heavy
CC chain and at least one light chain, of a fully defined sequence of SEQ ID
CC NOS: 48, 49, 59, 60, 69, 70, 79 and 80, respectively. Also described are:
CC (i) at least one isolated mammalian amyloid antibody that binds to the
CC same region of an amyloid polypeptide as an antibody comprising at least
CC one heavy chain or light chain complementarity determining region (CDR)
CC having the amino acid sequence of at least one of SEQ ID NO: 73-78, (ii)
CC at least one isolated mammalian amyloid antibody, comprising at least one
CC human CDR, where the antibody specifically binds at least one epitope
CC selected from amino acids 2-7, 3-8, 33-42, or 34-40 of a fully defined
CC sequence of 42 amino acids (SEQ ID NO: 50), (iii) an isolated nucleic
CC acid encoding at least one of any of the isolated mammalian amyloid
CC antibodies mentioned and having at least one human CDR of a fully defined
CC sequence of SEQ ID NO: 51, 52, 61, 62, 71, 72, 81 and 82, (iv) an
CC isolated nucleic acid vector comprising an isolated nucleic acid encoding
CC an amyloid antibody, (v) a prokaryotic or eukaryotic host cell comprising
CC an isolated nucleic acid encoding an amyloid antibody, (vi) a method of
CC producing at least one amyloid antibody, (vii) a composition comprising
CC at least one of any of the isolated mammalian amyloid antibodies
CC mentioned, and at least one pharmaceutical carrier or diluent, (viii) an
CC anti-idiotype antibody or fragment that specifically binds at least one
CC of the amyloid antibodies mentioned, (ix) a method of diagnosing or
CC treating an amyloid related condition in a cell, tissue, organ or animal,
CC comprising contacting or administering a composition comprising at least
CC one of the antibodies mentioned, with, or to, the cell, tissue, organ or
CC animal, (x) a medical device comprising at least one amyloid antibody
CC mentioned, where the device is suitable for contacting or administering
CC at least one amyloid antibody, (xi) an article of manufacture for human
CC pharmaceutical or diagnostic use, comprising packaging material and a
CC container comprising a solution or a lyophilized form of at least one of
CC the amyloid antibodies mentioned, and (xii) a method of producing at
CC least one of the isolated mammalian amyloid antibodies, comprising
CC providing a host cell or transgenic animal or transgenic plant or plant
CC cell capable of expressing the antibody in recoverable amounts. The
CC methods and compositions of the present invention are useful for
CC producing therapeutic compositions and devices for treating amyloid-
CC associated disorders, such as Alzheimer's disease, cancer, allergies,
CC autoimmune disease, Parkinson's disease, AIDS, multiple sclerosis,
CC migraine, dementia and infections. This sequence represents a light chain
CC variable region useful in the antibody of the invention.
XX
SQ Sequence 73 AA;

Query Match 100.0%; Score 86; DB 9; Length 73;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||

```
Db         25 WYQQKPGKAPKLLIY 39


RESULT 48
AEA16517
ID   AEA16517 standard; protein; 73 AA.
XX
AC   AEA16517;
XX
DT   28-JUL-2005  (first entry)
XX
DE   Human MCP-1 immunoglobulin light chain variable region, kappa-1-4.
XX
KW   monocyte chemoattractant protein-1; MCP-1; immunoglobulin;
KW   immunosuppressive; immunostimulant; cardiovascular-Gen.; antimicrobial;
KW   cytostatic; neuroprotective; vulnerary; antirheumatic; Muscle relaxant;
KW   analgesic; anesthetic; antipsoriatic; antithyroid; antidiarrheic;
KW   antitussive; antiemetic; antiulcer; laxative; anticoagulant; metabolic;
KW   cytostatic; antidepressant; antimanic; neuroleptic; tranquilizer;
KW   hypnotic; CNS-Gen.; antiasthmatic; auditory; immune disorder;
KW   cardiovascular disease; infectious disease; malignant disease;
KW   neurological disease; wound healing; trauma.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .23
FT                   /note= "FR1 region"
FT   Misc-difference 24
FT                   /note= "CDR1 region"
FT   Region          25. .39
FT                   /note= "FR2 region"
FT   Misc-difference 40
FT                   /note= "CDR2 region"
FT   Region          41. .72
FT                   /note= "FR3 region"
FT   Misc-difference 73
FT                   /note= "CDR3 region"
XX
PN   WO2005044200-A2.
XX
PD   19-MAY-2005.
XX
PF   05-NOV-2004; 2004WO-US037024.
XX
PR   05-NOV-2003; 2003US-0517370P.
XX
PA   (CENZ ) CENTOCOR INC.
XX
PI   Yan L,  Nakada MT,  Das A;
XX
DR   WPI; 2005-356202/36.
XX
PT   Treating at least one human monocyte chemoattractant protein-1 (MCP-1)
PT   related pathology, e.g. immune, neurologic, or cardiovascular diseases,
PT   comprises administering at least one MCP-1 immunoglobulin-derived protein
PT   to the animal.
XX
PS   Disclosure; SEQ ID NO 10; 96pp; English.
XX
CC   The invention relates to a novel method for treating at least one human
CC   monocyte chemoattractant protein-1 (MCP-1) related pathology. The method
CC   comprises contacting or administering a therapeutically effective amount
CC   of at least one MCP-1 immunoglobulin (Ig) derived protein to the cells,
CC   tissue or animal, where the MCP-1 Ig derived protein inhibits a
CC   biological activity of MCP-1, in vivo, in vitro or in situ. The method
CC   and MCP-1 composition have the following activities: immunosuppressive,
CC   immunostimulant, cardiovascular-Gen., antimicrobial, cytostatic,
CC   neuroprotective, vulnerary, antirheumatic, muscle-relaxant, analgesic,
CC   anesthetic, sedative, antipsoriatic, antithyroid, antidiarrheic,
CC   antitussive, antiemetic, antiulcer, laxative, anticoagulant, metabolic,
CC   cytostatic, antidepressant, antimanic, neuroleptic, tranquilizer,
CC   hypnotic, CNS-Gen., antiasthmatic, and auditory. The method and
CC   composition are useful for treating at least one human MCP-1 related
CC   pathology, such as an immune related disease, a cardiovascular disease,
CC   an infectious disease, a malignant disease, a neurological disease, or
CC   any wound or trauma. This sequence represents a human monocyte
CC   chemoattractant protein-1 immunoglobulin derived protein of the
CC   invention.
XX
SQ   Sequence 73 AA;

  Query Match             100.0%;  Score 86;  DB 9;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         25 WYQQKPGKAPKLLIY 39


RESULT 49
AEB72752
ID   AEB72752 standard; protein; 73 AA.
XX
AC   AEB72752;
XX
DT   06-OCT-2005  (first entry)
XX
DE   Anti-LTalpha antibody light chain variable region kappa1-4.
XX
KW   antibody; Anorectic; Immunosuppressive; Cardiovascular-Gen; Cytostatic;
KW   Neuroprotective; Vaccine; lymphotoxin alpha; obesity; immune disorder;
KW   cardiovascular disease; infection; neurological disease.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .23
FT                   /label= FR1
FT   Region          24
FT                   /label= CDR1
FT   Region          25. .39
FT                   /label= FR2
FT   Region          40
FT                   /label= CDR2
FT   Region          41. .72
FT                   /label= FR3
FT   Region          73
FT                   /label= CDR3
XX
PN   WO2005067477-A2.
XX
PD   28-JUL-2005.
XX
PF   30-NOV-2004; 2004WO-US040018.
XX
PR   08-DEC-2003; 2003US-0527794P.
XX
PA   (CENZ ) CENTOCOR INC.
XX
PI   Giles-Komar J,  Scallon BJ,  Cai A;
XX
DR   WPI; 2005-522703/53.
XX
PT   New anti-human lymphotoxin alpha antibody, useful for diagnosing or
PT   treating immune, cardiovascular, infectious disease, malignant, or
PT   neurological disease, or obesity.
XX
PS   Disclosure; SEQ ID NO 10; 114pp; English.
XX
CC   This sequence represents a mammalian anti-lymphotoxin alpha (LTalpha)
CC   antibody light chain. The antibody preferably comprises at least one
CC   variable region AEB72785AEB72787, at least one light chain
CC   complementarity determining region (CDR) AEB72797AEB72798AEB72799 and at
CC   least one heavy chain CDR AEB72800AEB72801AEB72802. The antibody binds
```

CC LTalpha with an affinity of 10 -9 to 10 -2 M. The antibody substantially
CC neutralizes at least one activity of at least one LTalpha protein. The
CC antibody and compositions, medical devices, and methods for its
CC production, are useful for diagnosing or treating a LTalpha related
CC condition, e.g. obesity, an immune related disease, a cardiovascular
CC disease, an infectious disease, a malignant disease, or a neurological
CC disease.
XX
SQ Sequence 73 AA;

Query Match 100.0%; Score 86; DB 9; Length 73;
Best Local Similarity 100.0%; Pred. No. 8.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 25 WYQQKPGKAPKLLIY 39

RESULT 50
AAW62805
ID AAW62805 standard; peptide; 74 AA.
XX
AC AAW62805;
XX
DT 23-SEP-1998 (first entry)
XX
DE Amino acid sequence of a human antibody fragment.
XX
KW Human; immunoglobulin; Ig; transgenic; non-human mammal;
KW inactivated endogenous Ig locus; B-cell development;
KW human heavy chain Ig locus; micro constant region; J-H; D-H; V-H gene;
KW kappa light chain Ig locus; kappa constant region; J-kappa gene; V-kappa;
KW production; antibody.
XX
OS Homo sapiens.
XX
PN WO9824893-A2.
XX
PD 11-JUN-1998.
XX
PF 03-DEC-1997; 97WO-US023091.
XX
PR 03-DEC-1996; 96US-00759620.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Jakobovits A, Kucherlapati R, Klapholz S, Mendez M, Green L;
XX
DR WPI; 1998-333314/29.
XX
PT New transgenic non-human mammals - having an inactivated immunoglobulin
PT locus and a near complete human immunoglobulin locus, used for production
PT of human antibodies.
XX
PS Disclosure; Page 77; 128pp; English.
XX
CC AAW62793-822 represent fragments of human antibodies produced by
CC transgenic Xenomice, created using the method of the invention. The
CC specification describes a transgenic non-human mammal which has genome
CC modifications that comprise an inactivated endogenous immunoglobulin (Ig)
CC locus, so that the mammal does not display normal B-cell development. The
CC modified genome also has an inserted human heavy chain Ig locus in
CC germline configuration, the human heavy chain Ig locus comprising a human
CC micro constant region and regulatory and switch sequences, human J-H
CC genes, human D-H genes, and human V-H genes and an inserted human kappa
CC light chain Ig locus in germline configuration, the human kappa light
CC chain Ig locus comprising a human kappa constant region, J-kappa genes,
CC and V-kappa genes, where the number of V-H and V-kappa genes inserted are
CC selected to restore normal B-cell development in the mammal. The
CC transgenic animals have a near complete human Ig locus, including both a
CC human heavy chain locus and a human kappa light chain locus. They can be
CC used for the production of human antibodies when exposed to particular
CC antigens e.g. when exposed to human IL-8, EGFR or TNF- alpha the mice
CC will produce antibodies to IL-8, EGFR or TNF- alpha respectively
XX
SQ Sequence 74 AA;

Query Match 100.0%; Score 86; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 14 WYQQKPGKAPKLLIY 28

Search completed: March 23, 2006, 01:54:01
Job time : 141.479 secs

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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:54:26 ; Search time 20.7534 Seconds
(without alignments)
69.543 Million cell updates/sec

Title: US-10-755-382-27
Perfect score: 86
Sequence: 1 WYQQKPGKAPKLLIY 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	86	100.0	53	2	PH0881	Ig kappa chain V r
2	86	100.0	62	2	S42265	Ig kappa chain V r
3	86	100.0	65	2	PH0880	Ig kappa chain V r
4	86	100.0	82	2	S34090	Ig kappa chain V r
5	86	100.0	86	2	S34086	Ig kappa chain V r
6	86	100.0	86	2	S16840	Ig kappa chain V r
7	86	100.0	87	2	S34084	Ig kappa chain V r
8	86	100.0	87	2	S21523	Ig kappa chain V r
9	86	100.0	87	2	I52592	Ig kappa chain V r
10	86	100.0	87	2	S34083	Ig kappa chain V r
11	86	100.0	88	2	S34087	Ig kappa chain V r
12	86	100.0	88	2	S21522	Ig kappa chain V r
13	86	100.0	88	2	S21528	Ig kappa chain V r
14	86	100.0	88	2	S21520	Ig kappa chain V r
15	86	100.0	88	2	S34104	Ig kappa chain V r
16	86	100.0	88	2	S34088	Ig kappa chain V r
17	86	100.0	88	2	S21524	Ig kappa chain V r
18	86	100.0	95	2	PH0864	Ig kappa chain V r
19	86	100.0	95	2	PH0862	Ig kappa chain V r
20	86	100.0	98	2	S41813	Ig kappa chain V r
21	86	100.0	106	2	PC2397	anti-tetanus toxin
22	86	100.0	107	2	S36264	Ig lambda chain V
23	86	100.0	107	2	S36262	Ig lambda chain V
24	86	100.0	107	2	S36269	Ig lambda chain V
25	86	100.0	108	1	K1HUAU	Ig kappa chain V-I
26	86	100.0	108	1	K1HUKA	Ig kappa chain V-I
27	86	100.0	108	1	K1HURY	Ig kappa chain V-I
28	86	100.0	108	2	S19674	Ig kappa chain V r
29	86	100.0	108	2	S36277	Ig lambda chain V
30	86	100.0	108	2	S36279	Ig lambda chain V
31	86	100.0	108	2	S47182	Ig kappa chain - h
32	86	100.0	108	2	B49047	Ig kappa chain V r
33	86	100.0	110	2	S44118	Ig kappa chain V-J
34	86	100.0	116	2	A27594	Ig kappa chain pre
35	86	100.0	117	1	K1HU12	Ig kappa chain pre
36	86	100.0	117	2	S24206	Ig kappa chain V r
37	86	100.0	117	2	S42264	Ig kappa chain V r
38	86	100.0	117	2	S11700	Ig kappa chain pre
39	86	100.0	117	2	S21527	Ig kappa chain pre
40	86	100.0	117	2	S46371	Ig kappa chain V-J
41	86	100.0	117	2	S46376	Ig kappa chain V-J
42	86	100.0	117	2	S42263	Ig kappa chain V r
43	86	100.0	117	2	S43528	Ig kappa chain V r
44	86	100.0	123	2	S40331	Ig kappa chain - h
45	86	100.0	124	2	S40336	Ig kappa chain V-J
46	86	100.0	125	2	S40333	Ig kappa chain V-J
47	86	100.0	125	2	S40349	Ig kappa chain V-J
48	86	100.0	128	2	S46372	IG light chain var
49	86	100.0	129	1	K1HUWK	Ig kappa chain pre
50	86	100.0	132	2	S38646	Ig kappa chain V r
51	86	100.0	132	2	S40334	Ig kappa chain - h
52	83	96.5	95	2	PH0865	Ig kappa chain V r
53	83	96.5	107	1	K1HUAR	Ig kappa chain V-I
54	83	96.5	108	1	K1HUEU	Ig kappa chain V-I
55	83	96.5	108	2	S34007	Ig kappa chain V r
56	83	96.5	108	2	S30521	Ig kappa chain V r
57	83	96.5	129	2	S52793	Ig kappa chain V r
58	82	95.3	71	2	S21526	Ig kappa chain V r
59	82	95.3	88	2	S21525	Ig kappa chain V r
60	82	95.3	95	2	PH0863	Ig kappa chain V r
61	82	95.3	101	2	S44117	Ig kappa chain V-J
62	82	95.3	103	2	S18731	Ig kappa chain V-J
63	82	95.3	105	2	A27585	Ig kappa chain V-I
64	82	95.3	107	2	S36275	Ig lambda chain V
65	82	95.3	107	2	S40366	Ig kappa chain V-J
66	82	95.3	108	1	K1HUBI	Ig kappa chain V-I
67	82	95.3	108	1	KVMS06	Ig kappa chain V r
68	82	95.3	108	1	KVMS09	Ig kappa chain V r
69	82	95.3	108	1	KVMS61	Ig kappa chain V r
70	82	95.3	108	1	KVMS82	Ig kappa chain V r
71	82	95.3	108	2	S31977	Ig kappa chain - h
72	82	95.3	109	1	K1HUMV	Ig kappa chain V-I
73	82	95.3	109	2	S31998	Ig kappa chain - h
74	82	95.3	117	2	S41812	Ig kappa chain V r
75	82	95.3	120	2	S21667	Ig kappa chain V r
76	82	95.3	120	2	S46370	Ig kappa chain V-J
77	82	95.3	126	2	S40335	Ig kappa chain V-J
78	82	95.3	127	2	S40367	Ig kappa chain V-J
79	82	95.3	127	2	S11240	Ig kappa chain V r
80	82	95.3	129	2	S40317	Ig kappa chain - h
81	82	95.3	131	2	S40352	Ig kappa chain V-J
82	82	95.3	230	2	S33161	Ig kappa chain - s
83	81	94.2	103	2	S44121	Ig kappa chain V-J
84	81	94.2	105	2	S36266	Ig lambda chain V
85	81	94.2	105	2	B27585	Ig kappa chain V-I
86	81	94.2	109	2	S31981	Ig kappa chain - h
87	81	94.2	123	2	S40354	Ig kappa chain - h
88	81	94.2	125	2	S40316	Ig kappa chain - h
89	81	94.2	125	2	S40350	Ig kappa chain - h
90	81	94.2	129	2	S52789	Ig kappa chain V r
91	81	94.2	141	2	A49134	Ig kappa chain V-I
92	80	93.0	108	1	K1HURE	Ig kappa chain V-I
93	80	93.0	110	2	S20635	Ig kappa chain V r
94	80	93.0	111	2	S46397	Ig lambda chain V
95	80	93.0	112	1	L2HUNG	Ig lambda chain V-
96	80	93.0	117	2	S41809	Ig kappa chain V r
97	80	93.0	125	2	S40353	Ig kappa chain V-J
98	80	93.0	129	1	K1HUDI	Ig kappa chain pre
99	80	93.0	130	2	S40368	Ig kappa chain - h
100	79	91.9	57	2	PH0879	Ig kappa chain V r
101	79	91.9	62	2	I30601	Ig kappa chain V-I
102	79	91.9	77	2	S70443	Ig kappa chain V r

103	79	91.9	78	2	S34102	Ig kappa chain V r
104	79	91.9	81	2	PH1048	Ig light chain V r
105	79	91.9	82	2	S38560	Ig light chain V r
106	79	91.9	83	2	I30607	Ig kappa chain V-I
107	79	91.9	83	2	S78489	Ig kappa chain V r
108	79	91.9	84	2	S34099	Ig kappa chain V r
109	79	91.9	86	2	S16834	Ig kappa chain V r
110	79	91.9	86	2	S16824	Ig kappa chain V r
111	79	91.9	86	2	S16832	Ig kappa chain V r
112	79	91.9	86	2	S16827	Ig kappa chain V r
113	79	91.9	86	2	S16831	Ig kappa chain V r
114	79	91.9	86	2	S16830	Ig kappa chain V r
115	79	91.9	86	2	S16833	Ig kappa chain V-I
116	79	91.9	86	2	S16828	Ig kappa chain V r
117	79	91.9	86	2	S16829	Ig kappa chain V r
118	79	91.9	86	2	S16826	Ig kappa chain V r
119	79	91.9	86	2	S16835	Ig kappa chain V r
120	79	91.9	87	2	S16823	Ig kappa chain V r
121	79	91.9	87	2	S34097	Ig kappa chain V r
122	79	91.9	87	2	S16841	Ig kappa chain V r
123	79	91.9	87	2	S34098	Ig kappa chain V r
124	79	91.9	89	2	S34096	Ig kappa chain V r
125	79	91.9	90	2	I38601	Ig kappa chain V r
126	79	91.9	90	2	S38561	Ig light chain V r
127	79	91.9	91	2	S37521	Ig kappa chain V r
128	79	91.9	91	2	S37520	Ig kappa chain V r
129	79	91.9	91	2	S37525	Ig kappa chain V r
130	79	91.9	91	2	S67940	Ig kappa chain V r
131	79	91.9	91	2	S37527	Ig kappa chain V r
132	79	91.9	92	2	S37504	Ig kappa chain V r
133	79	91.9	92	2	S37509	Ig kappa chain V r
134	79	91.9	92	2	S37513	Ig kappa chain V r
135	79	91.9	92	2	S37522	Ig kappa chain V r
136	79	91.9	92	2	S37502	Ig kappa chain V r
137	79	91.9	92	2	S37518	Ig kappa chain V r
138	79	91.9	92	2	S37517	Ig kappa chain V r
139	79	91.9	92	2	S37523	Ig kappa chain V r
140	79	91.9	92	2	S37516	Ig kappa chain V r
141	79	91.9	92	2	S37524	Ig kappa chain V r
142	79	91.9	92	2	S37519	Ig kappa chain V r
143	79	91.9	92	2	S38622	Ig kappa chain V r
144	79	91.9	93	2	S37526	Ig kappa chain V r
145	79	91.9	93	2	S37508	Ig kappa chain V r
146	79	91.9	93	2	S37501	Ig kappa chain V r
147	79	91.9	93	2	S37528	Ig kappa chain V r
148	79	91.9	93	2	S37505	Ig kappa chain V r
149	79	91.9	93	2	S38559	Ig light chain V r
150	79	91.9	95	2	PH0868	Ig kappa chain V r
151	79	91.9	96	2	S45441	Ig kappa chain V r
152	79	91.9	96	2	G38601	Ig kappa chain V r
153	79	91.9	96	2	A30601	Ig kappa chain V-I
154	79	91.9	98	2	S36046	Ig lambda chain -
155	79	91.9	98	2	S19974	Ig kappa chain V r
156	79	91.9	98	2	PH1073	Ig light chain V r
157	79	91.9	100	1	K3HUNG	Ig kappa chain pre
158	79	91.9	100	2	H38601	Ig kappa chain V r
159	79	91.9	101	2	PH1046	Ig light chain V r
160	79	91.9	101	2	S26337	Ig light chain V r
161	79	91.9	101	2	B37262	Ig kappa chain V r
162	79	91.9	103	2	PH1047	Ig light chain V r
163	79	91.9	103	2	PH1051	Ig light chain V r
164	79	91.9	103	2	PH1052	Ig light chain V r
165	79	91.9	103	2	PH1050	Ig light chain V r
166	79	91.9	103	2	PH1054	Ig light chain V r
167	79	91.9	104	2	PH1101	Ig light chain V r
168	79	91.9	104	2	F38601	Ig kappa chain V r
169	79	91.9	104	2	PH1102	Ig light chain V r
170	79	91.9	104	2	PH1104	Ig light chain V r
171	79	91.9	104	2	PH0964	Ig kappa chain V r
172	79	91.9	106	2	PC4282	Ig kappa chain (an
173	79	91.9	107	2	S34005	Ig kappa chain V r
174	79	91.9	107	2	S32191	Ig kappa chain V r
175	79	91.9	107	2	S32192	Ig kappa chain V r
176	79	91.9	107	2	S12954	Ig kappa chain V r
177	79	91.9	107	2	PH0965	Ig kappa chain V r
178	79	91.9	108	1	K1HUDE	Ig kappa chain V-I
179	79	91.9	108	1	K1HUGL	Ig kappa chain V-I
180	79	91.9	108	1	K1HUHU	Ig kappa chain V-I
181	79	91.9	108	1	K1HULY	Ig kappa chain V-I
182	79	91.9	108	2	G44151	Ig kappa chain V r
183	79	91.9	108	2	S40377	Ig kappa chain - h
184	79	91.9	108	2	E30609	Ig kappa chain V-I
185	79	91.9	108	2	B30608	Ig kappa chain V-I
186	79	91.9	108	2	PL0083	Ig kappa chain V r
187	79	91.9	108	2	H44151	Ig kappa chain V r
188	79	91.9	108	2	S33988	Ig kappa chain V r
189	79	91.9	108	2	C30608	Ig kappa chain V-I
190	79	91.9	109	1	K3HUSI	Ig kappa chain V-I
191	79	91.9	109	1	K3HUTI	Ig kappa chain V-I
192	79	91.9	109	1	K3HUWL	Ig kappa chain V-I
193	79	91.9	109	2	S47181	Ig kappa chain - h
194	79	91.9	109	2	F30601	Ig kappa chain V-I
195	79	91.9	109	2	H30601	Ig kappa chain V-I
196	79	91.9	109	2	F44151	Ig kappa chain V r
197	79	91.9	109	2	G30607	Ig kappa chain V-I
198	79	91.9	109	2	A30608	Ig kappa chain V-I
199	79	91.9	109	2	G30601	Ig kappa chain V-I
200	79	91.9	109	2	B30601	Ig kappa chain V-I
201	79	91.9	109	2	PH0963	Ig kappa chain V r
202	79	91.9	109	2	D30601	Ig kappa chain V-I
203	79	91.9	109	2	F30607	Ig kappa chain V-I
204	79	91.9	110	2	E30607	Ig kappa chain V-I
205	79	91.9	110	2	S40326	Ig kappa chain V-J
206	79	91.9	111	1	L2HUNI	Ig lambda chain V-
207	79	91.9	111	2	S23628	Ig kappa chain V r
208	79	91.9	111	2	PN0537	Ig kappa chain V r
209	79	91.9	111	2	S36281	Ig lambda chain V
210	79	91.9	111	2	S03304	Ig kappa chain V r
211	79	91.9	111	2	G30502	Ig kappa chain V r
212	79	91.9	112	2	S09970	Ig kappa chain V-J
213	79	91.9	112	2	PL0265	Ig kappa chain V r
214	79	91.9	112	2	S41393	Ig kappa chain V r
215	79	91.9	112	2	S43103	Ig kappa chain V-J
216	79	91.9	113	2	PT0408	Ig light chain V r
217	79	91.9	113	2	PT0407	Ig light chain V r
218	79	91.9	113	2	A49260	antitumor monoclon
219	79	91.9	114	2	S46375	Ig kappa chain V-J
220	79	91.9	114	2	S54905	Ig kappa chain V r
221	79	91.9	115	1	K3HUVG	Ig kappa chain pre
222	79	91.9	115	2	A30553	Ig kappa chain pre
223	79	91.9	115	2	S11697	Ig kappa chain pre
224	79	91.9	115	2	B25924	Ig kappa chain pre
225	79	91.9	115	2	A25924	Ig kappa chain pre
226	79	91.9	116	1	K3HUVH	Ig kappa chain pre
227	79	91.9	116	2	B26555	Ig kappa chain V-I
228	79	91.9	116	2	S41817	Ig kappa chain V r
229	79	91.9	116	2	C27594	Ig kappa chain pre
230	79	91.9	116	2	B27594	Ig kappa chain pre
231	79	91.9	117	2	S40362	Ig kappa chain - h
232	79	91.9	117	2	S42466	Ig kappa chain V r
233	79	91.9	118	2	PT0356	Ig kappa chain V r
234	79	91.9	119	2	S41816	Ig kappa chain V r
235	79	91.9	119	2	PQ0265	Ig kappa chain V r
236	79	91.9	120	2	G33932	Ig kappa chain pre
237	79	91.9	121	2	S40327	Ig kappa chain - h
238	79	91.9	124	2	S20633	Ig kappa chain - h
239	79	91.9	124	2	S40348	Ig kappa chain V-J
240	79	91.9	127	2	S04577	Ig kappa chain pre
241	79	91.9	128	2	S20636	Ig kappa chain V r
242	79	91.9	128	2	A56701	Ig kappa chain V r
243	79	91.9	128	2	S40345	Ig kappa chain V-J
244	79	91.9	129	1	K3HUHA	Ig kappa chain pre
245	79	91.9	129	1	K3HUHI	Ig kappa chain pre
246	79	91.9	129	2	S52792	Ig kappa chain V r
247	79	91.9	129	2	S40363	Ig kappa chain - h
248	79	91.9	129	2	S46369	IG light chain var

249	79	91.9	129	2	S49532	anti-Sm antibody V
250	79	91.9	130	2	S20637	Ig kappa chain V r
251	79	91.9	130	2	S40360	Ig kappa chain - h
252	79	91.9	131	2	S40328	Ig kappa chain - h
253	79	91.9	131	2	PL0207	anti-idiotypic ant
254	79	91.9	133	2	PS0023	Ig kappa chain pre
255	79	91.9	134	2	S38643	Ig kappa chain V r
256	79	91.9	134	2	PC1214	Ig kappa chain pre
257	79	91.9	138	2	S26040	Ig kappa chain pre
258	79	91.9	145	2	PL0014	Ig kappa chain pre
259	79	91.9	149	1	KVMS11	Ig kappa chain pre
260	79	91.9	215	2	A23746	Ig kappa chain V-I
261	79	91.9	215	2	JE0244	Ig kappa chain NIG
262	79	91.9	225	2	S37484	Ig kappa chain - m
263	79	91.9	233	2	S29577	Ig light chain - r
264	79	91.9	240	2	S06084	Ig kappa chain pre
265	78	90.7	79	2	S24215	Ig kappa chain - m
266	78	90.7	99	2	S36055	Ig lambda chain -
267	78	90.7	99	2	S36057	Ig lambda chain -
268	78	90.7	99	2	S36056	Ig lambda chain -
269	78	90.7	108	1	K1HUKU	Ig kappa chain V-I
270	78	90.7	108	1	K1HUSW	Ig kappa chain V-I
271	78	90.7	108	1	K1HUWS	Ig kappa chain V-I
272	78	90.7	108	2	PS0073	Ig kappa chain V r
273	78	90.7	108	2	S19112	Ig kappa chain V r
274	78	90.7	109	1	L2HUBR	Ig lambda chain V-
275	78	90.7	109	2	S32001	Ig kappa chain - h
276	78	90.7	109	2	S31980	Ig kappa chain - h
277	78	90.7	109	2	S31979	Ig kappa chain - h
278	78	90.7	109	2	S26336	Ig light chain V r
279	78	90.7	110	1	L2HU58	Ig lambda chain V-
280	78	90.7	110	2	S57442	Ig lambda chain V-
281	78	90.7	110	2	PN0535	Ig kappa chain V r
282	78	90.7	110	2	S51149	antibody light cha
283	78	90.7	111	1	L2HUBH	Ig lambda chain V-
284	78	90.7	112	1	K1HUNY	Ig kappa chain V-I
285	78	90.7	112	2	S46395	Ig lambda chain V
286	78	90.7	112	2	S44123	Ig lambda chain V-
287	78	90.7	112	2	S31515	Ig lambda chain V
288	78	90.7	112	2	S44105	Ig lambda chain V-
289	78	90.7	112	2	S19976	Ig kappa chain V r
290	78	90.7	113	2	JC2270	PL7-6 antibody lig
291	78	90.7	117	2	S21668	Ig kappa chain V r
292	78	90.7	117	2	S24207	Ig kappa chain V r
293	78	90.7	118	2	S04519	Ig lambda chain pr
294	78	90.7	125	2	S20634	Ig kappa chain V r
295	78	90.7	125	2	S40315	Ig kappa chain - h
296	78	90.7	214	2	S68212	Ig kappa chain (Ma
297	78	90.7	235	2	S25758	Ig lambda chain -
298	77	89.5	77	2	D30502	Ig kappa chain V r
299	77	89.5	81	2	S42193	Ig kappa chain V r
300	77	89.5	91	2	S25462	Ig kappa chain V r
301	77	89.5	92	2	S37532	Ig kappa chain V r
302	77	89.5	92	2	S37533	Ig kappa chain V r
303	77	89.5	92	2	S37530	Ig kappa chain V r
304	77	89.5	92	2	S37535	Ig kappa chain V r
305	77	89.5	92	2	S37534	Ig kappa chain V r
306	77	89.5	92	2	S37529	Ig kappa chain V r
307	77	89.5	93	2	A38601	Ig kappa chain V r
308	77	89.5	96	2	B49442	Ig light chain V r
309	77	89.5	101	2	PH0869	Ig kappa chain V r
310	77	89.5	102	2	PH1076	Ig light chain V r
311	77	89.5	104	2	PH1103	Ig light chain V r
312	77	89.5	105	2	C30535	Ig kappa chain V r
313	77	89.5	107	2	S36268	Ig lambda chain V
314	77	89.5	107	2	S26343	Ig kappa chain V r
315	77	89.5	107	2	S26344	Ig kappa chain V r
316	77	89.5	107	2	F30535	Ig kappa chain V r
317	77	89.5	107	2	D30535	Ig kappa chain V r
318	77	89.5	107	2	G30535	Ig kappa chain V r
319	77	89.5	107	2	B30535	Ig kappa chain V r
320	77	89.5	108	1	K1HUOU	Ig kappa chain V-I
321	77	89.5	108	1	KVMSAA	Ig kappa chain V r
322	77	89.5	108	1	KVRB2K	Ig kappa chain V r
323	77	89.5	108	2	S40330	Ig kappa chain V-J
324	77	89.5	108	2	E30535	Ig kappa chain V r
325	77	89.5	110	1	KVMS10	Ig kappa chain V r
326	77	89.5	110	1	KVRB54	Ig kappa chain V r
327	77	89.5	111	1	KVMS08	Ig kappa chain V r
328	77	89.5	111	1	KVMS37	Ig kappa chain V r
329	77	89.5	111	1	KVMS40	Ig kappa chain V r
330	77	89.5	111	1	KVMS43	Ig kappa chain V r
331	77	89.5	111	1	KVMS75	Ig kappa chain V r
332	77	89.5	111	1	KVMS83	Ig kappa chain V r
333	77	89.5	111	1	KVMS84	Ig kappa chain V r
334	77	89.5	111	1	KVMS85	Ig kappa chain V r
335	77	89.5	111	1	KVRB36	Ig kappa chain V r
336	77	89.5	111	2	D45722	anti-glycoprotein
337	77	89.5	112	2	S19972	Ig kappa chain V r
338	77	89.5	112	2	F30538	Ig kappa chain V r
339	77	89.5	112	2	E30538	Ig kappa chain V r
340	77	89.5	112	2	S19971	Ig kappa chain V r
341	77	89.5	113	2	S34002	Ig kappa chain V r
342	77	89.5	113	2	PL0263	Ig kappa chain V r
343	77	89.5	114	1	K4HULN	Ig kappa chain V-I
344	77	89.5	114	2	S46377	Ig kappa chain V-J
345	77	89.5	115	2	S63596	Ig kappa chain V r
346	77	89.5	117	1	K4RBF2	Ig kappa chain pre
347	77	89.5	120	2	S51147	antibody light cha
348	77	89.5	120	2	S06731	Ig kappa chain pre
349	77	89.5	121	1	K4HU	Ig kappa chain pre
350	77	89.5	130	2	S08079	Ig kappa chain pre
351	77	89.5	131	1	KVMSM6	Ig kappa chain pre
352	77	89.5	131	2	S55027	Ig light chain pre
353	77	89.5	131	2	PH1226	Ig kappa chain pre
354	77	89.5	133	1	K4HUJI	Ig kappa chain pre
355	77	89.5	134	1	K4HU17	Ig kappa chain pre
356	77	89.5	134	2	S49531	anti-Sm antibody V
357	77	89.5	135	2	S38807	Ig light chain V-J
358	77	89.5	138	2	A53261	Ig kappa chain pre
359	77	89.5	215	2	JE0242	Ig kappa chain NIG
360	77	89.5	229	2	A20969	Ig kappa chain pre
361	76	88.4	86	2	S16836	Ig kappa chain V r
362	76	88.4	86	2	S16837	Ig kappa chain V r
363	76	88.4	92	2	S37514	Ig kappa chain V r
364	76	88.4	98	2	PH1067	Ig light chain V r
365	76	88.4	98	2	PH1066	Ig light chain V r
366	76	88.4	107	2	S47183	Ig kappa chain - h
367	76	88.4	107	2	S09968	Ig kappa chain V-J
368	76	88.4	108	1	K1HUBN	Ig kappa chain V-I
369	76	88.4	108	1	K3HUB6	Ig kappa chain V-I
370	76	88.4	108	2	S44122	Ig kappa chain V r
371	76	88.4	109	1	K3HUGO	Ig kappa chain V-I
372	76	88.4	109	2	C30601	Ig kappa chain V-I
373	76	88.4	112	2	A44151	Ig lambda chain V
374	76	88.4	116	2	B25521	Ig kappa chain pre
375	76	88.4	117	2	C21056	Ig kappa chain pre
376	76	88.4	117	2	S10227	Ig kappa chain pre
377	76	88.4	117	2	S41814	Ig kappa chain V r
378	76	88.4	123	2	S40313	Ig kappa chain V-J
379	76	88.4	129	2	S40325	Ig kappa chain - h
380	76	88.4	129	2	S40369	Ig kappa chain - h
381	76	88.4	129	2	S40332	Ig kappa chain - h
382	76	88.4	139	2	S40365	Ig kappa chain - h
383	76	88.4	144	2	PL0106	Ig kappa chain pre
384	75	87.2	60	2	A24626	Ig lambda chain V-
385	75	87.2	86	2	S16825	Ig kappa chain V r
386	75	87.2	91	2	S37511	Ig kappa chain V r
387	75	87.2	92	2	S37510	Ig kappa chain V r
388	75	87.2	93	2	S17633	Ig kappa chain V r
389	75	87.2	93	2	S17632	Ig kappa chain V r
390	75	87.2	93	2	S17635	Ig kappa chain V r
391	75	87.2	93	2	S17634	Ig kappa chain V r
392	75	87.2	93	2	S17636	Ig kappa chain V r
393	75	87.2	93	2	S17624	Ig kappa chain V r
394	75	87.2	95	2	PH0867	Ig kappa chain V r

395	75	87.2	102	2	S29582	Ig kappa chain V r
396	75	87.2	102	2	S29588	Ig kappa chain V r
397	75	87.2	103	2	S13695	Ig kappa chain - m
398	75	87.2	108	1	KVRBB1	Ig kappa chain V r
399	75	87.2	108	1	KVRBB5	Ig kappa chain V r
400	75	87.2	108	2	PS0069	Ig kappa chain V r
401	75	87.2	109	2	S38494	Ig lambda chain -
402	75	87.2	109	2	JN0296	Ig kappa chain V-J
403	75	87.2	109	2	S13699	Ig kappa chain V r
404	75	87.2	111	2	S40359	Ig kappa chain V-J
405	75	87.2	120	2	S66536	Ig light chain V r
406	75	87.2	123	2	S05269	Ig kappa chain pre
407	75	87.2	124	2	S05267	Ig kappa chain pre
408	75	87.2	127	2	S40380	Ig kappa chain V-J
409	75	87.2	152	2	S30751	Ig kappa chain pre
410	75	87.2	228	2	S29575	Ig light chain - r
411	75	87.2	235	2	S25759	Ig lambda chain -
412	75	87.2	235	2	S20000	Ig light chain pre
413	74	86.0	75	2	A34966	Ig heavy chain V r
414	74	86.0	86	2	S78488	Ig kappa chain V r
415	74	86.0	87	2	S16842	Ig kappa chain V r
416	74	86.0	91	2	S37515	Ig kappa chain V r
417	74	86.0	92	2	S37506	Ig kappa chain V r
418	74	86.0	92	2	S37531	Ig kappa chain V r
419	74	86.0	92	2	S37507	Ig kappa chain V r
420	74	86.0	94	2	F33730	Ig kappa chain V r
421	74	86.0	95	2	PH0866	Ig kappa chain V r
422	74	86.0	97	2	A42575	Ig kappa chain V r
423	74	86.0	98	2	I30608	Ig kappa chain V-I
424	74	86.0	98	2	PH1072	Ig light chain V r
425	74	86.0	107	2	S57444	Ig kappa chain V-J
426	74	86.0	108	1	K1HUWE	Ig kappa chain V-I
427	74	86.0	108	2	B44371	Ig kappa chain V r
428	74	86.0	108	2	PH0092	Ig kappa chain V r
429	74	86.0	108	2	PL0204	anti-DNA autoantib
430	74	86.0	109	1	KVRB37	Ig kappa chain V r
431	74	86.0	109	2	S31978	Ig kappa chain - h
432	74	86.0	111	1	KVMSC1	Ig kappa chain V r
433	74	86.0	111	1	L2HUTR	Ig lambda chain V-
434	74	86.0	111	1	L2HUWN	Ig lambda chain V-
435	74	86.0	111	2	S38497	Ig lambda chain -
436	74	86.0	112	2	S45715	Ig kappa chain V r
437	74	86.0	113	2	S30520	Ig kappa chain V r
438	74	86.0	115	1	K3HUCL	Ig kappa chain pre
439	74	86.0	115	1	KVMSL6	Ig kappa chain pre
440	74	86.0	115	2	B46518	Ig L1 chain V regi
441	74	86.0	120	2	S21666	Ig kappa chain V r
442	74	86.0	125	2	S04936	Ig kappa chain pre
443	74	86.0	127	2	S52447	Ig kappa chain V r
444	74	86.0	128	2	S40379	Ig kappa chain V-J
445	74	86.0	128	2	PL0101	Ig kappa chain pre
446	74	86.0	128	2	A47159	Ig lambda chain V
447	74	86.0	130	2	PL0113	Ig kappa chain pre
448	74	86.0	131	2	S40346	Ig kappa chain V-J
449	74	86.0	145	2	S20631	Ig kappa chain - h
450	74	86.0	210	2	A56169	Ig kappa chain V r
451	74	86.0	216	2	S69130	Ig lambda chain (D
452	74	86.0	220	2	A31790	Ig kappa chain V r
453	74	86.0	235	2	S14675	Ig lambda chain -
454	73	84.9	87	2	S78490	Ig kappa chain V r
455	73	84.9	95	2	S69898	Ig kappa chain V r
456	73	84.9	95	2	S49571	Ig lambda chain pr
457	73	84.9	95	2	S25177	Ig kappa chain V r
458	73	84.9	98	2	S36068	Ig lambda chain -
459	73	84.9	98	2	S36047	Ig lambda chain -
460	73	84.9	98	2	S36050	Ig lambda chain -
461	73	84.9	98	2	S36048	Ig lambda chain -
462	73	84.9	99	2	JH0429	Ig kappa chain V-I
463	73	84.9	99	2	S36053	Ig lambda chain -
464	73	84.9	99	2	S36051	Ig lambda chain -
465	73	84.9	99	2	S36052	Ig lambda chain -
466	73	84.9	99	2	S36054	Ig lambda chain -
467	73	84.9	102	2	PH1079	Ig light chain V r
468	73	84.9	106	2	S03303	Ig kappa chain V r
469	73	84.9	107	2	S09964	Ig kappa chain V-J
470	73	84.9	108	1	KVRB12	Ig kappa chain V r
471	73	84.9	109	1	KVRB16	Ig kappa chain V r
472	73	84.9	109	2	S31983	Ig kappa chain - h
473	73	84.9	109	2	PH0093	Ig kappa chain V r
474	73	84.9	110	1	KVRB29	Ig kappa chain V r
475	73	84.9	110	2	S57408	Ig lambda chain V-
476	73	84.9	111	1	KVMS13	Ig kappa chain V r
477	73	84.9	111	1	KVMS50	Ig kappa chain V r
478	73	84.9	111	1	KVMS80	Ig kappa chain V r
479	73	84.9	111	1	L1HUNG	Ig lambda chain V-
480	73	84.9	111	2	S47185	Ig lambda chain -
481	73	84.9	111	2	S47009	Ig lambda chain V1
482	73	84.9	111	2	S36274	Ig lambda chain V
483	73	84.9	111	2	PL0081	Ig kappa chain V r
484	73	84.9	111	2	E53285	Ig kappa chain V a
485	73	84.9	111	2	S37202	Ig kappa chain V r
486	73	84.9	111	2	S09965	Ig kappa chain V-J
487	73	84.9	112	1	L1HUHA	Ig lambda chain V-
488	73	84.9	112	1	L1HUMM	Ig lambda chain V-
489	73	84.9	112	2	C44151	Ig lambda chain V
490	73	84.9	112	2	D44151	Ig lambda chain V
491	73	84.9	112	2	B44151	Ig lambda chain V
492	73	84.9	112	2	S51148	antibody light cha
493	73	84.9	117	2	S04525	Ig lambda chain pr
494	73	84.9	117	2	S23627	Ig lambda chain pr
495	73	84.9	118	2	T03036	Ig light chain - h
496	73	84.9	118	2	S12627	Ig lambda chain pr
497	73	84.9	119	2	S08077	Ig kappa chain pre
498	73	84.9	120	2	S46374	Ig kappa chain V-J
499	73	84.9	120	2	S06732	Ig kappa chain pre
500	73	84.9	128	2	S40343	Ig kappa chain V-J
501	73	84.9	129	2	S78058	Ig lambda chain pr
502	73	84.9	129	2	S40347	Ig kappa chain - h
503	73	84.9	130	1	L1HUBL	Ig lambda chain pr
504	73	84.9	130	2	S78057	Ig lambda chain pr
505	73	84.9	130	2	S09712	Ig lambda chain V
506	73	84.9	131	2	S24321	Ig lambda chain pr
507	73	84.9	132	1	KVMS32	Ig kappa chain pre
508	73	84.9	149	2	S23626	Ig lambda chain V
509	73	84.9	213	2	S21066	Ig lambda chain V
510	73	84.9	216	2	A42193	Ig lambda chain (B
511	73	84.9	216	2	S03401	Ig lambda chain (K
512	73	84.9	216	2	S29258	Ig lambda chain V
513	73	84.9	233	2	S25744	Ig lambda chain -
514	73	84.9	233	2	S25752	Ig lambda chain -
515	73	84.9	235	2	S05270	Ig lambda chain pr
516	73	84.9	236	2	S25746	Ig lambda chain -
517	72	83.7	86	2	S16839	Ig kappa chain V r
518	72	83.7	86	2	S20651	Ig heavy chain V r
519	72	83.7	87	2	S16843	Ig kappa chain V r
520	72	83.7	93	2	PH1039	Ig light chain V r
521	72	83.7	93	2	S24502	Ig kappa chain V r
522	72	83.7	96	2	S36060	Ig lambda chain -
523	72	83.7	96	2	C33730	Ig kappa chain V r
524	72	83.7	96	2	S55366	Ig kappa chain V r
525	72	83.7	98	2	B33936	Ig kappa chain V r
526	72	83.7	98	2	PH1061	Ig light chain V r
527	72	83.7	99	2	S36058	Ig lambda chain -
528	72	83.7	99	2	PH1059	Ig light chain V r
529	72	83.7	99	2	PH1060	Ig light chain V r
530	72	83.7	99	2	S24504	Ig kappa chain V r
531	72	83.7	99	2	S24501	Ig kappa chain V r
532	72	83.7	99	2	PH1058	Ig light chain V r
533	72	83.7	100	2	S26334	Ig light chain V r
534	72	83.7	101	2	S11126	Ig kappa chain V r
535	72	83.7	102	2	S14590	Ig kappa chain V r
536	72	83.7	102	2	S14591	Ig kappa chain V r
537	72	83.7	102	2	S14594	Ig kappa chain V r
538	72	83.7	102	2	S14592	Ig kappa chain V r
539	72	83.7	102	2	S14593	Ig kappa chain V r
540	72	83.7	102	2	PH1035	Ig light chain V r

541	72	83.7	102	2	E28195	Ig kappa chain V r
542	72	83.7	102	2	PH1044	Ig light chain V r
543	72	83.7	103	2	PH1045	Ig light chain V r
544	72	83.7	103	2	PH1042	Ig light chain V r
545	72	83.7	103	2	PH1031	Ig light chain V r
546	72	83.7	103	2	PH1034	Ig light chain V r
547	72	83.7	103	2	PH1038	Ig light chain V r
548	72	83.7	103	2	PH1030	Ig light chain V r
549	72	83.7	103	2	PH1043	Ig light chain V r
550	72	83.7	103	2	PH1036	Ig light chain V r
551	72	83.7	103	2	PH1037	Ig light chain V r
552	72	83.7	104	2	PH1053	Ig light chain V r
553	72	83.7	105	2	S49533	anti-Sm antibody V
554	72	83.7	106	2	A49138	IgA kappa rheumato
555	72	83.7	107	2	JL0139	Ig kappa chain V r
556	72	83.7	107	2	D32530	Ig kappa chain V r
557	72	83.7	107	2	S09967	Ig kappa chain V-J
558	72	83.7	108	1	L3HUSH	Ig lambda chain V-
559	72	83.7	108	2	S38498	Ig lambda chain -
560	72	83.7	108	2	S47184	Ig lambda chain -
561	72	83.7	108	2	E32530	Ig kappa chain V r
562	72	83.7	109	2	S19663	Ig lambda chain V
563	72	83.7	110	2	S57428	Ig light chain V-J
564	72	83.7	110	2	S19672	Ig lambda chain V
565	72	83.7	110	2	S36272	Ig lambda chain V
566	72	83.7	110	2	S26335	Ig kappa chain V r
567	72	83.7	111	1	L2HUTG	Ig lambda chain V-
568	72	83.7	111	2	S09963	Ig kappa chain V-J
569	72	83.7	111	2	PL0257	Ig kappa chain V r
570	72	83.7	112	2	E27887	Ig kappa chain V r
571	72	83.7	112	2	S32189	Ig kappa chain V r
572	72	83.7	112	2	S38719	Ig light chain V r
573	72	83.7	112	2	F27887	Ig kappa chain V r
574	72	83.7	112	2	B27887	Ig kappa chain V r
575	72	83.7	112	2	S53750	antibody Fab Jel 1
576	72	83.7	112	2	A27887	Ig kappa chain V r
577	72	83.7	112	2	D28195	Ig kappa chain V r
578	72	83.7	112	2	A31807	Ig kappa chain V r
579	72	83.7	113	2	PL0203	anti-DNA autoantib
580	72	83.7	113	2	PL0205	anti-DNA autoantib
581	72	83.7	113	2	B41940	Ig light chain V r
582	72	83.7	114	2	A32967	Ig kappa chain V-I
583	72	83.7	114	2	A34353	anti-peptide Fab'
584	72	83.7	115	2	S13726	Ig lambda chain V
585	72	83.7	115	2	S60066	Ig kappa chain V r
586	72	83.7	117	1	K1HU11	Ig kappa chain pre
587	72	83.7	117	2	B21056	Ig kappa chain pre
588	72	83.7	118	2	S24510	Ig kappa chain V r
589	72	83.7	118	2	S24538	Ig kappa chain V r
590	72	83.7	118	2	PT0359	Ig kappa chain V r
591	72	83.7	118	2	S24536	Ig kappa chain V r
592	72	83.7	118	2	S24503	Ig kappa chain V r
593	72	83.7	118	2	S24531	Ig kappa chain V r
594	72	83.7	118	2	S24533	Ig kappa chain V r
595	72	83.7	118	2	S24535	Ig kappa chain V r
596	72	83.7	118	2	S24498	Ig kappa chain V r
597	72	83.7	118	2	S24500	Ig kappa chain V r
598	72	83.7	118	2	S24529	Ig kappa chain V r
599	72	83.7	118	2	S24506	Ig kappa chain V r
600	72	83.7	118	2	S24509	Ig kappa chain V r
601	72	83.7	118	2	S24507	Ig kappa chain V r
602	72	83.7	118	2	S24537	Ig kappa chain V r
603	72	83.7	118	2	S24530	Ig kappa chain V r
604	72	83.7	119	2	A49032	Ig kappa chain V r
605	72	83.7	119	2	S30526	Ig lambda chain V
606	72	83.7	121	2	S40371	Ig kappa chain - h
607	72	83.7	127	2	S70444	Ig lambda chain pr
608	72	83.7	128	1	KVMST1	Ig kappa chain pre
609	72	83.7	129	2	S29627	Ig kappa chain V r
610	72	83.7	129	2	A32274	Ig kappa chain pre
611	72	83.7	130	2	C29380	Ig kappa chain pre
612	72	83.7	130	2	A32513	Ig kappa chain pre
613	72	83.7	131	2	B34904	Ig kappa chain pre
614	72	83.7	131	2	B39276	Ig light chain pre
615	72	83.7	131	2	G34903	Ig kappa chain pre
616	72	83.7	131	2	S09259	Ig kappa chain pre
617	72	83.7	131	2	B32513	Ig kappa chain pre
618	72	83.7	131	2	D29380	Ig kappa chain pre
619	72	83.7	131	2	PT0178	Ig kappa chain pre
620	72	83.7	131	2	C34904	Ig kappa chain pre
621	72	83.7	131	2	B30577	Ig kappa chain pre
622	72	83.7	146	2	S02083	Ig lambda chain V-
623	72	83.7	212	2	S70431	Ig lambda chain -
624	72	83.7	219	2	S52028	Ig kappa chain - m
625	72	83.7	219	2	PC4203	Ig kappa chain (mo
626	72	83.7	232	2	S25742	Ig lambda chain -
627	71	82.6	92	2	S37503	Ig kappa chain V r
628	71	82.6	93	2	S17631	Ig kappa chain V r
629	71	82.6	95	2	S45324	Ig kappa chain V r
630	71	82.6	107	1	L4HUHL	Ig lambda chain V-
631	71	82.6	107	2	S38713	Ig light chain V r
632	71	82.6	107	2	S24290	Ig kappa chain V r
633	71	82.6	107	2	S33132	Ig kappa chain V r
634	71	82.6	108	2	I39154	Ig kappa chain (BR
635	71	82.6	108	2	PL0278	Ig kappa chain V r
636	71	82.6	108	2	PL0277	Ig kappa chain V r
637	71	82.6	108	2	PL0276	Ig kappa chain V r
638	71	82.6	111	2	S46396	Ig lambda chain V
639	71	82.6	111	2	D37266	Ig kappa chain V r
640	71	82.6	117	2	S41810	Ig kappa chain V r
641	71	82.6	118	2	I33932	Ig kappa chain pre
642	71	82.6	120	2	S30527	Ig lambda chain V
643	71	82.6	122	2	S40370	Ig kappa chain - h
644	71	82.6	125	2	S40344	Ig kappa chain V-J
645	71	82.6	132	2	S09713	Ig lambda chain V
646	71	82.6	136	1	KVMS21	Ig kappa chain pre
647	71	82.6	216	2	JE0245	Ig lambda chain NI
648	71	82.6	232	2	S25756	Ig lambda chain -
649	71	82.6	233	2	S25747	Ig lambda chain -
650	71	82.6	235	2	S25754	Ig lambda chain -
651	70	81.4	81	2	S22024	Ig kappa chain - m
652	70	81.4	88	2	S38562	Ig kappa chain V r
653	70	81.4	92	2	S37512	Ig kappa chain V r
654	70	81.4	97	2	S36066	Ig lambda chain -
655	70	81.4	97	2	PH1068	Ig light chain V r
656	70	81.4	98	2	S36062	Ig lambda chain -
657	70	81.4	98	2	PH1069	Ig light chain V r
658	70	81.4	98	2	PH1074	Ig light chain V r
659	70	81.4	99	2	E28833	Ig heavy chain V r
660	70	81.4	100	2	C28833	Ig heavy chain V r
661	70	81.4	100	2	B28833	Ig heavy chain V r
662	70	81.4	100	2	D28833	Ig heavy chain V r
663	70	81.4	101	2	S20810	Ig kappa chain V r
664	70	81.4	101	2	S13701	Ig kappa chain V r
665	70	81.4	102	2	PH1077	Ig light chain V r
666	70	81.4	103	2	H30502	Ig kappa chain V r
667	70	81.4	103	2	S13703	Ig kappa chain V r
668	70	81.4	104	2	S13700	Ig kappa chain V r
669	70	81.4	106	2	S26345	Ig light chain V r
670	70	81.4	106	2	PS0070	Ig kappa chain V r
671	70	81.4	106	2	B47329	Ig kappa chain V r
672	70	81.4	107	2	PL0080	Ig kappa chain V r
673	70	81.4	108	1	KVMS49	Ig kappa chain V r
674	70	81.4	108	1	KVMS54	Ig kappa chain V r
675	70	81.4	108	2	S36283	Ig lambda chain V
676	70	81.4	110	1	K4RB27	Ig kappa chain V r
677	70	81.4	111	1	KVMS69	Ig kappa chain V r
678	70	81.4	111	1	L2HUBO	Ig lambda chain V-
679	70	81.4	113	2	A29700	Ig lambda chain V
680	70	81.4	114	2	S44116	Ig kappa chain V-J
681	70	81.4	115	1	KVMSK2	Ig kappa chain pre
682	70	81.4	116	2	PT0357	Ig kappa chain V r
683	70	81.4	117	1	LVHU2	Ig lambda chain pr
684	70	81.4	117	2	S41811	Ig kappa chain V r
685	70	81.4	117	2	S04526	Ig lambda chain pr
686	70	81.4	118	2	S24508	Ig kappa chain V r

687	70	81.4	124	2	S40318	Ig kappa chain V r
688	70	81.4	127	2	S04574	Ig kappa chain pre
689	70	81.4	127	2	S09230	Ig kappa chain pre
690	70	81.4	128	2	S31488	Ig kappa chain pre
691	70	81.4	129	2	B23986	Ig kappa chain pre
692	70	81.4	132	2	S05268	Ig kappa chain pre
693	70	81.4	134	2	A30563	T-cell receptor be
694	70	81.4	134	2	S11245	Ig kappa chain pre
695	70	81.4	135	2	S24320	Ig kappa chain pre
696	70	81.4	136	2	S16848	Ig lambda chain V-
697	70	81.4	213	2	JE0247	Ig lambda chain NI
698	70	81.4	218	2	S68241	Ig kappa chain V r
699	70	81.4	218	2	JC5810	monoclonal antibod
700	70	81.4	234	2	S25757	Ig lambda chain -
701	70	81.4	234	2	S14237	Ig kappa chain pre
702	70	81.4	234	2	S01320	Ig kappa chain pre
703	69	80.2	48	2	PH0884	Ig kappa chain V r
704	69	80.2	72	2	H36025	Ig heavy chain V r
705	69	80.2	81	2	G36025	Ig light chain V r
706	69	80.2	85	2	F36025	Ig light chain V r
707	69	80.2	94	2	S20648	Ig heavy chain V r
708	69	80.2	94	2	E33730	Ig kappa chain V r
709	69	80.2	94	2	PH1063	Ig light chain V r
710	69	80.2	94	2	PL0258	Ig kappa chain V r
711	69	80.2	95	2	S36065	Ig lambda chain -
712	69	80.2	97	2	PH1064	Ig light chain V r
713	69	80.2	98	2	PH1083	Ig light chain V r
714	69	80.2	103	1	L1HUNM	Ig lambda chain V-
715	69	80.2	104	2	S26330	Ig kappa chain V r
716	69	80.2	104	2	S26329	Ig kappa chain V r
717	69	80.2	106	1	L4HUBU	Ig lambda chain V-
718	69	80.2	106	2	C33936	Ig kappa chain V r
719	69	80.2	107	1	K4RB41	Ig kappa chain V r
720	69	80.2	107	2	PC4283	anti-SS-A/Ro 60K p
721	69	80.2	107	2	B28195	Ig kappa chain V r
722	69	80.2	107	2	A28195	Ig kappa chain V r
723	69	80.2	108	1	K1HUAG	Ig kappa chain V-I
724	69	80.2	109	1	L1HUEP	Ig lambda chain V-
725	69	80.2	109	1	L1HUWA	Ig lambda chain V-
726	69	80.2	109	2	S38496	Ig lambda chain -
727	69	80.2	111	2	S09969	Ig kappa chain V-J
728	69	80.2	112	2	A49715	Ig kappa chain V r
729	69	80.2	112	2	B31485	Ig kappa chain V r
730	69	80.2	113	2	S34003	Ig kappa chain V r
731	69	80.2	113	2	S30523	Ig kappa chain V r
732	69	80.2	113	2	PL0264	Ig kappa chain V r
733	69	80.2	114	2	S16440	Ig lambda chain -
734	69	80.2	114	2	S44119	Ig kappa chain V-J
735	69	80.2	115	2	S38715	Ig kappa chain V r
736	69	80.2	120	2	A49043	Ig kappa chain V r
737	69	80.2	122	2	S40314	Ig kappa chain - h
738	69	80.2	124	2	S40364	Ig kappa chain - h
739	69	80.2	125	2	S09365	Ig kappa chain - m
740	69	80.2	129	2	S40329	Ig kappa chain V-J
741	69	80.2	129	2	S32806	Ig kappa chain pre
742	69	80.2	131	2	D34904	Ig kappa chain pre
743	69	80.2	132	2	S46373	Ig kappa chain V-J
744	69	80.2	208	2	B49444	Ig lambda chain (N
745	69	80.2	217	2	S42772	Ig kappa chain - m
746	69	80.2	219	2	S38865	Ig kappa chain - m
747	69	80.2	233	2	S25741	Ig lambda chain -
748	68	79.1	54	2	S34093	Ig kappa chain V r
749	68	79.1	87	2	S34091	Ig kappa chain V r
750	68	79.1	92	1	KVRB38	Ig kappa chain V r
751	68	79.1	96	2	S40320	Ig kappa chain - h
752	68	79.1	98	2	S36063	Ig lambda chain -
753	68	79.1	100	2	S24681	Ig kappa chain - h
754	68	79.1	103	2	PH1099	Ig light chain V r
755	68	79.1	103	2	PH1041	Ig light chain V r
756	68	79.1	103	2	PH1098	Ig light chain V r
757	68	79.1	103	2	PH1040	Ig light chain V r
758	68	79.1	106	2	PL0088	Ig kappa chain V r
759	68	79.1	106	2	S20652	Ig kappa chain V r
760	68	79.1	107	2	I69017	anti-HIV1 envelope
761	68	79.1	109	2	PH0091	Ig kappa chain V r
762	68	79.1	109	2	PH0089	Ig kappa chain V r
763	68	79.1	110	2	S36258	Ig lambda chain V
764	68	79.1	110	2	S60591	Ig light chain var
765	68	79.1	110	2	S44120	Ig kappa chain V-J
766	68	79.1	110	2	S57465	Ig lambda chain V-
767	68	79.1	110	2	PH0090	Ig light chain V r
768	68	79.1	111	2	S19671	Ig lambda chain V
769	68	79.1	111	2	S36256	Ig lambda chain V
770	68	79.1	111	2	S15673	Ig kappa chain V r
771	68	79.1	112	1	KVMSS1	Ig kappa chain V r
772	68	79.1	112	2	S26655	Ig lambda chain V
773	68	79.1	112	2	S58207	Ig light chain V r
774	68	79.1	112	2	S58206	Ig light chain V r
775	68	79.1	112	2	D27887	Ig kappa chain V r
776	68	79.1	113	1	K2HUFR	Ig kappa chain V-I
777	68	79.1	113	1	K2HUTW	Ig kappa chain V-I
778	68	79.1	113	2	F30534	Ig kappa chain V r
779	68	79.1	114	2	S40340	Ig kappa chain V-J
780	68	79.1	114	2	S40375	Ig kappa chain - h
781	68	79.1	114	2	B32967	Ig kappa chain V-I
782	68	79.1	115	2	S10146	Ig kappa chain pre
783	68	79.1	116	2	S20708	Ig kappa chain V r
784	68	79.1	119	2	B27588	Ig kappa chain pre
785	68	79.1	120	2	S30528	Ig lambda chain V
786	68	79.1	120	2	S41815	Ig kappa chain V r
787	68	79.1	121	2	S24205	Ig kappa chain V r
788	68	79.1	123	2	S40319	Ig kappa chain V r
789	68	79.1	125	2	S40356	Ig kappa chain - h
790	68	79.1	126	2	S40339	Ig kappa chain - h
791	68	79.1	130	2	S40321	Ig kappa chain - h
792	68	79.1	131	2	S40372	Ig kappa chain V-J
793	68	79.1	132	2	S26882	Ig kappa chain V r
794	68	79.1	134	2	S21917	Ig kappa chain V r
795	68	79.1	135	2	S40342	Ig kappa chain - h
796	68	79.1	136	2	S42610	ARMVlambda protein
797	68	79.1	136	2	S40357	Ig kappa chain V-J
798	68	79.1	181	2	PT0220	Ig lambda chain V-
799	68	79.1	197	2	S29574	Ig light chain - A
800	67	77.9	88	2	A37262	Ig kappa chain V r
801	67	77.9	91	2	S17630	Ig kappa chain V r
802	67	77.9	91	2	S17626	Ig kappa chain V r
803	67	77.9	95	2	S26333	Ig kappa chain V r
804	67	77.9	98	2	S40361	Ig kappa chain V-J
805	67	77.9	101	2	S59640	Ig light chain V r
806	67	77.9	102	2	I30534	Ig kappa chain V r
807	67	77.9	104	2	C30534	Ig kappa chain V r
808	67	77.9	105	2	A30534	Ig kappa chain V r
809	67	77.9	106	2	B54378	Ig light chain V r
810	67	77.9	107	2	B46516	Ig lambda chain V
811	67	77.9	109	1	K3HUPM	Ig kappa chain V-I
812	67	77.9	111	1	L2HUMC	Ig lambda chain V-
813	67	77.9	111	2	S24217	Ig kappa chain - m
814	67	77.9	113	2	H30534	Ig kappa chain V r
815	67	77.9	114	1	KVMS7A	Ig kappa chain V r
816	67	77.9	114	2	PT0358	Ig kappa chain V r
817	67	77.9	115	1	KVRB31	Ig kappa chain V-J
818	67	77.9	122	2	S40351	Ig kappa chain V r
819	67	77.9	133	2	S40324	Ig kappa chain pre
820	67	77.9	136	2	A49137	Ig kappa chain pre
821	67	77.9	225	2	JL0029	Ig lambda chain -
822	67	77.9	231	2	S25753	Ig kappa chain V r
823	66	76.7	91	2	S25463	Ig kappa chain V r
824	66	76.7	98	2	PH1065	Ig heavy chain V r
825	66	76.7	101	2	S13696	Ig heavy chain V r
826	66	76.7	102	2	S13697	Ig lambda chain V
827	66	76.7	105	2	S44124	Ig lambda chain V-
828	66	76.7	106	1	L4HUX	Ig kappa chain V r
829	66	76.7	106	2	S29583	Ig lambda chain V-
830	66	76.7	108	1	L5HUDL	Ig kappa chain V r
831	66	76.7	109	1	KVRT21	Ig kappa chain V-I
832	66	76.7	112	1	K2HUML	

833	66	76.7	113	1	KVMS17	Ig kappa chain V r
834	66	76.7	113	2	PT0409	Ig light chain V r
835	66	76.7	114	2	PH0133	Ig lambda chain V
836	66	76.7	118	2	S24532	Ig kappa chain V r
837	66	76.7	120	2	S42266	Ig kappa chain V r
838	66	76.7	120	2	S30525	Ig lambda chain V
839	66	76.7	123	2	S40378	Ig kappa chain - h
840	66	76.7	123	2	S35302	B-cell protein 8HS
841	66	76.7	131	2	S52449	Ig kappa chain V r
842	66	76.7	217	2	JE0246	Ig lambda chain NI
843	66	76.7	233	2	S25748	Ig lambda chain -
844	66	76.7	243	2	S25755	Ig lambda chain -
845	65	75.6	79	2	A28840	Ig kappa chain V r
846	65	75.6	90	2	S26339	Ig kappa chain V r
847	65	75.6	91	2	S17628	Ig kappa chain V r
848	65	75.6	94	2	S20653	Ig heavy chain V r
849	65	75.6	94	2	S20650	Ig heavy chain V r
850	65	75.6	94	2	S26340	Ig light chain V r
851	65	75.6	99	2	C46518	Ig L1 chain V regi
852	65	75.6	99	2	S29585	Ig kappa chain V r
853	65	75.6	100	2	A28833	Ig heavy chain V r
854	65	75.6	100	2	H33730	Ig kappa chain V r
855	65	75.6	102	2	B34153	Ig kappa chain V-I
856	65	75.6	102	2	PC6027	acetylcoline recep
857	65	75.6	105	2	S26338	Ig kappa chain V r
858	65	75.6	106	2	G27887	Ig kappa chain V r
859	65	75.6	107	2	PD0011	Ig kappa chain V r
860	65	75.6	107	2	D53285	Ig kappa chain V a
861	65	75.6	107	2	A42848	Ig light chain V r
862	65	75.6	107	2	PC4405	Ig kappa chain V r
863	65	75.6	110	2	S24288	Ig kappa chain V r
864	65	75.6	111	1	L7HUMT	Ig lambda chain V-
865	65	75.6	111	2	S38499	VL lambda protein
866	65	75.6	111	2	S19673	Ig lambda chain V
867	65	75.6	112	2	C27887	Ig kappa chain V r
868	65	75.6	114	1	KVRBAH	Ig kappa chain V r
869	65	75.6	114	2	S00996	Ig kappa chain pre
870	65	75.6	119	2	A27588	Ig kappa chain pre
871	65	75.6	126	2	S40341	Ig kappa chain - h
872	65	75.6	127	2	S40323	Ig kappa chain - h
873	65	75.6	127	2	A23986	Ig kappa chain pre
874	65	75.6	128	2	S52448	Ig kappa chain V r
875	65	75.6	128	2	JL0073	aberrant kappa tra
876	65	75.6	129	2	D32513	Ig kappa chain pre
877	65	75.6	140	2	PN0446	Ig kappa chain pre
878	65	75.6	140	2	PH0134	Ig lambda chain pr
879	65	75.6	219	2	S16112	Ig kappa chain V r
880	65	75.6	233	2	JC5322	p53 specific singl
881	65	75.6	235	2	S25750	Ig lambda chain -
882	65	75.6	235	2	S25749	Ig lambda chain -
883	64	74.4	47	2	B30607	Ig kappa chain V-I
884	64	74.4	84	2	E28840	Ig kappa chain V r
885	64	74.4	93	2	S17625	Ig kappa chain V r
886	64	74.4	94	2	A01955	Ig kappa-B5 chain
887	64	74.4	103	2	PH1100	Ig light chain V r
888	64	74.4	106	1	L4HUML	Ig lambda chain V-
889	64	74.4	108	2	S11125	Ig kappa chain V r
890	64	74.4	111	1	L1HUVO	Ig lambda chain V-
891	64	74.4	112	1	L6HUAR	Ig lambda chain V-
892	64	74.4	113	1	KVMS26	Ig kappa chain V r
893	64	74.4	113	2	S03410	Ig kappa chain pre
894	64	74.4	121	2	B56700	Ig kappa chain (an
895	64	74.4	132	2	A24402	T-cell receptor al
896	64	74.4	132	2	PH0106	anti-digoxin trans
897	64	74.4	140	2	PH0132	Ig lambda chain pr
898	64	74.4	215	2	JE0243	Ig kappa chain NIG
899	63	73.3	83	2	S34095	Ig kappa chain V r
900	63	73.3	86	2	C28195	Ig kappa chain V r
901	63	73.3	87	2	S34094	Ig kappa chain V r
902	63	73.3	90	2	S24218	Ig kappa chain - m
903	63	73.3	93	2	S17642	Ig kappa chain V r
904	63	73.3	93	2	S17641	Ig kappa chain V r
905	63	73.3	96	2	PH1070	Ig light chain V r
906	63	73.3	111	1	L1HUNW	Ig lambda chain V-
907	63	73.3	111	2	S19664	Ig lambda chain V
908	63	73.3	111	2	PS0074	Ig kappa chain V r
909	63	73.3	111	2	S09966	Ig kappa chain V-J
910	63	73.3	112	2	S37203	Ig kappa chain V r
911	63	73.3	113	2	E30560	Ig kappa chain V r
912	63	73.3	113	2	H30560	Ig kappa chain V r
913	63	73.3	114	2	S49572	Ig kappa chain pre
914	63	73.3	114	2	D46516	Ig lambda chain V
915	63	73.3	114	2	B49002	Ig kappa chain V r
916	63	73.3	120	2	S42270	Ig kappa chain V r
917	63	73.3	120	2	S42268	Ig kappa chain V r
918	63	73.3	120	2	S42267	Ig kappa chain V r
919	63	73.3	122	2	S40338	Ig kappa chain - h
920	63	73.3	124	2	S03876	Ig kappa chain V-I
921	63	73.3	126	2	S40312	Ig kappa chain - h
922	63	73.3	128	2	S40373	Ig kappa chain - h
923	63	73.3	131	2	S40355	Ig kappa chain - h
924	63	73.3	132	2	B25912	Ig kappa chain pre
925	63	73.3	133	1	A24452	Ig kappa chain pre
926	63	73.3	133	1	K2HURP	Ig kappa chain pre
927	63	73.3	133	2	S23230	Ig kappa chain pre
928	63	73.3	133	2	S42611	HUNVK protein prec
929	63	73.3	140	2	S22658	Ig kappa chain pre
930	63	73.3	142	2	S22902	Ig kappa chain V r
931	63	73.3	151	2	S25739	Ig lambda chain -
932	63	73.3	231	2	S25738	Ig lambda chain -
933	62.5	72.7	216	2	JE0241	Ig kappa chain Am3
934	62	72.1	89	2	A22775	Ig kappa chain pre
935	62	72.1	93	2	S17640	Ig kappa chain V r
936	62	72.1	103	2	S26332	Ig light chain V r
937	62	72.1	106	1	L4HUKN	Ig lambda chain V-
938	62	72.1	106	2	S38495	Ig lambda chain -
939	62	72.1	111	1	L6HULT	Ig lambda chain V-
940	62	72.1	111	1	L6HUST	Ig lambda chain V-
941	62	72.1	130	2	B32456	Ig kappa chain pre
942	62	72.1	190	2	S25740	Ig lambda chain -
943	61	70.9	74	2	G30538	Ig kappa chain V r
944	61	70.9	92	2	A28762	Ig kappa chain V r
945	61	70.9	97	2	PH1085	Ig light chain V r
946	61	70.9	100	2	PH1075	Ig light chain V r
947	61	70.9	101	2	PH1057	Ig light chain V r
948	61	70.9	103	2	PH1056	Ig light chain V r
949	61	70.9	103	2	PH1055	Ig light chain V r
950	61	70.9	107	2	PL0270	Ig kappa chain V r
951	61	70.9	107	2	PL0272	Ig kappa chain V r
952	61	70.9	107	2	PL0271	Ig kappa chain V r
953	61	70.9	107	2	S11122	Ig kappa chain V r
954	61	70.9	107	2	PL0269	Ig kappa chain V r
955	61	70.9	111	1	L2HUVL	Ig lambda chain V-
956	61	70.9	112	1	L6HU48	Ig lambda chain V-
957	61	70.9	112	2	PL0275	Ig kappa chain V r
958	61	70.9	112	2	C26317	Ig kappa chain V r
959	61	70.9	112	2	E26317	Ig kappa chain V r
960	61	70.9	112	2	S38716	Ig light chain V r
961	61	70.9	112	2	A26317	Ig kappa chain V r
962	61	70.9	112	2	PL0274	Ig kappa chain V r
963	61	70.9	112	2	F26317	Ig kappa chain V r
964	61	70.9	112	2	G26317	Ig kappa chain V r
965	61	70.9	112	2	I26317	Ig kappa chain V r
966	61	70.9	112	2	B26317	Ig kappa chain V r
967	61	70.9	119	2	S40137	T-cell receptor V-
968	61	70.9	120	1	KVMS67	Ig kappa chain pre
969	61	70.9	120	2	A29775	Ig kappa chain pre
970	61	70.9	120	2	D29775	Ig kappa chain pre
971	61	70.9	197	2	S29593	Ig kappa chain (WM
972	61	70.9	226	2	S25745	Ig lambda chain -
973	61	70.9	231	2	S25751	Ig lambda chain -
974	61	70.9	238	2	A49633	Ig lambda-like cha
975	61	70.9	249	2	S41374	single chain Fv an
976	60	69.8	46	2	A30609	Ig kappa chain V-I
977	60	69.8	93	2	S17623	Ig kappa chain V r
978	60	69.8	112	2	H28840	Ig kappa chain V r

979	60	69.8	113	1	KVMS7S	Ig kappa chain V r
980	60	69.8	115	1	K2HUCM	Ig kappa chain V-I
981	60	69.8	117	1	K2HUGM	Ig kappa chain pre
982	60	69.8	121	2	S67944	Ig kappa chain BrE
983	60	69.8	128	1	K3HU41	Ig kappa chain pre
984	60	69.8	130	2	S04573	Ig kappa chain pre
985	60	69.8	134	2	S40376	Ig kappa chain - h
986	60	69.8	140	2	PL0013	Ig kappa chain pre
987	60	69.8	145	2	S25743	Ig lambda chain -
988	59.5	69.2	103	2	A38923	AL type amyloid fi
989	59	68.6	81	2	A49039	T-cell receptor be
990	59	68.6	93	2	S38564	Ig kappa chain V r
991	59	68.6	93	2	S17643	Ig kappa chain V r
992	59	68.6	101	2	C34153	Ig kappa chain V-I
993	59	68.6	101	2	S07706	T-cell receptor al
994	59	68.6	103	2	S13698	Ig heavy chain V r
995	59	68.6	104	2	S36064	Ig lambda chain -
996	59	68.6	106	2	PL0082	Ig kappa chain V r
997	59	68.6	107	2	S69901	Ig kappa chain (cl
998	59	68.6	107	2	B48677	Ig kappa chain V-J
999	59	68.6	107	2	C48677	Ig light chain V-J
1000	59	68.6	107	2	A28044	Ig kappa chain V r

ALIGNMENTS

RESULT 1
PH0881
Ig kappa chain V region (GOU) - human (fragment)
N;Alternate names: myeloma protein
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-May-1997
C;Accession: PH0881
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0881
A;Molecule type: protein
A;Residues: 1-53 <MAN>
A;Cross-references: UNIPARC:UPI0000176D8A
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-53/Region: complementarity-determining 2

Query Match 100.0%; Score 86; DB 2; Length 53;
Best Local Similarity 100.0%; Pred. No. 3.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 WYQQKPGKAPKLLIY 15
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Db         35 WYQQKPGKAPKLLIY 49
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RESULT 2
S42265
Ig kappa chain V region (018) - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 17-Mar-1999
C;Accession: S42265
R;Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que
J. Immunol. 147, 4007-4013, 1991
A;Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus inf
A;Reference number: S42263; MUID:92043792; PMID:1940382
A;Accession: S42265
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-62 <SCO>
A;Cross-references: UNIPARC:UPI0000176D84; EMBL:M64856
C;Genetics:
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 86; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 4.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49
```

RESULT 3
PH0880
Ig kappa chain V region (SCH) - human (fragment)
N;Alternate names: myeloma protein
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-May-1997
C;Accession: PH0880
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype.
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0880
A;Molecule type: protein
A;Residues: 1-65 <MAN>
A;Cross-references: UNIPARC:UPI0000176D82
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-65/Region: framework 3

Query Match 100.0%; Score 86; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 4.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49
```

RESULT 4
S34090
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34090
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34090
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-82 <WAG>
A;Cross-references: UNIPROT:Q9UL79; UNIPARC:UPI0000176DA2; EMBL:X67174
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         26 WYQQKPGKAPKLLIY 40
```

RESULT 5
S34086
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S34086
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34086
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86 <WAG>
A;Cross-references: UNIPROT:Q96SA9; UNIPARC:UPI0000176D9E; EMBL:X67169
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

 Query Match 100.0%; Score 86; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 6.4e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 28 WYQQKPGKAPKLLIY 42

RESULT 6
S16840
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S16840
R;Blaison, G.; Kuntz, J.L.; Pasquali, J.L.
Eur. J. Immunol. 21, 1221-1227, 1991
A;Title: Molecular analysis of V(kappa)III variable regions of polyclonal rheumatoid fac
A;Reference number: S16823; MUID:91243737; PMID:1903706
A;Accession: S16840
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-86 <BLA>
A;Cross-references: UNIPROT:Q96SA9; UNIPARC:UPI0000176DA5; EMBL:X54838
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-81/Domain: immunoglobulin homology <IMM>

 Query Match 100.0%; Score 86; DB 2; Length 86;
 Best Local Similarity 100.0%; Pred. No. 6.4e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 26 WYQQKPGKAPKLLIY 40

RESULT 7
S34084
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34084
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34084
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-87 <WAG>
A;Cross-references: UNIPARC:UPI00001198BC; EMBL:X67167
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

 Query Match 100.0%; Score 86; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 6.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 28 WYQQKPGKAPKLLIY 42

RESULT 8
S21523
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jan-2000
C;Accession: S34079; S21523
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34079
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-87 <WA2>
A;Cross-references: UNIPARC:UPI000011604C; EMBL:X66039; NID:g33312; PIDN:CAA46838.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

 Query Match 100.0%; Score 86; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 6.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 28 WYQQKPGKAPKLLIY 42

RESULT 9
I52592
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I52592
R;Wagner, S.D.; Martinelli, V.; Luzzatto, L.
Blood 83, 3647-3653, 1994
A;Title: Similar patterns of V kappa gene usage but different degrees of somatic mutation
A;Reference number: I52592; MUID:94264318; PMID:8204889
A;Accession: I52592
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-87 <RES>
A;Cross-references: UNIPARC:UPI0000113F67; GB:S71057; NID:g547053; PIDN:AAB30971.1; PID:g
C;Genetics:
A;Gene: IgKV
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;9-83/Domain: immunoglobulin homology <IMM>

 Query Match 100.0%; Score 86; DB 2; Length 87;
 Best Local Similarity 100.0%; Pred. No. 6.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 28 WYQQKPGKAPKLLIY 42

RESULT 10
S34083
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)

```
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S34083
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34083
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-87 <WAG>
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77; UNIPARC:UPI0000176D9F; EMBL:X66045
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             100.0%;  Score 86;  DB 2;  Length 87;
  Best Local Similarity   100.0%;  Pred. No. 6.5e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         28 WYQQKPGKAPKLLIY 42


RESULT 11
S34087
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34087
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34087
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WAG>
A;Cross-references: UNIPARC:UPI0000176D9B; EMBL:X67171
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         28 WYQQKPGKAPKLLIY 42


RESULT 12
S21522
Ig kappa chain V region (patient 10 and 12) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jan-2000
C;Accession: S34078; S34085; S21522
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34078
A;Molecule type: DNA
A;Residues: 1-88 <WA2>
A;Cross-references: UNIPARC:UPI0000116052; EMBL:X66046; NID:g33308; PIDN:CAA46845.1; PID
A;Experimental source: patient 10
A;Accession: S34085
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-88 <WAG>
A;Cross-references: UNIPARC:UPI0000116052; EMBL:X67168
A;Experimental source: patient 12
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         28 WYQQKPGKAPKLLIY 42


RESULT 13
S21528
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S21528
R;Wagner, S.D.; Luzzatto, L.
submitted to the EMBL Data Library, May 1992
A;Description: Vk genes rearranged in chronic lymphocytic leukaemia do not show somatic m
A;Reference number: S21520
A;Accession: S21528
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WAG>
A;Cross-references: UNIPARC:UPI0000116051; EMBL:X66045; NID:g33322; PIDN:CAA46844.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

  Query Match             100.0%;  Score 86;  DB 2;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         28 WYQQKPGKAPKLLIY 42


RESULT 14
S21520
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jan-2000
C;Accession: S34077; S21520
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34077
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WA2>
A;Cross-references: UNIPARC:UPI000011604A; EMBL:X66037; NID:g33306; PIDN:CAA46836.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         28 WYQQKPGKAPKLLIY 42


RESULT 15
S34104
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
```

```
C;Accession: S34104
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34104
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WAG>
A;Cross-references: UNIPARC:UPI000011604B; EMBL:X66038; NID:g33310; PIDN:CAA46837.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         28 WYQQKPGKAPKLLIY 42


RESULT 16
S34088
Ig kappa chain V region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S34088
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34088
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WAG>
A;Cross-references: UNIPARC:UPI0000176D9A; EMBL:X67172
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         28 WYQQKPGKAPKLLIY 42


RESULT 17
S21524
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 25-Oct-1996 #text_change 21-Jan-2000
C;Accession: S34080; S21524
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34080
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <WA2>
A;Cross-references: UNIPARC:UPI000011604D; EMBL:X66040; NID:g33314; PIDN:CAA46839.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;9-83/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         28 WYQQKPGKAPKLLIY 42


RESULT 18
PH0864
Ig kappa chain V region (anti-DNA, IC4) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH0864
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0864
A;Molecule type: DNA
A;Residues: 1-95 <MAN>
A;Cross-references: UNIPARC:UPI0000176D9D
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3

  Query Match             100.0%;  Score 86;  DB 2;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 19
PH0862
Ig kappa chain V region (anti-DNA, III-3R) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jan-2000
C;Accession: PH0862
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotype
A;Reference number: PH0862; MUID:92078875; PMID:1660528
A;Accession: PH0862
A;Molecule type: DNA
A;Residues: 1-95 <MAN>
A;Cross-references: UNIPARC:UPI0000176D9C
C;Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bears
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-23/Region: framework 1
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity-determining 1
F;35-49/Region: framework 2
F;50-56/Region: complementarity-determining 2
F;57-88/Region: framework 3
F;89-95/Region: complementarity-determining 3

  Query Match             100.0%;  Score 86;  DB 2;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49
```

RESULT 20
S41813
Ig kappa chain V region L12 - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S41813
R;Huber, C.; Schaeble, K.F.; Huber, E.; Klein, R.; Meindl, A.; Thiebe, R.; Lamm, R.; Zac
Eur. J. Immunol. 23, 2868-2875, 1993
A;Title: The V(kappa) genes of the L regions and the repertoire of V(kappa) gene sequenc
A;Reference number: S41809; MUID:94039386; PMID:8223863
A;Accession: S41813
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-98 <HUB>
A;Cross-references: UNIPARC:UPI000011618D; EMBL:X72813; NID:g415363; PIDN:CAA51332.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-93/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 7.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 38 WYQQKPGKAPKLLIY 52

RESULT 21
PC2397
anti-tetanus toxin 9F12 Fab light-chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000
C;Accession: PC2397
R;Esposito, G.; Scarselli, E.; Traboni, C.
Gene 148, 167-168, 1994
A;Title: Phage display of a human antibody against Clostridium tetani toxin.
A;Reference number: PC2397; MUID:95011651; PMID:7926831
A;Accession: PC2397
A;Molecule type: mRNA
A;Residues: 1-106 <ESP>
A;Cross-references: UNIPARC:UPI0000176D47; EMBL:X75387
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
F;24-34/Region: complementarity determining region 1
F;50-56/Region: complementarity determining region 2

Query Match 100.0%; Score 86; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 35 WYQQKPGKAPKLLIY 49

RESULT 22
S36264
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36264
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36264
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
A;Cross-references: UNIPARC:UPI0000118DF4; EMBL:Z18845; NID:g33426; PIDN:CAA79297.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 35 WYQQKPGKAPKLLIY 49

RESULT 23
S36262
Ig lambda chain V region (clone alpha-TNF-E7) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36262
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36262
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
A;Cross-references: UNIPARC:UPI0000176D2C; EMBL:Z18842
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 35 WYQQKPGKAPKLLIY 49

RESULT 24
S36269
Ig lambda chain V region (clone alpha-TNF-A1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36269
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.;
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36269
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-107 <GRI>
A;Cross-references: UNIPARC:UPI0000118DF1; EMBL:Z18838; NID:g33422; PIDN:CAA79290.1; PID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 35 WYQQKPGKAPKLLIY 49

RESULT 25
K1HUAU
Ig kappa chain V-I region (Au) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004

C;Accession: A91653; A01862; S02573
R;Schiechl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 353, 345-370, 1972
A;Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ, Sub
A;Reference number: A91653; MUID:72189444; PMID:5028201
A;Accession: A91653
A;Molecule type: protein
A;Residues: 1-108 <SCH>
A;Cross-references: UNIPROT:P01594; UNIPARC:UPI000012E13E
A;Note: the C region of this chain has the Inv (3) marker
R;Fehlhammer, H.; Schiffer, M.; Epp, O.; Colman, P.M.; Lattman, E.E.; Schwager, P.; Stei
Biophys. Struct. Mech. 1, 139-146, 1975
A;Title: The structure determination of the variable portion of the Bence-Jones protein
A;Reference number: A90729; MUID:77022433; PMID:1234024
A;Contents: annotation; X-ray crystallography
A;Note: the structure of the V region was determined by molecular replacement methods us
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 100.0%; Score 86; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 35 WYQQKPGKAPKLLIY 49

RESULT 26
K1HUKA
Ig kappa chain V-I region (Ka) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C;Accession: A01869
R;Shinoda, T.
J. Biochem. 77, 1277-1296, 1975
A;Title: Comparative structural studies on the light chains of human immunoglobulins. I.
A;Reference number: A01869; MUID:76189985; PMID:818073
A;Accession: A01869
A;Molecule type: protein
A;Residues: 1-108 <SHI>
A;Cross-references: UNIPROT:P01603; UNIPARC:UPI000012E146
A;Note: the C region of this chain has the Inv (3) marker
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 100.0%; Score 86; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 35 WYQQKPGKAPKLLIY 49

RESULT 27
K1HURY
Ig kappa chain V-I region (Roy) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Jul-1998 #text_change 09-Jul-2004
C;Accession: A91638; B94417; A01874; S02575
R;Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 348, 1077-1080, 1967
A;Title: Die chemische Struktur von zwei Bence-Jones-Proteinen (Roy und Cum.) vom kappa-T
A;Reference number: A91638; MUID:68362076; PMID:5595110
A;Accession: A91638
A;Molecule type: protein
A;Residues: 1-38,'GPK',42-108 <HIL>
A;Cross-references: UNIPROT:P01608; UNIPARC:UPI0000173704
A;Note: the sequence of the C region, which has the Inv (1,2) marker, is also given
R;Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne, M
in Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-74, A
A;Reference number: A94417
A;Contents: revisions to residues 39 and 41
A;Accession: B94417
A;Molecule type: protein
A;Residues: 39;41 <HI2>
A;Cross-references: UNIPARC:UPI000011ECBE; UNIPARC:UPI000011ED5D
R;Steiner, V.; Chang, J.Y.
FEBS Lett. 222, 6-10, 1987
A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the
A;Reference number: S02572; MUID:88005152; PMID:3115831
A;Contents: annotation
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kapp
hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
F;23-88/Disulfide bonds: #status predicted

Query Match 100.0%; Score 86; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 8.1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 35 WYQQKPGKAPKLLIY 49

RESULT 28
S19674
Ig kappa chain V region (clone alpha-TEL9) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19674
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter,
J. Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on pha
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19674
A;Molecule type: mRNA
A;Residues: 1-108 <MAR>
A;Cross-references: UNIPARC:UPI0000115FE1; EMBL:X61642; NID:g37860; PIDN:CAA43823.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 86; DB 2; Length 108;

```
  Best Local Similarity   100.0%;  Pred. No. 8.1e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 29
S36277
Ig lambda chain V region (clone alpha-FOG1-G8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36277
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36277
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-108 <GRI>
A;Cross-references: UNIPARC:UPI0000118DEE; EMBL:Z18829; NID:g33417; PIDN:CAA79281.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 30
S36279
Ig lambda chain V region (clone alpha-THY-23) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36279
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36279
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-108 <GRI>
A;Cross-references: UNIPARC:UPI0000118DEF; EMBL:Z18831; NID:g33418; PIDN:CAA79283.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 31
S47182
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S47182
R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A;Description: Cloning and analysis of IgM anti-thyroglobulin autoantibodies from patien
A;Reference number: S47181
A;Accession: S47182
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <MCI>
A;Cross-references: UNIPARC:UPI00001161E5; EMBL:X79786; NID:g506422; PIDN:CAA56182.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 32
B49047
Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragme
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B49047
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes c
A;Reference number: A49047; MUID:92387224; PMID:1516616
A;Accession: B49047
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-108 <VIC>
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77; UNIPARC:UPI0000176B44
A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 33
S44118
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44118
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable re
A;Reference number: S44105
A;Accession: S44118
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 <HAW>
A;Cross-references: UNIPARC:UPI0000116635; EMBL:Z31395; NID:g472972; PIDN:CAA83270.1; PID
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 110;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
```

```
Db         35 WYQQKPGKAPKLLIY 49


RESULT 34
A27594
Ig kappa chain precursor V-I region (Nalm-6) - human
C;Species: Homo sapiens (man)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 21-Jan-2000
C;Accession: A27594
R;Graninger, W.B.; Goldman, P.L.; Morton, C.C.; O'Brien, S.J.; Korsmeyer, S.J.
J. Exp. Med. 167, 488-501, 1988
A;Title: The kappa-deleting element. Germline and rearranged, duplicated and dispersed f
A;Reference number: A92779; MUID:88154739; PMID:3126251
A;Accession: A27594
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-116 <GRA>
A;Cross-references: UNIPARC:UPI00001769D9
A;Note: this sequence was translated from an aberrantly rearranged kappa gene from lambd
C;Genetics:
A;Map position: 2
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;38-112/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 116;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         57 WYQQKPGKAPKLLIY 71


RESULT 35
K1HU12
Ig kappa chain precursor V-I region (HK102) - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 09-Jul-2004
C;Accession: A01882
R;Bentley, D.L.; Rabbitts, T.H.
Nature 288, 730-733, 1980
A;Title: Human immunoglobulin variable region genes - DNA sequences of two V-kappa genes
A;Reference number: A93241; MUID:81098966; PMID:6779204
A;Accession: A01882
A;Molecule type: DNA
A;Residues: 1-117 <BEN>
A;Cross-references: UNIPROT:P01602; UNIPARC:UPI000012E145; GB:J00245; NID:g185981; PIDN:
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
A;Introns: 19/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-117/Product: Ig kappa chain V-I region (HK102) #status predicted <MAT>
F;38-112/Domain: immunoglobulin homology <IMM>
F;45-110/Disulfide bonds: #status predicted

  Query Match             100.0%;  Score 86;  DB 1;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         57 WYQQKPGKAPKLLIY 71


RESULT 36
S24206
Ig kappa chain V region (Vx O12 and Vx O2) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: S24206; S24209
R;Pargent, W.; Meindl, A.; Thiebe, R.; Mitzel, S.; Zachau, H.G.
Eur. J. Immunol. 21, 1821-1827, 1991
A;Title: The human immunoglobulin kappa locus. Characterization of the duplicated O regic
A;Reference number: S24205; MUID:91330953; PMID:1907917
A;Accession: S24206
A;Molecule type: DNA
A;Residues: 1-117 <PAR>
A;Cross-references: UNIPARC:UPI0000115F90; EMBL:X59315; NID:g33247; PIDN:CAA42002.1; PID
A;Experimental source: placenta
A;Genetics: G1
A;Accession: S24209
A;Molecule type: DNA
A;Residues: 1-117 <PAW>
A;Cross-references: UNIPARC:UPI0000115F90; EMBL:X59312; NID:g33252; PIDN:CAA41999.1; PID
A;Experimental source: placenta
A;Genetics: G2
C;Genetics: <G1>
A;Gene: Vx O12
A;Map position: 2
A;Introns: 19/1
C;Genetics: <G2>
A;Gene: Vx O2
A;Map position: 2
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         57 WYQQKPGKAPKLLIY 71


RESULT 37
S42264
Ig kappa chain V region (L11) - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42264
R;Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Quer
J. Immunol. 147, 4007-4013, 1991
A;Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus infl
A;Reference number: S42263; MUID:92043792; PMID:1940382
A;Accession: S42264
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <SCO>
A;Cross-references: UNIPARC:UPI0000113B4D; EMBL:M64858; NID:g185952; PIDN:AAA58924.1; PII
C;Genetics:
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         57 WYQQKPGKAPKLLIY 71
```

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RESULT 38
S11700
Ig kappa chain precursor V-I region - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S11700
R;Pech, M.; Smola, H.; Pohlenz, H.D.; Straubinger, B.; Gerl, R.; Zachau, H.G.
J. Mol. Biol. 183, 291-299, 1985
A;Title: A large section of the gene locus encoding human immunoglobulin variable region
A;Reference number: S11697; MUID:85264787; PMID:3927006
A;Accession: S11700
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-117 <PEC>
A;Cross-references: UNIPARC:UPI0000115E40; EMBL:X17262; NID:g37873; PIDN:CAA35166.1; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1989
C;Genetics:
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         57 WYQQKPGKAPKLLIY 71


RESULT 39
S21527
Ig kappa chain precursor V-I region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: S11699; S34076; S34105; S21521; S21527
R;Pech, M.; Smola, H.; Pohlenz, H.D.; Straubinger, B.; Gerl, R.; Zachau, H.G.
J. Mol. Biol. 183, 291-299, 1985
A;Title: A large section of the gene locus encoding human immunoglobulin variable region
A;Reference number: S11697; MUID:85264787; PMID:3927006
A;Accession: S11699
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-117 <PEC>
A;Cross-references: UNIPARC:UPI000011148EB; EMBL:X17263; NID:g37889; PIDN:CAA35167.1; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1989
R;Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A;Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute
A;Reference number: S34076; MUID:93170387; PMID:8436174
A;Accession: S34076
A;Molecule type: DNA
A;Residues: 30-117 <WA2>
A;Cross-references: UNIPARC:UPI0000116050; EMBL:X66044; NID:g33320; PIDN:CAA46843.1; PID
A;Experimental source: patient 7
A;Accession: S34105
A;Molecule type: DNA
A;Residues: 30-117 <WAG>
A;Cross-references: UNIPARC:UPI0000116050; EMBL:X66044; NID:g33320; PIDN:CAA46843.1; PID
A;Experimental source: patient 8
C;Genetics:
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         57 WYQQKPGKAPKLLIY 71


RESULT 40
S46371
Ig kappa chain V-J region (T24-3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S46371; S38645
R;Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea
A;Reference number: S46369; MUID:94313975; PMID:8039491
A;Accession: S46371
A;Molecule type: mRNA
A;Residues: 1-117 <BEN>
A;Cross-references: UNIPARC:UPI00001165A4; EMBL:Z27172; NID:g415959; PIDN:CAA81696.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;23-97/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         42 WYQQKPGKAPKLLIY 56


RESULT 41
S46376
Ig kappa chain V-J region (T33-14) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C;Accession: S46376; S38649
R;Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea
A;Reference number: S46369; MUID:94313975; PMID:8039491
A;Accession: S46376
A;Molecule type: mRNA
A;Residues: 1-117 <BEN>
A;Cross-references: UNIPARC:UPI00001165A9; EMBL:Z27177; NID:g415969; PIDN:CAA81701.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-99/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         44 WYQQKPGKAPKLLIY 58


RESULT 42
S42263
Ig kappa chain V region (08) - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S42263
R;Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Quer
J. Immunol. 147, 4007-4013, 1991
A;Title: Clonal characterization of the human IgG antibody repertoire to Haemophilus infl
A;Reference number: S42263; MUID:92043792; PMID:1940382
A;Accession: S42263
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <SCO>
A;Cross-references: UNIPARC:UPI0000113B51; EMBL:M64855; NID:g185963; PIDN:AAA58925.1; PII
```

```
C;Genetics:
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;38-112/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         57 WYQQKPGKAPKLLIY 71


RESULT 43
S43528
Ig kappa chain V region (018) - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: S43528
R;Scott, M.G.; Crimmins, D.L.; McCourt, D.W.; Chung, G.; Schaeble, K.F.; Thiebe, R.; Que
submitted to the EMBL Data Library, December 1991
A;Reference number: S43528
A;Accession: S43528
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-117 <SCO>
A;Cross-references: UNIPARC:UPI0000113B52; EMBL:M64856
C;Genetics:
A;Introns: 19/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;38-112/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         57 WYQQKPGKAPKLLIY 71


RESULT 44
S40331
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40331
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40331
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 <KLE>
A;Cross-references: UNIPARC:UPI0000116151; EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-106/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 123;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         51 WYQQKPGKAPKLLIY 65


RESULT 45
S40336
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40336
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40336
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-124 <KLE>
A;Cross-references: UNIPARC:UPI0000116156; EMBL:X72446; NID:g441360; PIDN:CAA51114.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-105/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 124;
  Best Local Similarity   100.0%;  Pred. No. 9.3e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         50 WYQQKPGKAPKLLIY 64


RESULT 46
S40333
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40333
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40333
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: UNIPARC:UPI0000116153; EMBL:X72443; NID:g441354; PIDN:CAA51111.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-108/Domain: immunoglobulin homology <IMM>

  Query Match             100.0%;  Score 86;  DB 2;  Length 125;
  Best Local Similarity   100.0%;  Pred. No. 9.4e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         53 WYQQKPGKAPKLLIY 67


RESULT 47
S40349
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S40349
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40349
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: UNIPARC:UPI0000116163; EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PI
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>
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```
  Query Match            100.0%;  Score 86;  DB 2;  Length 125;
  Best Local Similarity   100.0%;  Pred. No. 9.4e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         52 WYQQKPGKAPKLLIY 66


RESULT 48
S46372
IG light chain variable region (VJ) - human
C;Species: Homo sapiens (man)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S46372
R;Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A;Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rea
A;Reference number: S46369; MUID:94313975; PMID:8039491
A;Accession: S46372
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-128 <BEN>
A;Cross-references: UNIPARC:UPI0000176CA4; EMBL:Z27173
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;36-110/Domain: immunoglobulin homology <IMM>

  Query Match            100.0%;  Score 86;  DB 2;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         55 WYQQKPGKAPKLLIY 69


RESULT 49
K1HUWK
Ig kappa chain precursor V-I region (Walker) - human
C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C;Accession: A01883
R;Klobeck, H.G.; Combriato, G.; Zachau, H.G.
Nucleic Acids Res. 12, 6995-7006, 1984
A;Title: Immunoglobulin genes of the kappa light chain type from two human lymphoid cell
A;Reference number: A93534; MUID:85014148; PMID:6091049
A;Accession: A01883
A;Molecule type: DNA
A;Residues: 1-129 <KLO>
A;Cross-references: UNIPROT:P04431; UNIPARC:UPI000012E151
A;Note: the sequence was determined from the differentiated gene
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-129/Product: Ig kappa chain V-I region (Walker) #status predicted <MAT>
F;23-45/Region: framework 1
F;38-112/Domain: immunoglobulin homology <IMM>
F;46-56/Region: complementarity-determining 1
F;57-71/Region: framework 2
F;72-78/Region: complementarity-determining 2
F;79-110/Region: framework 3
F;111-119/Region: complementarity-determining 3
F;120-129/Region: framework 4
F;45-110/Disulfide bonds: #status predicted

  Query Match            100.0%;  Score 86;  DB 1;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         57 WYQQKPGKAPKLLIY 71


RESULT 50
S38646
Ig kappa chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38646
R;Bensimon, C.; Chastagner, P.; Zouali, M.
submitted to the EMBL Data Library, November 1993
A;Description: Low rate of receptor-editing in human lupus anti-DNA autoantibodies.
A;Reference number: S38643
A;Accession: S38646
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-132 <BEN>
A;Cross-references: UNIPARC:UPI00001165A5; EMBL:Z27173; NID:g415961; PIDN:CAA81697.1; PII
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;40-114/Domain: immunoglobulin homology <IMM>

  Query Match            100.0%;  Score 86;  DB 2;  Length 132;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         59 WYQQKPGKAPKLLIY 73


Search completed: March 23, 2006, 02:05:03
Job time : 22.7534 secs
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 01:40:40 ; Search time 129.041 Seconds
(without alignments)
82.012 Million cell updates/sec

Title: US-10-755-382-27
Perfect score: 86
Sequence: 1 WYQQKPGKAPKLLIY 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	86	100.0	107	2	Q96SA9_HUMAN	Q96sa9 homo sapien
2	86	100.0	108	1	KV1B_HUMAN	P01594 homo sapien
3	86	100.0	108	1	KV1K_HUMAN	P01603 homo sapien
4	86	100.0	108	1	KV1P_HUMAN	P01608 homo sapien
5	86	100.0	117	1	KV1J_HUMAN	P01602 homo sapien
6	86	100.0	129	1	KV1W_HUMAN	P04431 homo sapien
7	86	100.0	236	2	Q6PIH4_HUMAN	Q6pih4 homo sapien
8	86	100.0	236	2	Q6GMX8_HUMAN	Q6gmx8 homo sapien
9	86	100.0	236	2	Q6GMW1_HUMAN	Q6gmw1 homo sapien
10	86	100.0	240	2	Q65ZC9_HUMAN	Q65zc9 homo sapien
11	83	96.5	107	1	KV1D_HUMAN	P01596 homo sapien
12	83	96.5	108	1	KV1F_HUMAN	P01598 homo sapien
13	82	95.3	108	1	KV1C_HUMAN	P01595 homo sapien
14	82	95.3	108	1	KV5Q_MOUSE	P01650 mus musculu
15	82	95.3	108	1	KV5R_MOUSE	P01651 mus musculu
16	82	95.3	108	1	KV5S_MOUSE	P01652 mus musculu
17	82	95.3	108	1	KV5T_MOUSE	P01653 mus musculu
18	82	95.3	108	2	Q9UL79_HUMAN	Q9ul79 homo sapien
19	82	95.3	109	1	KV1T_HUMAN	P01612 homo sapien
20	82	95.3	189	2	Q569I7_HUMAN	Q569i7 homo sapien
21	82	95.3	234	2	Q569I9_HUMAN	Q569i9 homo sapien
22	82	95.3	234	2	Q7Z473_HUMAN	Q7z473 homo sapien
23	82	95.3	244	2	Q65ZC8_HUMAN	Q65zc8 homo sapien
24	82	95.3	266	2	Q566X2_BRARE	Q566x2 brachydanio
25	81	94.2	107	2	Q9UL81_HUMAN	Q9ul81 homo sapien
26	81	94.2	108	2	Q9UL77_HUMAN	Q9ul77 homo sapien
27	81	94.2	236	2	Q6PIT5_HUMAN	Q6pit5 homo sapien
28	81	94.2	236	2	Q6PIH7_HUMAN	Q6pih7 homo sapien
29	80	93.0	108	1	KV1O_HUMAN	P01607 homo sapien
30	80	93.0	112	1	LV2K_HUMAN	P04209 homo sapien
31	80	93.0	129	1	KV1X_HUMAN	P04432 homo sapien
32	79	91.9	97	2	Q5NV70_HUMAN	Q5nv70 homo sapien
33	79	91.9	99	2	Q5NV67_HUMAN	Q5nv67 homo sapien
34	79	91.9	99	2	Q9JL74_MOUSE	Q9jl74 mus musculu
35	79	91.9	100	1	KV3C_HUMAN	P01621 homo sapien
36	79	91.9	108	1	KV1E_HUMAN	P01597 homo sapien
37	79	91.9	108	1	KV1G_HUMAN	P01599 homo sapien
38	79	91.9	108	1	KV1H_HUMAN	P01600 homo sapien
39	79	91.9	108	1	KV1M_HUMAN	P01605 homo sapien
40	79	91.9	108	2	Q9UL83_HUMAN	Q9ul83 homo sapien
41	79	91.9	109	1	KV3B_HUMAN	P01620 homo sapien
42	79	91.9	109	1	KV3D_HUMAN	P01622 homo sapien
43	79	91.9	109	1	KV3E_HUMAN	P01623 homo sapien
44	79	91.9	109	2	Q9UL85_HUMAN	Q9ul85 homo sapien
45	79	91.9	109	2	Q9UL86_HUMAN	Q9ul86 homo sapien
46	79	91.9	109	2	Q9UL78_HUMAN	Q9ul78 homo sapien
47	79	91.9	111	1	LV2B_HUMAN	P01705 homo sapien
48	79	91.9	115	1	KV3I_HUMAN	P04433 homo sapien
49	79	91.9	116	1	KV3J_HUMAN	P04434 homo sapien
50	79	91.9	129	1	KV3L_HUMAN	P18135 homo sapien
51	79	91.9	129	1	KV3M_HUMAN	P18136 homo sapien
52	79	91.9	130	2	Q9NP29_HUMAN	Q9np29 homo sapien
53	79	91.9	149	1	KV5A_MOUSE	P01633 mus musculu
54	79	91.9	234	2	Q4KM66_RAT	Q4km66 rattus norv
55	79	91.9	236	2	Q6P5S3_HUMAN	Q6p5s3 homo sapien
56	79	91.9	236	2	Q6PIL8_HUMAN	Q6pil8 homo sapien
57	79	91.9	240	2	Q52L64_MOUSE	Q52l64 mus musculu
58	79	91.9	255	2	Q6KB05_MOUSE	Q6kb05 mus musculu
59	78	90.7	99	2	Q5NV63_HUMAN	Q5nv63 homo sapien
60	78	90.7	99	2	Q5NV84_HUMAN	Q5nv84 homo sapien
61	78	90.7	99	2	Q5NV89_HUMAN	Q5nv89 homo sapien
62	78	90.7	108	1	KV1L_HUMAN	P01604 homo sapien
63	78	90.7	108	1	KV1Q_HUMAN	P01609 homo sapien
64	78	90.7	108	1	KV1S_HUMAN	P01611 homo sapien
65	78	90.7	109	1	LV2E_HUMAN	P01708 homo sapien
66	78	90.7	110	1	LV2J_HUMAN	P01713 homo sapien
67	78	90.7	111	1	LV2C_HUMAN	P01706 homo sapien
68	78	90.7	112	1	KV1U_HUMAN	P01613 homo sapien
69	78	90.7	233	2	Q6PJA3_HUMAN	Q6pja3 homo sapien
70	78	90.7	235	2	Q6PIK1_HUMAN	Q6pik1 homo sapien
71	77	89.5	103	2	Q9JL80_MOUSE	Q9jl80 mus musculu
72	77	89.5	108	1	KV07_RABIT	P01688 oryctolagus
73	77	89.5	108	1	KV1N_HUMAN	P01606 homo sapien
74	77	89.5	108	1	KV5P_MOUSE	P01649 mus musculu
75	77	89.5	110	1	KV13_RABIT	P01694 oryctolagus
76	77	89.5	110	1	KV3P_MOUSE	P01668 mus musculu
77	77	89.5	111	1	KV12_RABIT	P01693 oryctolagus
78	77	89.5	111	1	KV3H_MOUSE	P01660 mus musculu
79	77	89.5	111	1	KV3J_MOUSE	P01662 mus musculu
80	77	89.5	111	1	KV3K_MOUSE	P01663 mus musculu
81	77	89.5	111	1	KV3M_MOUSE	P01665 mus musculu
82	77	89.5	111	1	KV3N_MOUSE	P01666 mus musculu
83	77	89.5	111	1	KV3O_MOUSE	P01667 mus musculu
84	77	89.5	111	1	KV3R_MOUSE	P01670 mus musculu
85	77	89.5	111	1	KV3S_MOUSE	P01671 mus musculu
86	77	89.5	111	1	KV3T_MOUSE	P01672 mus musculu
87	77	89.5	111	1	KV3U_MOUSE	P01673 mus musculu
88	77	89.5	111	2	Q811U6_MOUSE	Q811u6 mus musculu
89	77	89.5	111	2	Q920E9_MOUSE	Q920e9 mus musculu
90	77	89.5	114	1	KV4A_HUMAN	P01625 homo sapien
91	77	89.5	117	1	KV10_RABIT	P01691 oryctolagus
92	77	89.5	121	1	KV40_HUMAN	P06312 homo sapien
93	77	89.5	131	1	KV3I_MOUSE	P01661 mus musculu
94	77	89.5	133	1	KV4B_HUMAN	P06313 homo sapien
95	77	89.5	134	1	KV4C_HUMAN	P06314 homo sapien
96	76	88.4	108	1	KV1V_HUMAN	P04430 homo sapien
97	76	88.4	108	1	KV3A_HUMAN	P01619 homo sapien
98	76	88.4	108	2	Q9UL70_HUMAN	Q9ul70 homo sapien
99	76	88.4	109	1	KV3G_HUMAN	P04206 homo sapien
100	76	88.4	235	2	Q6GMV9_HUMAN	Q6gmv9 homo sapien
101	76	88.4	235	2	Q6GMW0_HUMAN	Q6gmw0 homo sapien
102	76	88.4	236	2	Q6P5S8_HUMAN	Q6p5s8 homo sapien
103	76	88.4	236	2	Q7Z3Y4_HUMAN	Q7z3y4 homo sapien
104	76	88.4	236	2	Q502W4_HUMAN	Q502w4 homo sapien

105	75	87.2	50	2	Q6LBV5_HUMAN	Q6lbv5 homo sapien
106	75	87.2	95	2	Q5NV75_HUMAN	Q5nv75 homo sapien
107	75	87.2	101	2	Q9JL78_MOUSE	Q9jl78 mus musculu
108	75	87.2	108	1	KV05_RABIT	P01686 oryctolagus
109	75	87.2	108	1	KV06_RABIT	P01687 oryctolagus
110	75	87.2	108	1	KV6K_MOUSE	P04945 mus musculu
111	75	87.2	122	2	Q4T5Y4_TETNG	Q4t5y4 tetraodon n
112	74	86.0	108	1	KV1R_HUMAN	P01610 homo sapien
113	74	86.0	108	2	Q8VIJ0_MOUSE	Q8vij0 mus musculu
114	74	86.0	109	1	KV03_RABIT	P01684 oryctolagus
115	74	86.0	111	1	KV3L_MOUSE	P01664 mus musculu
116	74	86.0	111	1	LV2D_HUMAN	P01707 homo sapien
117	74	86.0	111	1	LV2I_HUMAN	P01712 homo sapien
118	74	86.0	111	1	LV2L_HUMAN	P80422 homo sapien
119	74	86.0	115	1	KV5F_MOUSE	P01638 mus musculu
120	74	86.0	116	2	Q96PF6_HUMAN	Q96pf6 homo sapien
121	74	86.0	129	1	KV3H_HUMAN	P04207 homo sapien
122	74	86.0	134	2	Q5M8V1_XENTR	Q5m8v1 xenopus tro
123	74	86.0	234	2	Q5EFE6_HUMAN	Q5efe6 homo sapien
124	74	86.0	236	2	Q6GMX0_HUMAN	Q6gmx0 homo sapien
125	74	86.0	236	2	Q6PIQ7_HUMAN	Q6piq7 homo sapien
126	74	86.0	236	2	Q6IPQ0_HUMAN	Q6ipq0 homo sapien
127	74	86.0	236	2	Q7TS98_MOUSE	Q7ts98 mus musculu
128	74	86.0	243	2	Q6NTU5_XENLA	Q6ntu5 xenopus lae
129	73	84.9	99	2	Q5NV81_HUMAN	Q5nv81 homo sapien
130	73	84.9	100	2	Q5NV69_HUMAN	Q5nv69 homo sapien
131	73	84.9	108	1	KV08_RABIT	P01689 oryctolagus
132	73	84.9	108	2	Q96SB0_HUMAN	Q96sb0 homo sapien
133	73	84.9	109	1	KV14_RABIT	P01695 oryctolagus
134	73	84.9	110	1	KV15_RABIT	P01696 oryctolagus
135	73	84.9	111	1	KV3A_MOUSE	P01654 mus musculu
136	73	84.9	111	1	KV3C_MOUSE	P01656 mus musculu
137	73	84.9	111	1	KV3D_MOUSE	P03977 mus musculu
138	73	84.9	111	1	KV3E_MOUSE	P01657 mus musculu
139	73	84.9	111	1	LV1D_HUMAN	P01702 homo sapien
140	73	84.9	112	1	KV3B_MOUSE	P01655 mus musculu
141	73	84.9	112	1	KV3G_MOUSE	P01659 mus musculu
142	73	84.9	112	1	LV1B_HUMAN	P01700 homo sapien
143	73	84.9	112	1	LV1H_HUMAN	P06887 homo sapien
144	73	84.9	116	2	Q4T5Y6_TETNG	Q4t5y6 tetraodon n
145	73	84.9	130	1	LV1G_HUMAN	P06316 homo sapien
146	73	84.9	132	1	KV3F_MOUSE	P01658 mus musculu
147	73	84.9	218	2	Q925S1_MOUSE	Q925s1 mus musculu
148	73	84.9	236	2	Q8NEJ1_HUMAN	Q8nej1 homo sapien
149	72	83.7	81	2	Q7Z2E8_HUMAN	Q7z2e8 homo sapien
150	72	83.7	97	2	Q5NV73_HUMAN	Q5nv73 homo sapien
151	72	83.7	97	2	Q5NV90_HUMAN	Q5nv90 homo sapien
152	72	83.7	99	2	Q5NV65_HUMAN	Q5nv65 homo sapien
153	72	83.7	107	2	Q9NSD6_HUMAN	Q9nsd6 homo sapien
154	72	83.7	108	1	KV1Y_HUMAN	P80362 homo sapien
155	72	83.7	108	1	LV3A_HUMAN	P01714 homo sapien
156	72	83.7	110	2	Q8TE63_HUMAN	Q8te63 homo sapien
157	72	83.7	111	1	LV2A_HUMAN	P01704 homo sapien
158	72	83.7	111	1	LV3B_HUMAN	P80748 homo sapien
159	72	83.7	115	2	Q5F2I0_MOUSE	Q5f2i0 mus musculu
160	72	83.7	117	1	KV1I_HUMAN	P01601 homo sapien
161	72	83.7	128	1	KV5E_MOUSE	P01637 mus musculu
162	72	83.7	131	2	Q811C3_MOUSE	Q811c3 mus musculu
163	72	83.7	233	2	Q6GMW4_HUMAN	Q6gmw4 homo sapien
164	72	83.7	233	2	Q8TBC9_HUMAN	Q8tbc9 homo sapien
165	72	83.7	234	2	Q6NS95_HUMAN	Q6ns95 homo sapien
166	72	83.7	235	2	Q567P1_HUMAN	Q567p1 homo sapien
167	72	83.7	235	2	Q6PJF2_HUMAN	Q6pjf2 homo sapien
168	72	83.7	235	2	Q6PJG0_HUMAN	Q6pjg0 homo sapien
169	72	83.7	248	2	Q65ZQ7_9MURI	Q65zq7 mus sp. b3(
170	71	82.6	97	2	Q5NV74_HUMAN	Q5nv74 homo sapien
171	71	82.6	107	1	LV4C_HUMAN	P01717 homo sapien
172	71	82.6	109	1	KV4D_HUMAN	P83593 homo sapien
173	71	82.6	136	1	KV5B_MOUSE	P01634 mus musculu
174	71	82.6	234	2	Q8N355_HUMAN	Q8n355 homo sapien
175	71	82.6	234	2	Q5M838_RAT	Q5m838 rattus norv
176	71	82.6	238	2	Q58EU4_MOUSE	Q58eu4 mus musculu
177	71	82.6	243	2	Q7TQM2_MOUSE	Q7tqm2 mus musculu
178	70	81.4	81	2	Q5R3T5_MOUSE	Q5r3t5 mus musculu
179	70	81.4	98	2	Q5NV80_HUMAN	Q5nv80 homo sapien
180	70	81.4	98	2	Q5NV83_HUMAN	Q5nv83 homo sapien
181	70	81.4	108	1	KV3V_MOUSE	P01674 mus musculu
182	70	81.4	108	1	KV5D_MOUSE	P01636 mus musculu
183	70	81.4	109	2	Q920E6_MOUSE	Q920e6 mus musculu
184	70	81.4	110	1	KV01_RABIT	P01682 oryctolagus
185	70	81.4	111	1	KV3Q_MOUSE	P01669 mus musculu
186	70	81.4	111	1	LV2G_HUMAN	P01710 homo sapien
187	70	81.4	111	2	Q65ZN3_MOUSE	Q65zn3 mus musculu
188	70	81.4	115	1	KV5C_MOUSE	P01635 mus musculu
189	70	81.4	117	1	LV0A_HUMAN	P04211 homo sapien
190	70	81.4	236	2	Q6GMX4_HUMAN	Q6gmx4 homo sapien
191	70	81.4	237	2	Q7SZ36_XENLA	Q7sz36 xenopus lae
192	70	81.4	238	2	Q66JS7_MOUSE	Q66js7 mus musculu
193	70	81.4	487	2	Q65ZL2_9MURI	Q65zl2 mus sp. fv/
194	69	80.2	59	2	Q4T3F9_TETNG	Q4t3f9 tetraodon n
195	69	80.2	96	2	Q4SX14_TETNG	Q4sx14 tetraodon n
196	69	80.2	103	1	LV1E_HUMAN	P01703 homo sapien
197	69	80.2	104	2	Q5NV87_HUMAN	Q5nv87 homo sapien
198	69	80.2	106	1	LV4A_HUMAN	P01715 homo sapien
199	69	80.2	107	1	KV04_RABIT	P01685 oryctolagus
200	69	80.2	108	1	KV1A_HUMAN	P01593 homo sapien
201	69	80.2	109	1	LV1F_HUMAN	P04208 homo sapien
202	69	80.2	109	1	LV1I_HUMAN	P06888 homo sapien
203	69	80.2	219	2	Q65ZC0_MOUSE	Q65zc0 mus musculu
204	69	80.2	233	2	Q6NS96_HUMAN	Q6ns96 homo sapien
205	69	80.2	235	2	Q6GMW6_HUMAN	Q6gmw6 homo sapien
206	69	80.2	236	2	Q96E61_HUMAN	Q96e61 homo sapien
207	69	80.2	236	2	Q6GMX9_HUMAN	Q6gmx9 homo sapien
208	69	80.2	239	2	Q5HZC6_XENTR	Q5hzc6 xenopus tro
209	68	79.1	92	1	KV09_RABIT	P01690 oryctolagus
210	68	79.1	95	2	Q5NV91_HUMAN	Q5nv91 homo sapien
211	68	79.1	96	2	Q4TJ02_TETNG	Q4tj02 tetraodon n
212	68	79.1	99	2	Q5NV62_HUMAN	Q5nv62 homo sapien
213	68	79.1	106	2	Q9U410_MOUSE	Q9u410 mus musculu
214	68	79.1	112	1	KV2D_MOUSE	P01629 mus musculu
215	68	79.1	113	1	KV2B_HUMAN	P01615 homo sapien
216	68	79.1	113	1	KV2D_HUMAN	P01617 homo sapien
217	68	79.1	234	2	Q6GMW3_HUMAN	Q6gmw3 homo sapien
218	68	79.1	235	2	Q6IN99_HUMAN	Q6in99 homo sapien
219	68	79.1	236	2	Q6GMV7_HUMAN	Q6gmv7 homo sapien
220	68	79.1	236	2	Q52L95_MOUSE	Q52l95 mus musculu
221	68	79.1	239	2	Q8NEK0_HUMAN	Q8nek0 homo sapien
222	68	79.1	240	2	Q6PIH6_HUMAN	Q6pih6 homo sapien
223	67	77.9	109	1	KV3F_HUMAN	P01624 homo sapien
224	67	77.9	111	1	LV2F_HUMAN	P01709 homo sapien
225	67	77.9	111	2	Q5F2I7_MOUSE	Q5f2i7 mus musculu
226	67	77.9	112	2	Q8K1F2_MOUSE	Q8k1f2 mus musculu
227	67	77.9	114	1	KV1A_MOUSE	P01632 mus musculu
228	67	77.9	115	1	KV02_RABIT	P01683 oryctolagus
229	67	77.9	165	2	Q6ZNX5_HUMAN	Q6znx5 homo sapien
230	66	76.7	97	2	Q5NV64_HUMAN	Q5nv64 homo sapien
231	66	76.7	97	2	Q5NV85_HUMAN	Q5nv85 homo sapien
232	66	76.7	104	2	Q5NV68_HUMAN	Q5nv68 homo sapien
233	66	76.7	106	1	LV4B_HUMAN	P01716 homo sapien
234	66	76.7	108	1	LV5A_HUMAN	P01719 homo sapien
235	66	76.7	109	1	KV01_RAT	P01681 rattus norv
236	66	76.7	112	1	KV2C_HUMAN	P01616 homo sapien
237	66	76.7	113	1	KV2E_MOUSE	P03976 mus musculu
238	66	76.7	123	2	Q61243_MOUSE	Q61243 mus musculu
239	66	76.7	135	2	Q9H5Z4_HUMAN	Q9h5z4 homo sapien
240	66	76.7	148	2	Q6PJ28_HUMAN	Q6pj28 homo sapien
241	66	76.7	234	2	Q5CZ94_HUMAN	Q5cz94 homo sapien
242	66	76.7	236	2	Q6GMX3_HUMAN	Q6gmx3 homo sapien
243	65	75.6	97	2	Q9JL76_MOUSE	Q9jl76 mus musculu
244	65	75.6	111	1	LV7A_HUMAN	P01720 homo sapien
245	65	75.6	112	2	Q96JD2_HUMAN	Q96jd2 homo sapien
246	65	75.6	112	2	Q5R1F4_MOUSE	Q5r1f4 mus musculu
247	65	75.6	112	2	Q8K1F3_MOUSE	Q8k1f3 mus musculu
248	65	75.6	114	1	KV16_RABIT	P01697 oryctolagus
249	65	75.6	134	2	Q8VDD0_MOUSE	Q8vdd0 mus musculu
250	65	75.6	235	2	Q6P2J1_HUMAN	Q6p2j1 homo sapien

251	65	75.6	235	2	Q5XFY8_MOUSE	Q5xfy8 mus musculu
252	65	75.6	237	2	Q6DHW4_HUMAN	Q6dhw4 homo sapien
253	64	74.4	94	1	KV11_RABIT	P01692 oryctolagus
254	64	74.4	101	2	Q8IZD8_HUMAN	Q8izd8 homo sapien
255	64	74.4	106	1	LV4E_HUMAN	P06889 homo sapien
256	64	74.4	111	1	LV1A_HUMAN	P01699 homo sapien
257	64	74.4	112	1	LV6A_HUMAN	P01721 homo sapien
258	64	74.4	112	2	Q96JD1_HUMAN	Q96jd1 homo sapien
259	64	74.4	113	1	KV2G_MOUSE	P01631 mus musculu
260	64	74.4	232	2	Q5FWF9_HUMAN	Q5fwf9 homo sapien
261	63	73.3	86	2	Q7Z3Y5_HUMAN	Q7z3y5 homo sapien
262	63	73.3	107	2	Q9UL82_HUMAN	Q9ul82 homo sapien
263	63	73.3	111	1	LV1C_HUMAN	P01701 homo sapien
264	63	73.3	114	2	Q9UL80_HUMAN	Q9ul80 homo sapien
265	63	73.3	114	2	Q8K1F1_MOUSE	Q8k1f1 mus musculu
266	63	73.3	133	1	KV2F_HUMAN	P06310 homo sapien
267	63	73.3	234	2	Q6GMV8_HUMAN	Q6gmv8 homo sapien
268	63	73.3	239	2	Q8TCD0_HUMAN	Q8tcd0 homo sapien
269	62	72.1	106	1	LV4D_HUMAN	P01718 homo sapien
270	62	72.1	111	1	LV6C_HUMAN	P06317 homo sapien
271	62	72.1	111	1	LV6D_HUMAN	P06318 homo sapien
272	61	70.9	98	2	Q5NV88_HUMAN	Q5nv88 homo sapien
273	61	70.9	111	1	LV2H_HUMAN	P01711 homo sapien
274	61	70.9	112	1	LV6B_HUMAN	P01722 homo sapien
275	61	70.9	112	2	Q6LEM8_MOUSE	Q6lem8 mus musculu
276	61	70.9	120	1	KV2B_MOUSE	P01627 mus musculu
277	61	70.9	234	2	Q5XKG4_MOUSE	Q5xkg4 mus musculu
278	61	70.9	239	2	Q58EU8_MOUSE	Q58eu8 mus musculu
279	60	69.8	109	2	Q9N0W5_RABIT	Q9n0w5 oryctolagus
280	60	69.8	112	2	Q5R1B8_MOUSE	Q5r1b8 mus musculu
281	60	69.8	112	2	Q53VP8_MOUSE	Q53vp8 mus musculu
282	60	69.8	113	1	KV2F_MOUSE	P01630 mus musculu
283	60	69.8	115	1	KV2A_HUMAN	P01614 homo sapien
284	60	69.8	117	1	KV2E_HUMAN	P06309 homo sapien
285	60	69.8	123	1	VPRE3_HUMAN	Q9uki3 homo sapien
286	60	69.8	128	1	KV3K_HUMAN	P06311 homo sapien
287	60	69.8	233	2	Q96I69_HUMAN	Q96i69 homo sapien
288	60	69.8	233	2	Q8N5F4_HUMAN	Q8n5f4 homo sapien
289	59	68.6	99	2	Q5NV79_HUMAN	Q5nv79 homo sapien
290	59	68.6	108	1	KV5J_MOUSE	P01643 mus musculu
291	59	68.6	108	1	KV5K_MOUSE	P01644 mus musculu
292	59	68.6	108	1	KV5L_MOUSE	P01645 mus musculu
293	59	68.6	108	1	KV5M_MOUSE	P01646 mus musculu
294	59	68.6	108	1	KV5N_MOUSE	P01647 mus musculu
295	59	68.6	108	1	KV5U_MOUSE	P04946 mus musculu
296	59	68.6	114	2	Q5R1C0_MOUSE	Q5r1c0 mus musculu
297	59	68.6	114	2	Q5R1F6_MOUSE	Q5r1f6 mus musculu
298	59	68.6	132	2	Q8TBD0_HUMAN	Q8tbd0 homo sapien
299	58.5	68.0	113	1	LV1_CHICK	P04210 gallus gall
300	58	67.4	104	2	Q5NV82_HUMAN	Q5nv82 homo sapien
301	58	67.4	121	2	Q5R1G1_MOUSE	Q5r1g1 mus musculu
302	58	67.4	237	2	Q569Y8_MOUSE	Q569y8 mus musculu
303	58	67.4	239	2	Q6P491_HUMAN	Q6p491 homo sapien
304	57	66.3	107	1	KV6F_MOUSE	P04940 mus musculu
305	57	66.3	107	1	KV6G_MOUSE	P04941 mus musculu
306	57	66.3	107	1	KV6H_MOUSE	P04942 mus musculu
307	57	66.3	107	1	KV6I_MOUSE	P04943 mus musculu
308	57	66.3	107	1	KV6J_MOUSE	P04944 mus musculu
309	57	66.3	112	2	Q8K1F0_MOUSE	Q8k1f0 mus musculu
310	57	66.3	116	2	Q96JD0_HUMAN	Q96jd0 homo sapien
311	57	66.3	120	2	Q5R1B3_MOUSE	Q5r1b3 mus musculu
312	57	66.3	120	2	Q5R1E9_MOUSE	Q5r1e9 mus musculu
313	57	66.3	121	2	Q5R1D3_MOUSE	Q5r1d3 mus musculu
314	57	66.3	129	1	KV4A_MOUSE	P01680 mus musculu
315	57	66.3	235	2	Q58EV6_MOUSE	Q58ev6 mus musculu
316	57	66.3	240	2	Q5U4N2_XENLA	Q5u4n2 xenopus lae
317	56	65.1	100	2	O77624_BOVIN	O77624 bos taurus
318	56	65.1	103	2	Q5NV61_HUMAN	Q5nv61 homo sapien
319	56	65.1	105	2	Q8WVJ6_HUMAN	Q8wvj6 homo sapien
320	56	65.1	107	1	KV6A_MOUSE	P01675 mus musculu
321	56	65.1	107	1	KV6B_MOUSE	P01676 mus musculu
322	56	65.1	107	1	KV6C_MOUSE	P01677 mus musculu
323	56	65.1	107	1	KV6D_MOUSE	P01678 mus musculu
324	56	65.1	107	1	KV6E_MOUSE	P01679 mus musculu
325	56	65.1	112	2	Q5R1E8_MOUSE	Q5r1e8 mus musculu
326	56	65.1	142	1	VPRE1_MOUSE	P13372 mus musculu
327	56	65.1	142	1	VPRE2_MOUSE	P13373 mus musculu
328	56	65.1	142	2	Q5W1K4_MOUSE	Q5w1k4 mus musculu
329	56	65.1	142	2	Q545E0_MOUSE	Q545e0 m 13 days e
330	56	65.1	145	1	VPREB_HUMAN	P12018 homo sapien
331	56	65.1	147	2	Q6V4Z9_RABIT	Q6v4z9 oryctolagus
332	56	65.1	147	2	Q6V500_RABIT	Q6v500 oryctolagus
333	56	65.1	240	2	Q8WUK3_HUMAN	Q8wuk3 homo sapien
334	55	64.0	107	2	Q9JL84_MOUSE	Q9jl84 mus musculu
335	55	64.0	108	1	KV5O_MOUSE	P01648 mus musculu
336	55	64.0	112	2	Q5R1F2_MOUSE	Q5r1f2 mus musculu
337	55	64.0	241	2	Q921A6_MOUSE	Q921a6 mus musculu
338	55	64.0	266	2	Q6PIP7_HUMAN	Q6pip7 homo sapien
339	54	62.8	112	1	KV2A_MOUSE	P01626 mus musculu
340	54	62.8	230	2	Q7Z2U3_HUMAN	Q7z2u3 homo sapien
341	53	61.6	112	2	Q5R1E5_MOUSE	Q5r1e5 mus musculu
342	53	61.6	112	2	Q5R1I1_MOUSE	Q5r1i1 mus musculu
343	53	61.6	112	2	Q5R1I3_MOUSE	Q5r1i3 mus musculu
344	53	61.6	115	1	KV5A_HUMAN	P06315 homo sapien
345	53	61.6	132	1	TVA2_MOUSE	P01739 mus musculu
346	53	61.6	262	2	Q65ZI1_MOUSE	Q65zi1 mus musculu
347	53	61.6	273	2	Q6PIZ8_HUMAN	Q6piz8 homo sapien
348	52	60.5	110	2	Q5R1J0_MOUSE	Q5r1j0 mus musculu
349	52	60.5	113	2	Q4T9E0_TETNG	Q4t9e0 tetraodon n
350	52	60.5	229	2	Q5M8U3_XENTR	Q5m8u3 xenopus tro
351	52	60.5	260	2	Q6P4G7_HUMAN	Q6p4g7 homo sapien
352	52	60.5	321	1	TCB_FLV	P11364 feline leuk
353	51.5	59.9	104	1	KV17_RABIT	P01698 oryctolagus
354	51	59.3	112	2	Q5R1I6_MOUSE	Q5r1i6 mus musculu
355	51	59.3	113	2	Q5R1I4_MOUSE	Q5r1i4 mus musculu
356	51	59.3	115	2	Q5R1E4_MOUSE	Q5r1e4 mus musculu
357	51	59.3	115	2	Q5R1I0_MOUSE	Q5r1i0 mus musculu
358	51	59.3	231	2	Q58E08_XENLA	Q58e08 xenopus lae
359	51	59.3	234	2	Q7Z2U7_HUMAN	Q7z2u7 homo sapien
360	51	59.3	239	2	Q5XGQ4_XENLA	Q5xgq4 xenopus lae
361	50	58.1	108	1	KV1_CANFA	P01618 canis famil
362	50	58.1	113	1	KV2C_MOUSE	P01628 mus musculu
363	50	58.1	136	1	TVC_HUMAN	P03979 homo sapien
364	50	58.1	200	2	Q6IPT1_HUMAN	Q6ipt1 homo sapien
365	50	58.1	222	2	Q8IYM6_HUMAN	Q8iym6 homo sapien
366	50	58.1	231	2	Q6GNB8_XENLA	Q6gnb8 xenopus lae
367	50	58.1	233	2	Q6GNH3_XENLA	Q6gnh3 xenopus lae
368	49	57.0	93	2	Q5ZGJ4_HUMAN	Q5zgj4 homo sapien
369	49	57.0	112	2	Q5R1E0_MOUSE	Q5r1e0 mus musculu
370	49	57.0	112	2	Q5R1H6_MOUSE	Q5r1h6 mus musculu
371	49	57.0	115	1	KV5I_MOUSE	P01642 mus musculu
372	49	57.0	131	1	LV6E_HUMAN	P06319 homo sapien
373	49	57.0	197	2	Q7EZA4_ORYSA	Q7eza4 oryza sativ
374	49	57.0	235	2	Q99M11_MOUSE	Q99m11 mus musculu
375	49	57.0	240	2	Q63ZL4_XENLA	Q63zl4 xenopus lae
376	49	57.0	241	2	Q7EZA5_ORYSA	Q7eza5 oryza sativ
377	49	57.0	274	2	Q6GMW8_HUMAN	Q6gmw8 homo sapien
378	49	57.0	470	2	Q4G060_RAT	Q4g060 rattus norv
379	49	57.0	569	2	Q99ND6_RAT	Q99nd6 rattus norv
380	49	57.0	575	1	I10R1_MOUSE	Q61727 mus musculu
381	49	57.0	581	2	Q4WM23_ASPFU	Q4wm23 aspergillus
382	49	57.0	731	2	Q4N3Y3_THEPA	Q4n3y3 theileria p
383	48	55.8	88	2	Q5ZGJ2_HUMAN	Q5zgj2 homo sapien
384	48	55.8	91	2	Q5ZGJ3_HUMAN	Q5zgj3 homo sapien
385	48	55.8	93	2	Q5ZGI4_HUMAN	Q5zgi4 homo sapien
386	48	55.8	95	2	Q5ZGK4_HUMAN	Q5zgk4 homo sapien
387	48	55.8	95	2	Q5ZGK3_HUMAN	Q5zgk3 homo sapien
388	48	55.8	273	2	Q6NSA1_HUMAN	Q6nsa1 homo sapien
389	48	55.8	285	2	Q5YCY6_BRARE	Q5ycy6 brachydanio
390	48	55.8	311	2	Q6GMR4_HUMAN	Q6gmr4 homo sapien
391	48	55.8	328	2	Q76B98_XENLA	Q76b98 xenopus lae
392	47	54.7	98	2	Q5NV86_HUMAN	Q5nv86 homo sapien
393	47	54.7	99	2	Q5NV92_HUMAN	Q5nv92 homo sapien
394	47	54.7	112	2	Q5R1E2_MOUSE	Q5r1e2 mus musculu
395	47	54.7	112	2	Q5R1H8_MOUSE	Q5r1h8 mus musculu
396	47	54.7	121	2	Q5R1C5_MOUSE	Q5r1c5 mus musculu

397	47	54.7	269	2	Q4KLD3_XENLA	Q4kld3	xenopus lae
398	47	54.7	531	1	RO60_DEIRA	Q9ruw8	deinococcus
399	47	54.7	1067	2	Q7SHQ9_NEUCR	Q7shq9	neurospora
400	47	54.7	1190	2	Q6CLJ2_KLULA	Q6clj2	kluyveromyc
401	47	54.7	1288	2	Q5Y9B8_RAT	Q5y9b8	rattus norv
402	46.5	54.1	248	2	Q5M912_XENTR	Q5m912	xenopus tro
403	46.5	54.1	280	2	Q55ZR0_CRYNE	Q55zr0	cryptococcu
404	46	53.5	87	2	Q5ZGK6_HUMAN	Q5zgk6	homo sapien
405	46	53.5	112	2	Q5R1B6_MOUSE	Q5r1b6	mus musculu
406	46	53.5	114	2	Q5R1I7_MOUSE	Q5r1i7	mus musculu
407	46	53.5	117	1	KV5H_MOUSE	P01641	mus musculu
408	46	53.5	121	2	Q5R1G9_MOUSE	Q5r1g9	mus musculu
409	46	53.5	233	2	Q5U512_XENLA	Q5u512	xenopus lae
410	46	53.5	241	2	Q63ZX4_MOUSE	Q63zx4	mus musculu
411	46	53.5	594	2	Q5Z2C2_NOCFA	Q5z2c2	nocardia fa
412	46	53.5	1417	2	Q9C6G0_ARATH	Q9c6g0	arabidopsis
413	45	52.3	112	2	Q5R1B9_MOUSE	Q5r1b9	mus musculu
414	45	52.3	112	2	Q5R1F5_MOUSE	Q5r1f5	mus musculu
415	45	52.3	112	2	Q5R1I5_MOUSE	Q5r1i5	mus musculu
416	45	52.3	113	2	Q5R1E3_MOUSE	Q5r1e3	mus musculu
417	45	52.3	113	2	Q5R1H9_MOUSE	Q5r1h9	mus musculu
418	45	52.3	114	2	Q5R1C3_MOUSE	Q5r1c3	mus musculu
419	45	52.3	114	2	Q5R1F9_MOUSE	Q5r1f9	mus musculu
420	45	52.3	133	1	TVB2_HUMAN	P04435	homo sapien
421	45	52.3	243	2	Q5M8G7_XENTR	Q5m8g7	xenopus tro
422	45	52.3	270	2	Q6PIR9_MOUSE	Q6pir9	mus musculu
423	45	52.3	284	2	Q4WBI1_ASPFU	Q4wbi1	aspergillus
424	45	52.3	321	2	Q6DJ81_XENTR	Q6dj81	xenopus tro
425	45	52.3	323	2	Q6PI92_HUMAN	Q6pi92	homo sapien
426	45	52.3	333	2	Q8UV75_BRARE	Q8uv75	brachydanio
427	45	52.3	362	2	Q6WAX1_TOXGO	Q6wax1	toxoplasma
428	45	52.3	367	2	Q6WAW4_TOXGO	Q6waw4	toxoplasma
429	45	52.3	475	2	Q9B8D2_CANAL	Q9b8d2	candida alb
430	45	52.3	701	2	Q81DP9_BACCR	Q81dp9	bacillus ce
431	45	52.3	976	2	Q7QJ73_ANOGA	Q7qj73	anopheles g
432	45	52.3	2385	2	Q6HJ02_BACHK	Q6hj02	bacillus th
433	45	52.3	2385	2	Q81QP7_BACAN	Q81qp7	bacillus an
434	45	52.3	2385	2	Q63BJ5_BACCZ	Q63bj5	bacillus ce
435	45	52.3	2444	2	Q5B823_EMENI	Q5b823	aspergillus
436	44	51.2	89	2	Q5ZGI7_HUMAN	Q5zgi7	homo sapien
437	44	51.2	93	2	Q5ZGK7_HUMAN	Q5zgk7	homo sapien
438	44	51.2	113	2	Q5R1D5_MOUSE	Q5r1d5	mus musculu
439	44	51.2	114	2	Q5R1C9_MOUSE	Q5r1c9	mus musculu
440	44	51.2	114	2	Q5R1G5_MOUSE	Q5r1g5	mus musculu
441	44	51.2	114	2	Q5R1B2_MOUSE	Q5r1b2	mus musculu
442	44	51.2	117	2	Q8UV56_BRARE	Q8uv56	brachydanio
443	44	51.2	118	2	Q8UUG5_BRARE	Q8uug5	brachydanio
444	44	51.2	128	2	Q6PIW0_HUMAN	Q6piw0	homo sapien
445	44	51.2	136	1	TVB4_MOUSE	P04212	mus musculu
446	44	51.2	249	2	Q5VTN6_BRARE	Q5vtn6	brachydanio
447	44	51.2	267	2	Q4RWI5_TETNG	Q4rwi5	tetraodon n
448	44	51.2	285	2	Q5SNN8_BRARE	Q5snn8	brachydanio
449	44	51.2	316	2	Q5YCY7_BRARE	Q5ycy7	brachydanio
450	44	51.2	316	2	Q5SNN7_BRARE	Q5snn7	brachydanio
451	44	51.2	520	1	NIFK_KLEPN	P09772	klebsiella
452	44	51.2	541	1	LNT_CHLCV	Q824q5	chlamydophi
453	44	51.2	926	2	Q4KCP3_PSEF5	Q4kcp3	pseudomonas
454	44	51.2	2385	2	Q738J2_BACC1	Q738j2	bacillus ce
455	44	51.2	14474	2	Q5YPK6_NOCFA	Q5ypk6	nocardia fa
456	43	50.0	86	2	Q5ZGI9_HUMAN	Q5zgi9	homo sapien
457	43	50.0	92	2	Q5ZGJ0_HUMAN	Q5zgj0	homo sapien
458	43	50.0	98	2	Q7NE55_GLOVI	Q7ne55	gloeobacter
459	43	50.0	112	2	Q5R1E6_MOUSE	Q5r1e6	mus musculu
460	43	50.0	119	2	Q99601_HUMAN	Q99601	homo sapien
461	43	50.0	119	2	Q5R1A8_MOUSE	Q5r1a8	mus musculu
462	43	50.0	124	2	Q4SGJ3_TETNG	Q4sgj3	tetraodon n
463	43	50.0	147	2	Q8CFJ3_MOUSE	Q8cfj3	mus musculu
464	43	50.0	189	2	Q6VE09_9HEPC	Q6ve09	hepatitis c
465	43	50.0	191	2	Q7NSZ5_CHRVO	Q7nsz5	chromobacte
466	43	50.0	197	2	Q6B8P6_GRATL	Q6b8p6	gracilaria
467	43	50.0	205	2	Q4RCF0_TETNG	Q4rcf0	tetraodon n
468	43	50.0	223	2	Q8AW69_BRARE	Q8aw69	brachydanio
469	43	50.0	267	2	Q569B0_RAT	Q569b0	rattus norv
470	43	50.0	276	1	T702_FREDI	Q00462	fremyella d
471	43	50.0	287	2	Q5VTQ4_BRARE	Q5vtq4	brachydanio
472	43	50.0	306	2	Q6GMV6_HUMAN	Q6gmv6	homo sapien
473	43	50.0	310	2	Q8N2T6_HUMAN	Q8n2t6	homo sapien
474	43	50.0	313	2	Q8UV45_BRARE	Q8uv45	brachydanio
475	43	50.0	325	2	Q5VTQ7_BRARE	Q5vtq7	brachydanio
476	43	50.0	325	2	Q8UWL3_ICTPU	Q8uwl3	ictalurus p
477	43	50.0	328	2	Q5SPT3_BRARE	Q5spt3	brachydanio
478	43	50.0	361	2	Q6CZF0_ERWCT	Q6czf0	erwinia car
479	43	50.0	483	2	Q566J7_MOUSE	Q566j7	mus musculu
480	43	50.0	493	2	Q9XZ17_DROME	Q9xz17	drosophila
481	43	50.0	499	2	Q7VZP3_BORPE	Q7vzp3	bordetella
482	43	50.0	500	2	Q7W5B9_BORPA	Q7w5b9	bordetella
483	43	50.0	500	2	Q7WCV1_BORBR	Q7wcv1	bordetella
484	43	50.0	568	1	MPP3_MOUSE	O88910	mus musculu
485	43	50.0	585	1	MPP3_HUMAN	Q13368	homo sapien
486	43	50.0	585	2	Q6PGR3_HUMAN	Q6pgr3	homo sapien
487	43	50.0	585	2	Q6XE40_MOUSE	Q6xe40	mus musculu
488	43	50.0	754	2	Q4HXZ1_GIBZE	Q4hxz1	gibberella
489	43	50.0	984	2	Q4IR10_GIBZE	Q4ir10	gibberella
490	43	50.0	1134	2	Q4I0C0_GIBZE	Q4i0c0	gibberella
491	43	50.0	1186	2	Q4SWC3_TETNG	Q4swc3	tetraodon n
492	43	50.0	1677	2	Q54H96_DICDI	Q54h96	dictyosteli
493	43	50.0	2280	2	Q8UZ80_9CALI	Q8uz80	human calic
494	42.5	49.4	411	2	Q5BGV3_EMENI	Q5bgv3	aspergillus
495	42	48.8	32	2	Q9AZV9_9CAUD	Q9azv9	bacteriopha
496	42	48.8	32	2	Q9XJE2_BPTU2	Q9xje2	lactococcus
497	42	48.8	70	2	Q9B010_9CAUD	Q9b010	bacteriopha
498	42	48.8	90	2	Q5ZGJ1_HUMAN	Q5zgj1	homo sapien
499	42	48.8	99	2	Q5NV66_HUMAN	Q5nv66	homo sapien
500	42	48.8	109	2	Q5R1A9_MOUSE	Q5r1a9	mus musculu
501	42	48.8	109	2	Q5R1I9_MOUSE	Q5r1i9	mus musculu
502	42	48.8	122	2	Q99603_HUMAN	Q99603	homo sapien
503	42	48.8	122	2	Q99604_HUMAN	Q99604	homo sapien
504	42	48.8	125	1	HV2D_HUMAN	P01817	homo sapien
505	42	48.8	132	1	TVA3_MOUSE	P06323	mus musculu
506	42	48.8	170	2	Q63AE3_BACCZ	Q63ae3	bacillus ce
507	42	48.8	230	2	Q984B0_RHILO	Q984b0	rhizobium l
508	42	48.8	232	2	Q8UV53_BRARE	Q8uv53	brachydanio
509	42	48.8	232	2	Q8UV82_BRARE	Q8uv82	brachydanio
510	42	48.8	238	2	Q98NZ0_RHILO	Q98nz0	rhizobium l
511	42	48.8	245	2	Q7ZZ97_BRARE	Q7zz97	brachydanio
512	42	48.8	295	2	Q8IT85_PLAFA	Q8it85	plasmodium
513	42	48.8	298	2	Q6INA4_HUMAN	Q6ina4	homo sapien
514	42	48.8	301	2	Q5FPL7_GLUOX	Q5fpl7	gluconobact
515	42	48.8	315	2	Q6IN96_HUMAN	Q6in96	homo sapien
516	42	48.8	323	2	Q5VTR5_BRARE	Q5vtr5	brachydanio
517	42	48.8	337	2	Q5SYD7_BRARE	Q5syd7	brachydanio
518	42	48.8	338	2	Q5VTN7_BRARE	Q5vtn7	brachydanio
519	42	48.8	338	2	Q5YCZ1_BRARE	Q5ycz1	brachydanio
520	42	48.8	346	2	Q75R38_ONCMY	Q75r38	oncorhynchu
521	42	48.8	362	2	O15703_TOXGO	O15703	toxoplasma
522	42	48.8	362	2	Q6WAX2_TOXGO	Q6wax2	toxoplasma
523	42	48.8	367	2	O15728_TOXGO	O15728	toxoplasma
524	42	48.8	367	2	Q6WAW5_TOXGO	Q6waw5	toxoplasma
525	42	48.8	367	2	Q94802_TOXGO	Q94802	toxoplasma
526	42	48.8	380	2	Q5B344_EMENI	Q5b344	aspergillus
527	42	48.8	396	2	Q5AG63_CANAL	Q5ag63	candida alb
528	42	48.8	396	2	Q5AGK0_CANAL	Q5agk0	candida alb
529	42	48.8	396	2	Q8NMU0_CORGL	Q8nmu0	corynebacte
530	42	48.8	414	2	Q6M2Z4_CORGL	Q6m2z4	corynebacte
531	42	48.8	449	2	Q41251_TOBAC	Q41251	nicotiana t
532	42	48.8	530	2	Q5LEW9_BACFN	Q5lew9	bacteroides
533	42	48.8	530	2	Q64VW2_BACFR	Q64vw2	bacteroides
534	41.5	48.3	338	2	Q8XXI7_RALSO	Q8xxi7	ralstonia s
535	41.5	48.3	3989	2	Q9PYB2_9FLAV	Q9pyb2	pestivirus
536	41	47.7	64	2	Q5YSV1_NOCFA	Q5ysv1	nocardia fa
537	41	47.7	81	2	Q8YJW9_ANASP	Q8yjw9	anabaena sp
538	41	47.7	88	2	Q8TIK7_METAC	Q8tik7	methanosarc
539	41	47.7	97	2	Q5ZGJ9_HUMAN	Q5zgj9	homo sapien
540	41	47.7	101	2	Q9C112_SCHPO	Q9c112	schizosacch
541	41	47.7	103	2	Q6QMZ6_CHILA	Q6qmz6	chinchilla
542	41	47.7	117	2	Q8AW76_BRARE	Q8aw76	brachydanio

543	41	47.7	152	2	Q6LBN1_HUMAN	Q6lbn1 homo sapien
544	41	47.7	172	2	Q95JR8_MACFA	Q95jr8 macaca fasc
545	41	47.7	185	2	Q6J1M0_XENLA	Q6j1m0 xenopus lae
546	41	47.7	185	2	Q8UWK4_ICTPU	Q8uwk4 ictalurus p
547	41	47.7	202	2	Q8UWK6_ICTPU	Q8uwk6 ictalurus p
548	41	47.7	206	2	Q8UWG3_ICTPU	Q8uwg3 ictalurus p
549	41	47.7	206	2	Q8UWK5_ICTPU	Q8uwk5 ictalurus p
550	41	47.7	210	2	Q82AG8_STRAW	Q82ag8 streptomyce
551	41	47.7	215	2	Q8UWK7_ICTPU	Q8uwk7 ictalurus p
552	41	47.7	216	2	Q8WUL5_HUMAN	Q8wul5 homo sapien
553	41	47.7	223	2	Q8UWK8_ICTPU	Q8uwk8 ictalurus p
554	41	47.7	227	2	Q8UWK9_ICTPU	Q8uwk9 ictalurus p
555	41	47.7	240	2	Q5VSN6_BRARE	Q5vsn6 brachydanio
556	41	47.7	252	2	Q6NSA0_HUMAN	Q6nsa0 homo sapien
557	41	47.7	255	2	Q4IZP8_AZOVI	Q4izp8 azotobacter
558	41	47.7	281	2	Q8KH21_PSEAE	Q8kh21 pseudomonas
559	41	47.7	308	2	Q6PIV3_HUMAN	Q6piv3 homo sapien
560	41	47.7	313	2	Q6IPU1_HUMAN	Q6ipu1 homo sapien
561	41	47.7	317	2	Q5M858_RAT	Q5m858 rattus norv
562	41	47.7	323	2	Q8XZ00_RALSO	Q8xz00 ralstonia s
563	41	47.7	331	2	Q9IB01_9PERC	Q9ib01 sphoeroides
564	41	47.7	340	2	Q6FSD6_CANGA	Q6fsd6 candida gla
565	41	47.7	343	2	Q9KJN9_MYXXA	Q9kjn9 myxococcus
566	41	47.7	353	2	Q6QMY6_RAT	Q6qmy6 rattus norv
567	41	47.7	354	2	Q4W655_MOUSE	Q4w655 mus musculu
568	41	47.7	361	2	P94521_BACSU	P94521 bacillus su
569	41	47.7	372	2	Q8CBR6_MOUSE	Q8cbr6 mus musculu
570	41	47.7	470	2	Q6L0Q3_PICTO	Q6l0q3 picrophilus
571	41	47.7	471	2	Q84697_PEBV	Q84697 pea early b
572	41	47.7	521	2	Q8N4Y9_HUMAN	Q8n4y9 homo sapien
573	41	47.7	611	2	Q61DU3_CAEBR	Q61du3 caenorhabdi
574	41	47.7	614	2	Q7VEG9_PROMA	Q7veg9 prochloroco
575	41	47.7	681	2	Q6XMU2_RHOER	Q6xmu2 rhodococcus
576	41	47.7	709	2	Q4UG30_THEAN	Q4ug30 theileria a
577	41	47.7	746	2	Q7NEC9_GLOVI	Q7nec9 gloeobacter
578	41	47.7	872	2	O70011_STRCO	O70011 streptomyce
579	41	47.7	874	2	Q8CJR4_STRCO	Q8cjr4 streptomyce
580	41	47.7	1083	2	Q873F2_NEUCR	Q873f2 neurospora
581	41	47.7	1698	2	Q84918_9VIRU	Q84918 pepper ring
582	41	47.7	1707	1	194K_TRVSY	P05080 tobacco rat
583	41	47.7	1707	2	O56250_9VIRU	O56250 tobacco rat
584	41	47.7	1707	2	Q70BW7_9VIRU	Q70bw7 tobacco rat
585	41	47.7	1707	2	Q8JU32_9VIRU	Q8ju32 tobacco rat
586	41	47.7	1707	2	Q9DL34_9VIRU	Q9dl34 tobacco rat
587	41	47.7	1707	2	Q9J942_9VIRU	Q9j942 tobacco rat
588	41	47.7	1766	2	Q9WJD8_PEBV	Q9wjd8 pea early b
589	41	47.7	3008	2	Q4FY07_LEIMA	Q4fy07 leishmania
590	41	47.7	3342	2	Q80MM9_9POTV	Q80mm9 papaya ring
591	40.5	47.1	581	2	Q8EC82_SHEON	Q8ec82 shewanella
592	40	46.5	88	2	Q7P2T0_FUSNV	Q7p2t0 fusobacteri
593	40	46.5	112	2	Q5R1H2_MOUSE	Q5r1h2 mus musculu
594	40	46.5	120	1	HV3U_HUMAN	P01782 homo sapien
595	40	46.5	127	2	Q925S9_MOUSE	Q925s9 mus musculu
596	40	46.5	130	1	KV5G_MOUSE	P01639 mus musculu
597	40	46.5	133	2	Q8UV48_BRARE	Q8uv48 brachydanio
598	40	46.5	139	1	TVA2_HUMAN	P04437 homo sapien
599	40	46.5	142	2	Q924Q2_MOUSE	Q924q2 mus musculu
600	40	46.5	157	2	Q7Y2B5_BPR69	Q7y2b5 bacteriopha
601	40	46.5	178	2	Q6R4N4_PIG	Q6r4n4 sus scrofa
602	40	46.5	179	2	Q715C6_9POTV	Q715c6 papaya ring
603	40	46.5	192	2	Q86M72_HETGL	Q86m72 heterodera
604	40	46.5	195	2	Q6R2U9_PIG	Q6r2u9 sus scrofa
605	40	46.5	223	2	Q8AW68_BRARE	Q8aw68 brachydanio
606	40	46.5	223	2	Q8UV47_BRARE	Q8uv47 brachydanio
607	40	46.5	223	2	Q8UVA3_BRARE	Q8uva3 brachydanio
608	40	46.5	230	2	Q801W9_BRARE	Q801w9 brachydanio
609	40	46.5	230	2	Q8UV30_BRARE	Q8uv30 brachydanio
610	40	46.5	230	2	Q8UV76_BRARE	Q8uv76 brachydanio
611	40	46.5	230	2	Q90Z86_BRARE	Q90z86 brachydanio
612	40	46.5	230	2	Q5SNP6_BRARE	Q5snp6 brachydanio
613	40	46.5	236	2	Q6GYR4_PIG	Q6gyr4 sus scrofa
614	40	46.5	243	2	Q83EK4_COXBU	Q83ek4 coxiella bu
615	40	46.5	244	2	Q8UWL0_ICTPU	Q8uwl0 ictalurus p
616	40	46.5	263	2	Q8KHF5_PSEAE	Q8khf5 pseudomonas
617	40	46.5	275	2	Q8KHA8_PSEAE	Q8kha8 pseudomonas
618	40	46.5	275	2	Q8KIR3_PSEAE	Q8kir3 pseudomonas
619	40	46.5	278	2	Q6IPR8_HUMAN	Q6ipr8 homo sapien
620	40	46.5	281	2	Q8KHM9_PSEAE	Q8khm9 pseudomonas
621	40	46.5	281	2	Q8KI35_PSEAE	Q8ki35 pseudomonas
622	40	46.5	281	2	Q8KIP7_PSEAE	Q8kip7 pseudomonas
623	40	46.5	281	2	Q8KIQ4_PSEAE	Q8kiq4 pseudomonas
624	40	46.5	281	2	Q8KIU9_PSEAE	Q8kiu9 pseudomonas
625	40	46.5	282	2	Q8GGB3_PSEAE	Q8ggb3 pseudomonas
626	40	46.5	282	2	Q8GGC0_PSEAE	Q8ggc0 pseudomonas
627	40	46.5	292	2	Q66I72_BRARE	Q66i72 brachydanio
628	40	46.5	296	2	Q61DM8_CAEBR	Q61dm8 caenorhabdi
629	40	46.5	310	2	Q7N385_PHOLL	Q7n385 photorhabdu
630	40	46.5	322	2	Q5NRG8_ZYMMO	Q5nrg8 zymomonas m
631	40	46.5	353	2	O62197_CAEEL	O62197 caenorhabdi
632	40	46.5	357	2	Q73ZC7_MYCPA	Q73zc7 mycobacteri
633	40	46.5	358	2	Q5JZR3_9POTV	Q5jzr3 papaya ring
634	40	46.5	358	2	Q5JZS2_9POTV	Q5jzs2 papaya ring
635	40	46.5	358	2	Q5JZS6_9POTV	Q5jzs6 papaya ring
636	40	46.5	372	2	Q88HC0_PSEPK	Q88hc0 pseudomonas
637	40	46.5	381	1	CENA2_MOUSE	Q8r2v5 mus musculu
638	40	46.5	381	2	Q5SSK2_MOUSE	Q5ssk2 mus musculu
639	40	46.5	381	2	Q9WGB4_9POTV	Q9wgb4 papaya ring
640	40	46.5	389	2	Q6DBQ9_BRARE	Q6dbq9 brachydanio
641	40	46.5	404	2	Q51NZ5_MAGGR	Q51nz5 magnaporthe
642	40	46.5	415	2	Q4JVN7_CORJK	Q4jvn7 corynebacte
643	40	46.5	415	2	Q69ZB3_MOUSE	Q69zb3 mus musculu
644	40	46.5	425	2	Q8H4S4_ORYSA	Q8h4s4 oryza sativ
645	40	46.5	434	2	Q4SMC5_TETNG	Q4smc5 tetraodon n
646	40	46.5	461	2	Q9HWU0_PSEAE	Q9hwu0 pseudomonas
647	40	46.5	462	2	Q5F8W0_NEIG1	Q5f8w0 neisseria g
648	40	46.5	462	2	Q9JYY7_NEIMB	Q9jyy7 neisseria m
649	40	46.5	462	2	Q9JTY3_NEIMA	Q9jty3 neisseria m
650	40	46.5	462	2	Q5RI00_BRARE	Q5ri00 brachydanio
651	40	46.5	465	2	Q6R7C4_9HERP	Q6r7c4 ostreid her
652	40	46.5	480	2	Q8K0Z4_MOUSE	Q8k0z4 mus musculu
653	40	46.5	493	2	Q5D7Q5_9POTV	Q5d7q5 papaya ring
654	40	46.5	498	2	Q524P4_MAGGR	Q524p4 magnaporthe
655	40	46.5	517	2	Q4VYE9_9POTV	Q4vye9 papaya ring
656	40	46.5	526	2	Q620C8_CAEBR	Q620c8 caenorhabdi
657	40	46.5	570	2	Q5BJ31_BRARE	Q5bj31 brachydanio
658	40	46.5	575	1	VG05_BPT4	P16009 bacteriopha
659	40	46.5	590	2	Q5BG25_EMENI	Q5bg25 aspergillus
660	40	46.5	608	2	Q9Y027_TRYCR	Q9y027 trypanosoma
661	40	46.5	658	1	SYDM_YEAST	P15179 saccharomyc
662	40	46.5	665	2	P72145_PSEAE	P72145 pseudomonas
663	40	46.5	665	2	Q7X3T1_PSEAE	Q7x3t1 pseudomonas
664	40	46.5	665	2	Q9RHC7_PSEAE	Q9rhc7 pseudomonas
665	40	46.5	665	2	Q9HZ86_PSEAE	Q9hz86 pseudomonas
666	40	46.5	720	2	Q8FK38_ECOL6	Q8fk38 escherichia
667	40	46.5	734	2	Q6JC00_9VIRU	Q6jc00 adeno-assoc
668	40	46.5	745	1	NFRB_ECOLI	P31599 escherichia
669	40	46.5	745	2	Q83M21_SHIFL	Q83m21 shigella fl
670	40	46.5	754	1	MBP1_KLULA	P39679 kluyveromyc
671	40	46.5	754	2	Q5SVH2_HUMAN	Q5svh2 homo sapien
672	40	46.5	773	2	Q8IG87_DROME	Q8ig87 drosophila
673	40	46.5	988	2	Q5L6K1_CHLAB	Q5l6k1 chlamydophi
674	40	46.5	1374	2	Q4IU91_AZOVI	Q4iu91 azotobacter
675	40	46.5	1483	2	Q5SVH3_HUMAN	Q5svh3 homo sapien
676	40	46.5	1784	2	Q9VE54_DROME	Q9ve54 drosophila
677	40	46.5	1830	2	Q5VUY9_HUMAN	Q5vuy9 homo sapien
678	40	46.5	1836	2	Q8IVL2_HUMAN	Q8ivl2 homo sapien
679	40	46.5	1877	2	Q5SVH7_HUMAN	Q5svh7 homo sapien
680	40	46.5	1877	2	Q8NEY1_HUMAN	Q8ney1 homo sapien
681	40	46.5	2385	2	Q4MU45_BACCE	Q4mu45 bacillus ce
682	40	46.5	2420	2	Q96UQ6_ASPFU	Q96uq6 aspergillus
683	40	46.5	2420	2	Q4WFV3_ASPFU	Q4wfv3 aspergillus
684	40	46.5	2552	2	Q4IDL4_GIBZE	Q4idl4 gibberella
685	40	46.5	2838	2	Q8MP05_TENMO	Q8mp05 tenebrio mo
686	40	46.5	5005	2	Q9PPZ5_UREPA	Q9ppz5 ureaplasma
687	39.5	45.9	217	2	Q4PKG1_9BACT	Q4pkg1 uncultured
688	39.5	45.9	250	2	Q88VP5_LACPL	Q88vp5 lactobacill

689	39.5	45.9	288	2	Q5B4W5_EMENI	Q5b4w5	aspergillus
690	39.5	45.9	339	2	Q7VZM9_BORPE	Q7vzm9	bordetella
691	39.5	45.9	339	2	Q7W7N2_BORPA	Q7w7n2	bordetella
692	39.5	45.9	339	2	Q7WL20_BORBR	Q7wl20	bordetella
693	39.5	45.9	353	2	Q4RDK9_TETNG	Q4rdk9	tetraodon n
694	39.5	45.9	573	2	Q897F9_CLOTE	Q897f9	clostridium
695	39.5	45.9	3270	2	Q7N1E2_PHOLL	Q7n1e2	photorhabdu
696	39.5	45.9	3898	2	Q918S9_9FLAV	Q918s9	classical s
697	39	45.3	75	2	Q9AKG7_RICRI	Q9akg7	rickettsia
698	39	45.3	97	2	O43234_HUMAN	O43234	homo sapien
699	39	45.3	112	2	Q5R1D6_MOUSE	Q5r1d6	mus musculu
700	39	45.3	117	2	Q7ZZ67_BRARE	Q7zz67	brachydanio
701	39	45.3	117	2	Q7ZZ68_BRARE	Q7zz68	brachydanio
702	39	45.3	117	2	Q78AP1_BRARE	Q78ap1	brachydanio
703	39	45.3	118	2	Q7ZZ69_BRARE	Q7zz69	brachydanio
704	39	45.3	118	2	Q7ZZ98_BRARE	Q7zz98	brachydanio
705	39	45.3	120	2	Q715C3_9POTV	Q715c3	papaya ring
706	39	45.3	127	2	Q9D3G4_MOUSE	Q9d3g4	mus musculu
707	39	45.3	128	2	Q88IP5_PSEPK	Q88ip5	pseudomonas
708	39	45.3	128	2	Q5R1A2_MOUSE	Q5r1a2	mus musculu
709	39	45.3	130	1	TVB8_MOUSE	P06321	mus musculu
710	39	45.3	132	1	TVC3_MOUSE	P06324	mus musculu
711	39	45.3	133	1	TVB2_MOUSE	P01735	mus musculu
712	39	45.3	135	1	TVC1_MOUSE	P01740	mus musculu
713	39	45.3	138	2	Q6Y855_9POTV	Q6y855	papaya ring
714	39	45.3	140	2	Q9L5K9_SALTI	Q915k9	salmonella
715	39	45.3	141	2	Q8NA04_HUMAN	Q8na04	homo sapien
716	39	45.3	145	2	Q5CMF5_CRYHO	Q5cmf5	cryptospori
717	39	45.3	158	2	Q4KLG4_RAT	Q4klg4	rattus norv
718	39	45.3	160	2	Q8L3Y6_ORYSA	Q8l3y6	oryza sativ
719	39	45.3	162	2	Q5CSF1_CRYPV	Q5csf1	cryptospori
720	39	45.3	164	1	LYS_BPT4	P00720	bacteriopha
721	39	45.3	164	2	Q7M2A4_BPT2	Q7m2a4	bacteriopha
722	39	45.3	167	2	Q5WBD0_BACSK	Q5wbd0	bacillus cl
723	39	45.3	179	2	Q715C5_9POTV	Q715c5	papaya ring
724	39	45.3	180	2	Q715C4_9POTV	Q715c4	papaya ring
725	39	45.3	184	2	Q715C2_9POTV	Q715c2	papaya ring
726	39	45.3	198	2	Q7BV95_BACSU	Q7bv95	bacillus su
727	39	45.3	203	2	Q55581_SYNY3	Q55581	synechocyst
728	39	45.3	208	2	Q8UV39_BRARE	Q8uv39	brachydanio
729	39	45.3	213	2	O11877_9BROM	O11877	elm mottle
730	39	45.3	213	2	Q77P79_9BROM	Q77p79	hydrangea m
731	39	45.3	213	2	Q98703_9BROM	Q98703	elm mottle
732	39	45.3	214	2	Q71YW2_LISMF	Q71yw2	listeria mo
733	39	45.3	214	2	Q8Y6H9_LISMO	Q8y6h9	listeria mo
734	39	45.3	214	2	Q92AV2_LISIN	Q92av2	listeria in
735	39	45.3	217	2	Q66274_9BROM	Q66274	citrus vari
736	39	45.3	217	2	Q8V320_9BROM	Q8v320	citrus vari
737	39	45.3	217	2	Q8V321_9BROM	Q8v321	citrus vari
738	39	45.3	217	2	Q8V322_9BROM	Q8v322	citrus vari
739	39	45.3	217	2	Q8V323_9BROM	Q8v323	citrus vari
740	39	45.3	217	2	Q8V324_9BROM	Q8v324	citrus vari
741	39	45.3	217	2	Q8V325_9BROM	Q8v325	citrus vari
742	39	45.3	217	2	Q8V326_9BROM	Q8v326	citrus vari
743	39	45.3	217	2	Q8V327_9BROM	Q8v327	citrus vari
744	39	45.3	217	2	Q8V328_9BROM	Q8v328	citrus vari
745	39	45.3	217	2	Q8V329_9BROM	Q8v329	citrus vari
746	39	45.3	229	1	Y544_METJA	Q57964	methanococc
747	39	45.3	237	2	Q5VTN5_BRARE	Q5vtn5	brachydanio
748	39	45.3	239	2	Q53KG6_ORYSA	Q53kg6	oryza sativ
749	39	45.3	242	2	Q529L2_MAGGR	Q529l2	magnaporthe
750	39	45.3	242	2	Q9UG10_HUMAN	Q9ug10	homo sapien
751	39	45.3	250	2	Q4N193_THEPA	Q4n193	theileria p
752	39	45.3	251	2	Q8S6Z7_ORYSA	Q8s6z7	oryza sativ
753	39	45.3	255	2	Q9JIS2_MOUSE	Q9jis2	mus musculu
754	39	45.3	255	2	Q9Z0M1_MOUSE	Q9z0m1	mus musculu
755	39	45.3	256	2	Q68ES0_XENTR	Q68es0	xenopus tro
756	39	45.3	264	2	Q9DKT6_9POTV	Q9dkt6	papaya ring
757	39	45.3	268	2	Q569A8_RAT	Q569a8	rattus norv
758	39	45.3	270	2	Q8KIQ8_PSEAE	Q8kiq8	pseudomonas
759	39	45.3	270	2	Q8KIS0_PSEAE	Q8kis0	pseudomonas
760	39	45.3	270	2	Q8KIU7_PSEAE	Q8kiu7	pseudomonas
761	39	45.3	274	2	Q7NN65_GLOVI	Q7nn65	gloeobacter
762	39	45.3	281	2	Q8KIT8_PSEAE	Q8kit8	pseudomonas
763	39	45.3	287	2	Q5VTP2_BRARE	Q5vtp2	brachydanio
764	39	45.3	296	2	Q4FTL8_9GAMM	Q4ftl8	psychrobact
765	39	45.3	300	2	Q8PQ65_XANAC	Q8pq65	xanthomonas
766	39	45.3	303	2	Q7TND8_MOUSE	Q7tnd8	mus musculu
767	39	45.3	308	2	Q8UUG3_ICTPU	Q8uug3	ictalurus p
768	39	45.3	318	2	Q9IB03_9PERC	Q9ib03	sphoeroides
769	39	45.3	326	2	Q5SYA6_BRARE	Q5sya6	brachydanio
770	39	45.3	331	2	Q9IB07_9PERC	Q9ib07	sphoeroides
771	39	45.3	337	2	Q9IAZ4_9PERC	Q9iaz4	sphoeroides
772	39	45.3	338	2	Q8A0K7_BACTN	Q8a0k7	bacteroides
773	39	45.3	342	2	Q9IB00_9PERC	Q9ib00	sphoeroides
774	39	45.3	352	1	COFG_METMP	Q6lyv9	methanococc
775	39	45.3	353	2	Q9UJX9_HUMAN	Q9ujx9	homo sapien
776	39	45.3	353	2	Q8WUA8_HUMAN	Q8wua8	homo sapien
777	39	45.3	358	2	Q5JZR4_9POTV	Q5jzr4	papaya ring
778	39	45.3	358	2	Q5JZR5_9POTV	Q5jzr5	papaya ring
779	39	45.3	358	2	Q5JZR7_9POTV	Q5jzr7	papaya ring
780	39	45.3	358	2	Q5JZR8_9POTV	Q5jzr8	papaya ring
781	39	45.3	358	2	Q5JZS1_9POTV	Q5jzs1	papaya ring
782	39	45.3	358	2	Q5JZS3_9POTV	Q5jzs3	papaya ring
783	39	45.3	358	2	Q5JZS4_9POTV	Q5jzs4	papaya ring
784	39	45.3	358	2	Q5JZS7_9POTV	Q5jzs7	papaya ring
785	39	45.3	362	2	Q9IPP4_9POTV	Q9ipp4	papaya ring
786	39	45.3	362	2	Q9IPP7_9POTV	Q9ipp7	papaya ring
787	39	45.3	364	2	Q5LMB6_SILPO	Q5lmb6	silicibacte
788	39	45.3	366	1	YKK3_CAEEL	P34280	caenorhabdi
789	39	45.3	366	2	Q60IX6_CAEBR	Q60ix6	caenorhabdi
790	39	45.3	369	2	Q89GJ5_BRAJA	Q89gj5	bradyrhizob
791	39	45.3	375	1	LYS1_EMENI	Q870g1	emericella
792	39	45.3	377	2	Q63YX6_BURPS	Q63yx6	burkholderi
793	39	45.3	410	2	Q4HST9_CAMUP	Q4hst9	campylobact
794	39	45.3	420	2	O30227_ARCFU	O30227	archaeoglob
795	39	45.3	422	2	Q5XQA7_9ARCH	Q5xqa7	uncultured
796	39	45.3	441	2	Q4UY33_XANCP	Q4uy33	xanthomonas
797	39	45.3	441	2	Q8P5S9_XANCP	Q8p5s9	xanthomonas
798	39	45.3	441	2	Q8PH57_XANAC	Q8ph57	xanthomonas
799	39	45.3	448	2	Q745B7_MYCPA	Q745b7	mycobacteri
800	39	45.3	450	2	Q7SAQ9_NEUCR	Q7saq9	neurospora
801	39	45.3	484	2	Q65E96_BACLD	Q65e96	bacillus li
802	39	45.3	487	2	Q5BK15_RAT	Q5bk15	rattus norv
803	39	45.3	499	2	Q7SZQ3_BRARE	Q7szq3	brachydanio
804	39	45.3	503	2	Q5QPZ5_WHEAT	Q5qpz5	triticum ae
805	39	45.3	517	2	O89956_9POTV	O89956	papaya ring
806	39	45.3	518	2	O89957_9POTV	O89957	papaya ring
807	39	45.3	532	2	Q91HP0_9POTV	Q91hp0	papaya ring
808	39	45.3	532	2	Q91HP2_9POTV	Q91hp2	papaya ring
809	39	45.3	532	2	Q91HP3_9POTV	Q91hp3	papaya ring
810	39	45.3	533	2	Q8QY60_9POTV	Q8qy60	papaya ring
811	39	45.3	546	2	Q69K02_ORYSA	Q69k02	oryza sativ
812	39	45.3	555	2	Q4J6Y9_SULAC	Q4j6y9	sulfolobus
813	39	45.3	555	2	Q7YZI1_MONBE	Q7yzi1	monosiga br
814	39	45.3	574	2	Q5MA20_TOBAC	Q5ma20	nicotiana t
815	39	45.3	582	2	Q4P903_USTMA	Q4p903	ustilago ma
816	39	45.3	608	2	Q9FFD4_ARATH	Q9ffd4	arabidopsis
817	39	45.3	612	2	Q4WZA3_ASPFU	Q4wza3	aspergillus
818	39	45.3	618	2	Q5B114_EMENI	Q5b114	aspergillus
819	39	45.3	626	2	Q6VQR2_ORYSA	Q6vqr2	oryza sativ
820	39	45.3	628	2	Q619E9_CAEBR	Q619e9	caenorhabdi
821	39	45.3	637	2	Q6W5F5_ORYSA	Q6w5f5	oryza sativ
822	39	45.3	644	2	Q55VS9_CRYNE	Q55vs9	cryptococcu
823	39	45.3	644	2	Q5KKG0_CRYNE	Q5kkg0	cryptococcu
824	39	45.3	649	2	Q6W5F4_ORYSA	Q6w5f4	oryza sativ
825	39	45.3	653	2	Q9VBW7_DROME	Q9vbw7	drosophila
826	39	45.3	657	2	Q4WUJ0_ASPFU	Q4wuj0	aspergillus
827	39	45.3	665	2	P95428_PSEAE	P95428	pseudomonas
828	39	45.3	665	2	Q9KIC5_PSEAE	Q9kic5	pseudomonas
829	39	45.3	675	1	POLG_PRSVP	P19723	papaya ring
830	39	45.3	675	1	POLG_PRSVW	P19724	papaya ring
831	39	45.3	677	2	Q7Q5R7_ANOGA	Q7q5r7	anopheles g
832	39	45.3	680	1	DCP_ECOLI	P24171	escherichia
833	39	45.3	700	2	Q8WS94_CAEEL	Q8ws94	caenorhabdi
834	39	45.3	700	2	O62299_CAEEL	O62299	caenorhabdi

835	39	45.3	705	2	Q9H624_HUMAN	Q9h624	homo sapien
836	39	45.3	714	2	Q5AKL3_CANAL	Q5akl3	candida alb
837	39	45.3	714	2	Q5AK51_CANAL	Q5ak51	candida alb
838	39	45.3	715	2	Q7YY38_CRYPV	Q7yy38	cryptospori
839	39	45.3	716	2	Q58AC2_9BURK	Q58ac2	ralstonia m
840	39	45.3	716	2	Q82YF1_STRAW	Q82yf1	streptomyce
841	39	45.3	738	2	Q6K271_ORYSA	Q6k271	oryza sativ
842	39	45.3	738	2	Q6WQT6_ORYSA	Q6wqt6	oryza sativ
843	39	45.3	766	2	Q96UC7_NEUCR	Q96uc7	neurospora
844	39	45.3	791	2	Q66H54_RAT	Q66h54	rattus norv
845	39	45.3	854	2	Q8HZV9_9PRIM	Q8hzv9	gorilla gor
846	39	45.3	854	2	Q8HZW0_PANTR	Q8hzw0	pan troglod
847	39	45.3	862	1	CUTL1_RAT	P53565	rattus norv
848	39	45.3	886	2	Q8VDK9_MOUSE	Q8vdk9	mus musculu
849	39	45.3	897	2	Q4V516_DROME	Q4v516	drosophila
850	39	45.3	917	2	Q85029_9POTV	Q85029	papaya ring
851	39	45.3	920	2	Q80T93_MOUSE	Q80t93	mus musculu
852	39	45.3	923	2	Q8HZV5_MACFA	Q8hzv5	macaca fasc
853	39	45.3	923	2	Q8HZV6_PAPCY	Q8hzv6	papio cynoc
854	39	45.3	923	2	Q8HZV7_HYLLA	Q8hzv7	hylobates l
855	39	45.3	931	2	Q8HZV8_PONPY	Q8hzv8	pongo pygma
856	39	45.3	935	2	Q811J6_MOUSE	Q811j6	mus musculu
857	39	45.3	958	2	Q5GIA5_BACHD	Q5gia5	bacillus ha
858	39	45.3	958	2	Q9KFR4_BACHD	Q9kfr4	bacillus ha
859	39	45.3	972	2	Q8N612_HUMAN	Q8n612	homo sapien
860	39	45.3	972	2	Q5R8V2_PONPY	Q5r8v2	pongo pygma
861	39	45.3	975	1	CUTL1_CANFA	P39881	canis famil
862	39	45.3	975	2	Q6P543_MOUSE	Q6p543	mus musculu
863	39	45.3	982	2	Q5YYB5_NOCFA	Q5yyb5	nocardia fa
864	39	45.3	983	2	Q9C0A4_HUMAN	Q9c0a4	homo sapien
865	39	45.3	986	2	Q9H0N3_HUMAN	Q9h0n3	homo sapien
866	39	45.3	1026	2	Q5B9A7_EMENI	Q5b9a7	aspergillus
867	39	45.3	1040	2	Q4Q6W0_LEIMA	Q4q6w0	leishmania
868	39	45.3	1040	2	Q4NGY1_9MICC	Q4ngy1	arthrobacte
869	39	45.3	1098	2	Q4S024_TETNG	Q4s024	tetraodon n
870	39	45.3	1131	2	Q759C0_ASHGO	Q759c0	ashbya goss
871	39	45.3	1144	2	Q9HGS8_NEUCR	Q9hgs8	neurospora
872	39	45.3	1151	2	Q9CAP6_ARATH	Q9cap6	arabidopsis
873	39	45.3	1183	2	Q4SPL9_TETNG	Q4spl9	tetraodon n
874	39	45.3	1194	1	DPOL_VZVD	P09252	varicella-z
875	39	45.3	1194	2	Q6QCM7_HHV3	Q6qcm7	human herpe
876	39	45.3	1194	2	Q997M7_HHV3	Q997m7	human herpe
877	39	45.3	1194	2	Q997M8_HHV3	Q997m8	human herpe
878	39	45.3	1194	2	Q997M9_HHV3	Q997m9	human herpe
879	39	45.3	1194	2	Q997N0_HHV3	Q997n0	human herpe
880	39	45.3	1238	2	Q73Q63_TREDE	Q73q63	treponema d
881	39	45.3	1291	2	Q80UV9_MOUSE	Q80uv9	mus musculu
882	39	45.3	1303	2	Q4ZPR1_PSESY	Q4zpr1	pseudomonas
883	39	45.3	1395	1	CUTL1_MOUSE	P53564	mus musculu
884	39	45.3	1426	2	Q5BL05_MOUSE	Q5bl05	mus musculu
885	39	45.3	1497	2	Q7XG34_ORYSA	Q7xg34	oryza sativ
886	39	45.3	1497	2	Q94I18_ORYSA	Q94i18	oryza sativ
887	39	45.3	1505	1	CUTL1_HUMAN	P39880	homo sapien
888	39	45.3	1506	2	Q571L6_MOUSE	Q57116	mus musculu
889	39	45.3	1516	2	Q6NYH4_HUMAN	Q6nyh4	homo sapien
890	39	45.3	1517	2	Q91ZD2_MOUSE	Q91zd2	mus musculu
891	39	45.3	1826	1	TAF1L_HUMAN	Q8izx4	homo sapien
892	39	45.3	1865	2	Q60544_MESAU	Q60544	mesocricetu
893	39	45.3	1872	1	TAF1_HUMAN	P21675	homo sapien
894	39	45.3	1949	2	Q4S8V9_TETNG	Q4s8v9	tetraodon n
895	39	45.3	2075	2	Q4NRA4_9DELT	Q4nra4	anaeromyxob
896	39	45.3	2387	2	Q5B0P5_EMENI	Q5b0p5	aspergillus
897	39	45.3	3343	2	Q91HK6_PRSVW	Q91hk6	papaya ring
898	39	45.3	3344	1	POLG_PRSVH	Q01901	p genome po
899	39	45.3	3344	2	P90213_9POTV	P90213	papaya ring
900	39	45.3	3346	2	Q98WK5_PRSVW	Q98wk5	papaya ring
901	39	45.3	5579	2	Q5Z1X6_NOCFA	Q5z1x6	nocardia fa
902	38.5	44.8	159	2	Q8WXD6_HUMAN	Q8wxd6	homo sapien
903	38.5	44.8	246	1	DCHM_BPT2	P18029	bacteriopha
904	38.5	44.8	246	1	DCHM_BPT4	P08773	bacteriopha
905	38.5	44.8	246	1	DCHM_BPT6	P18030	bacteriopha
906	38.5	44.8	246	2	Q9S2R0_STRCO	Q9s2r0	streptomyce
907	38.5	44.8	257	2	Q5K9Q1_CRYNE	Q5k9q1	cryptococcu
908	38.5	44.8	368	2	Q9GYR9_CAEEL	Q9gyr9	caenorhabdi
909	38.5	44.8	510	2	Q5LJ17_BACFN	Q5lj17	bacteroides
910	38.5	44.8	526	2	Q650K5_BACFR	Q650k5	bacteroides
911	38.5	44.8	561	2	Q6F1Z7_MESFL	Q6f1z7	mesoplasma
912	38.5	44.8	733	2	Q808X8_9VIRU	Q808x8	non-human p
913	38.5	44.8	789	1	LSP1B_DROME	P11996	drosophila
914	38.5	44.8	852	2	Q73KW3_TREDE	Q73kw3	treponema d
915	38.5	44.8	2291	2	Q55JU9_CRYNE	Q55ju9	cryptococcu
916	38	44.2	55	1	CALU_CAVPO	P22075	cavia porce
917	38	44.2	76	2	Q91VF8_CAVPO	Q91vf8	cavia porce
918	38	44.2	98	2	Q7TLZ4_9ZZZZ	Q7tlz4	uncultured
919	38	44.2	99	2	Q601F2_MYCHY	Q601f2	mycoplasma
920	38	44.2	100	2	Q72TA1_LEPIC	Q72ta1	leptospira
921	38	44.2	100	2	Q8F236_LEPIN	Q8f236	leptospira
922	38	44.2	100	2	Q7TM48_9ZZZZ	Q7tm48	uncultured
923	38	44.2	110	2	Q5R1B4_MOUSE	Q5r1b4	mus musculu
924	38	44.2	114	2	Q5R1B0_MOUSE	Q5r1b0	mus musculu
925	38	44.2	116	1	RL34_ICTPU	Q90yt5	ictalurus p
926	38	44.2	120	1	TVB3_MOUSE	P01736	mus musculu
927	38	44.2	121	2	Q9UL96_HUMAN	Q9ul96	homo sapien
928	38	44.2	128	2	Q5W2T1_SULIS	Q5w2t1	sulfolobus
929	38	44.2	135	2	Q821G7_CHLCV	Q821g7	chlamydophi
930	38	44.2	149	2	Q64UL7_BACFR	Q64ul7	bacteroides
931	38	44.2	151	2	Q77ZJ5_HPV16	Q77zj5	human papil
932	38	44.2	151	2	Q89648_9PAPI	Q89648	human papil
933	38	44.2	160	2	Q9VKA2_DROME	Q9vka2	drosophila
934	38	44.2	163	2	Q4HUN9_GIBZE	Q4hun9	gibberella
935	38	44.2	166	2	Q9M4T9_WHEAT	Q9m4t9	triticum ae
936	38	44.2	169	2	Q4QPV4_DROME	Q4qpv4	drosophila
937	38	44.2	170	2	Q81CF9_BACCR	Q81cf9	bacillus ce
938	38	44.2	177	2	Q6DDL3_XENLA	Q6ddl3	xenopus lae
939	38	44.2	179	1	UCRI_RHOVI	P81380	rhodopseudo
940	38	44.2	182	2	Q7T2D3_BRARE	Q7t2d3	brachydanio
941	38	44.2	185	2	Q9P9R0_XYLFA	Q9p9r0	xylella fas
942	38	44.2	185	2	Q877T4_XYLFT	Q877t4	xylella fas
943	38	44.2	217	2	Q8V330_9BROM	Q8v330	citrus vari
944	38	44.2	217	2	Q8V331_9BROM	Q8v331	citrus vari
945	38	44.2	228	2	Q4H7R4_9DEIO	Q4h7r4	deinococcus
946	38	44.2	230	1	TREM2_HUMAN	Q9nzc2	homo sapien
947	38	44.2	230	2	Q5TCX1_HUMAN	Q5tcx1	homo sapien
948	38	44.2	230	2	Q9RXY3_DEIRA	Q9rxy3	deinococcus
949	38	44.2	232	2	Q8VY52_ARATH	Q8vy52	arabidopsis
950	38	44.2	236	1	STX8_HUMAN	Q9unk0	homo sapien
951	38	44.2	236	2	Q53XT8_HUMAN	Q53xt8	homo sapien
952	38	44.2	238	2	Q5XKI8_HUMAN	Q5xki8	homo sapien
953	38	44.2	238	2	Q7Z5X6_HUMAN	Q7z5x6	homo sapien
954	38	44.2	240	2	Q4ZRQ0_PSESY	Q4zrq0	pseudomonas
955	38	44.2	241	2	Q514X1_ENTHI	Q514x1	entamoeba h
956	38	44.2	245	2	Q6GNC5_XENLA	Q6gnc5	xenopus lae
957	38	44.2	248	2	Q7SYU1_XENLA	Q7syu1	xenopus lae
958	38	44.2	253	1	Y1424_MYCTU	P64851	mycobacteri
959	38	44.2	253	1	Y1459_MYCBO	P64852	mycobacteri
960	38	44.2	253	2	Q8MUG7_TAESO	Q8mug7	taenia soli
961	38	44.2	253	2	Q8MUH4_TAESO	Q8muh4	taenia soli
962	38	44.2	258	2	Q9XVM9_CAEEL	Q9xvm9	caenorhabdi
963	38	44.2	268	2	Q65ZL6_9MURI	Q65zl6	mus sp. t-c
964	38	44.2	268	2	Q5M790_XENTR	Q5m790	xenopus tro
965	38	44.2	273	2	Q5BAU8_EMENI	Q5bau8	aspergillus
966	38	44.2	277	2	Q9YH28_CHICK	Q9yh28	gallus gall
967	38	44.2	282	2	Q7ZYB6_XENLA	Q7zyb6	xenopus lae
968	38	44.2	289	2	Q4WNX7_ASPFU	Q4wnx7	aspergillus
969	38	44.2	290	2	Q9YHT2_CHICK	Q9yht2	gallus gall
970	38	44.2	291	2	O28428_ARCFU	O28428	archaeoglob
971	38	44.2	292	2	P73680_SYNY3	P73680	synechocyst
972	38	44.2	304	2	Q839Q7_ENTFA	Q839q7	enterococcu
973	38	44.2	306	2	Q4TNI9_9SPHN	Q4tni9	erythrobact
974	38	44.2	310	2	Q8VGN9_MOUSE	Q8vgn9	mus musculu
975	38	44.2	323	2	Q4HUM1_GIBZE	Q4hum1	gibberella
976	38	44.2	329	1	HEM2_MYCTU	O33357	mycobacteri
977	38	44.2	329	2	Q7U1W0_MYCBO	Q7u1w0	mycobacteri
978	38	44.2	336	2	Q4RFX8_TETNG	Q4rfx8	tetraodon n
979	38	44.2	342	2	Q7U156_MYCBO	Q7u156	mycobacteri
980	38	44.2	342	2	O53849_MYCTU	O53849	mycobacteri

981	38	44.2	342	2	Q8AXL4_ONCMY	Q8axl4 oncorhynchu
982	38	44.2	347	2	Q9VV41_DROME	Q9vv41 drosophila
983	38	44.2	355	2	Q5JZS0_9POTV	Q5jzs0 papaya ring
984	38	44.2	357	2	Q5AX82_EMENI	Q5ax82 aspergillus
985	38	44.2	358	2	Q5JZR9_9POTV	Q5jzr9 papaya ring
986	38	44.2	365	2	Q6NSR1_MOUSE	Q6nsr1 mus musculu
987	38	44.2	375	2	Q9JUV0_NEIMA	Q9juv0 neisseria m
988	38	44.2	396	2	Q5TVJ4_ANOGA	Q5tvj4 anopheles g
989	38	44.2	398	2	Q5F848_NEIG1	Q5f848 neisseria g
990	38	44.2	398	2	Q9JZR5_NEIMB	Q9jzr5 neisseria m
991	38	44.2	398	2	Q7TNS9_MOUSE	Q7tns9 mus musculu
992	38	44.2	401	2	Q5XJE3_MOUSE	Q5xje3 mus musculu
993	38	44.2	404	2	Q8BGL1_MOUSE	Q8bgl1 m mus muscu
994	38	44.2	407	2	Q5UR52_MIMIV	Q5ur52 mimivirus.
995	38	44.2	420	1	SYS_MYCGA	Q7nad6 mycoplasma
996	38	44.2	426	2	Q5ARB9_EMENI	Q5arb9 aspergillus
997	38	44.2	432	1	SYS_BUCBP	P59553 buchnera ap
998	38	44.2	442	2	Q64DE7_9ARCH	Q64de7 uncultured
999	38	44.2	448	2	Q6CED2_YARLI	Q6ced2 yarrowia li
1000	38	44.2	452	2	Q5XCZ7_STRP6	Q5xcz7 streptococc

ALIGNMENTS

```
RESULT 1
Q96SA9_HUMAN
ID   Q96SA9_HUMAN PRELIMINARY;      PRT;   107 AA.
AC   Q96SA9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
DE   variable region (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98375893; PubMed=9712075;
RA   Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT   "Molecular analysis of polyreactive monoclonal antibodies from
RT   rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT   antibody V region genes.";
RL   J. Immunol. 161:2020-2031(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1516616;
RA   Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT   "Human monoclonal striational autoantibodies isolated from thymic B
RT   lymphocytes of patients with myasthenia gravis use VH and VL gene
RT   segments associated with the autoimmune repertoire.";
RL   Eur. J. Immunol. 22:2231-2236(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=8436174;
RA   Wagner S.D., Luzzatto L.;
RT   "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT   distributed over a large portion of the V kappa locus and do not show
RT   somatic mutation.";
RL   Eur. J. Immunol. 23:391-397(1993).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1660528;
RA   Manheimer-Lory A., Katz J.B., Pillinger M., Ghossein C., Smith A.,
RA   Diamond B.;
RT   "Molecular characteristics of antibodies bearing an anti-DNA-
RT   associated idiotype.";
RL   J. Exp. Med. 174:1639-1652(1991).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1903706;
RA   Blaison G., Kuntz J.L., Pasquali J.L.;
RT   "Molecular analysis of V kappa III variable regions of polyclonal
RT   rheumatoid factors during rheumatoid arthritis.";
RL   Eur. J. Immunol. 21:1221-1227(1991).
DR   EMBL; U96396; AAB68785.1; -; mRNA.
DR   PIR; B49047; B49047.
DR   PIR; PH0867; PH0867.
DR   PIR; S16840; S16840.
DR   PIR; S31977; S31977.
DR   PIR; S34083; S34083.
DR   PIR; S34086; S34086.
DR   HSSP; P01607; 1BWW.
DR   SMR; Q96SA9; 1-107.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11520 MW;  4BB43E9C5B577F16 CRC64;

  Query Match             100.0%;  Score 86;  DB 2;  Length 107;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 2
KV1B_HUMAN
ID   KV1B_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01594;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region AU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=72189444; PubMed=5028201;
RA   Schiechl H., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
RT   protein Au).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX   MEDLINE=77022433; PubMed=1234024;
RA   Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
RA   Schwager P., Steigemann W., Schramm H.J.;
RT   "The structure determination of the variable portion of the Bence-
RT   Jones protein Au.";
RL   Biophys. Struct. Mech. 1:139-146(1975).
CC   -!- MISCELLANEOUS: The structure of the V region was determined by
CC       molecular replacement methods using the known structure of the V
CC       region of the kappa chain REI.
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A91653; K1HUAU.
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DR   PDB; 1JV5; X-ray; A=1-107.
DR   Ensembl; ENSG00000173782; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin domain; Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
FT   STRAND        4      5
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       44     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       85     90
FT   STRAND       97     98
FT   STRAND      102    106
SQ   SEQUENCE   108 AA;  11939 MW;  E8011187EE6F6FB9 CRC64;

  Query Match             100.0%;  Score 86;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 3
KV1K_HUMAN
ID   KV1K_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01603;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Ka.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=76189985; PubMed=818073;
RA   Shinoda T.;
RT   "Comparative structural studies on the light chains of human
RT   immunoglobulins. I. Protein Ka with the Inv(3) allotypic marker.";
RL   J. Biochem. 77:1277-1296(1975).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A01869; K1HUKA.
DR   HSSP; P80362; 1WTL.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11900 MW;  768839FBED5A2F4B CRC64;

  Query Match             100.0%;  Score 86;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 4
KV1P_HUMAN
ID   KV1P_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01608;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Roy.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=68362076; PubMed=5595110;
RA   Hilschmann N.;
RT   "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT   Cum.).";
RL   Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN   [2]
RP   SEQUENCE REVISION TO 39 AND 41.
RA   Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA   Steinmetz-Kayne M., Suter L., Watanabe S.;
RL   (In) Franek F., Shugar D. (eds.);
RL   Gamma globulins: structure and function, pp.57-74, Academic Press, New
RL   York (1969).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC       marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
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CC   ----------------------------------------------------------------------
DR   PIR; A91638; K1HURY.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01608; 1-108.
DR   Ensembl; ENSG00000173782; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11782 MW;  F5ACEDE5A313DF3A CRC64;

  Query Match             100.0%;  Score 86;  DB 1;  Length 108;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 5
KV1J_HUMAN
ID   KV1J_HUMAN     STANDARD;      PRT;   117 AA.
AC   P01602;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region HK102 precursor (Fragment).
GN   Name=IGKV1-5;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=81098966; PubMed=6779204;
RA   Bentley D.L., Rabbitts T.H.;
RT   "Human immunoglobulin variable region genes -- DNA sequences of two V
RT   kappa genes and a pseudogene.";
RL   Nature 288:730-733(1980).
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; J00245; AAA59087.1; -; Genomic_DNA.
DR   EMBL; Z00001; CAA77292.1; -; Genomic_DNA.
DR   PIR; A01882; K1HU12.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01602; 23-117.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   HGNC; HGNC:5741; IGKV1-5.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23   >117       Ig kappa chain V-I region HK102.
FT   REGION       23     45       Framework-1.
FT   REGION       46     56       Complementarity-determining-1.
FT   REGION       57     71       Framework-2.
FT   REGION       72     78       Complementarity-determining-2.
FT   REGION       79    110       Framework-3.
FT   REGION      111   >117       Complementarity-determining-3.
FT   DISULFID     45    110       By similarity.
FT   NON_TER     117    117
SQ   SEQUENCE   117 AA;  12768 MW;  AD1DF3A40AF1A49B CRC64;

  Query Match             100.0%;  Score 86;  DB 1;  Length 117;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         57 WYQQKPGKAPKLLIY 71


RESULT 6
KV1W_HUMAN
ID   KV1W_HUMAN     STANDARD;      PRT;   129 AA.
AC   P04431;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Walker precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; X00965; CAA25477.1; ALT_TERM; Genomic_DNA.
DR   PIR; A01883; K1HUWK.
DR   HSSP; P01607; 1BWW.
DR   SMR; P04431; 23-129.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       Ig kappa chain V-I region Walker.
FT   REGION       23     45       Framework-1.
FT   REGION       46     56       Complementarity-determining-1.
FT   REGION       57     71       Framework-2.
FT   REGION       72     78       Complementarity-determining-2.
FT   REGION       79    110       Framework-3.
FT   REGION      111    119       Complementarity-determining-3.
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FT   REGION      120    129       Framework-4.
FT   DISULFID     45    110       By similarity.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14069 MW;  F941FA07D4AFC2F9 CRC64;

  Query Match            100.0%;  Score 86;  DB 1;  Length 129;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         57 WYQQKPGKAPKLLIY 71


RESULT 7
Q6PIH4_HUMAN
ID   Q6PIH4_HUMAN PRELIMINARY;      PRT;   236 AA.
AC   Q6PIH4;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034146; AAH34146.1; -; mRNA.
DR   HSSP; P01607; 1AR2.
DR   SMR; Q6PIH4; 23-236.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25871 MW;  BE01A28CD06EEE26 CRC64;

  Query Match            100.0%;  Score 86;  DB 2;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         57 WYQQKPGKAPKLLIY 71


RESULT 8
Q6GMX8_HUMAN
ID   Q6GMX8_HUMAN PRELIMINARY;      PRT;   236 AA.
AC   Q6GMX8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGKC protein.
GN   Name=IGKC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Primary B-Cells;
RG   NIH MGC Project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073764; AAH73764.1; -; mRNA.
DR   SMR; Q6GMX8; 24-235.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   236 AA;  25707 MW;  4FC8E14B6559EFC9 CRC64;

  Query Match            100.0%;  Score 86;  DB 2;  Length 236;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
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                ||||||||||||||||
Db          57 WYQQKPGKAPKLLIY 71


RESULT 9
Q6GMW1_HUMAN
ID   Q6GMW1_HUMAN PRELIMINARY;      PRT;   236 AA.
AC   Q6GMW1;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGKC protein.
GN   Name=IGKC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RG   NIH MGC Project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC073791; AAH73791.1; -; mRNA.
DR   SMR; Q6GMW1; 24-236.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ   SEQUENCE   236 AA;  25751 MW;  5BFE6A087AFAC437 CRC64;

  Query Match           100.0%;  Score 86;  DB 2;  Length 236;
  Best Local Similarity  100.0%;  Pred. No. 8.2e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         57 WYQQKPGKAPKLLIY 71


RESULT 10
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Q65ZC9_HUMAN
ID   Q65ZC9_HUMAN PRELIMINARY;      PRT;   240 AA.
AC   Q65ZC9;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Single-chain Fv (Fragment).
GN   Name=scFv;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C1q/7;
RX   MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA   Kontermann R.E., Wing M.G., Winter G.;
RT   "Complement recruitment using bispecific diabodies.";
RL   Nat. Biotechnol. 15:629-631(1997).
DR   EMBL; Y13056; CAA73499.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1       1
FT   NON_TER     240     240
SQ   SEQUENCE   240 AA;  25569 MW;  FDCFD3645F64B373 CRC64;

  Query Match           100.0%;  Score 86;  DB 2;  Length 240;
  Best Local Similarity  100.0%;  Pred. No. 8.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db        167 WYQQKPGKAPKLLIY 181


RESULT 11
KV1D_HUMAN
ID   KV1D_HUMAN     STANDARD;      PRT;   107 AA.
AC   P01596;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region CAR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=75075135; PubMed=4216454;
RA   Milstein C.P., Deverson E.V.;
RT   "Primary structure of kappa light chain from a human myeloma
RT   protein.";
RL   Eur. J. Biochem. 49:377-391(1974).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC       marker.
CC   -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A01864; K1HUAR.
DR   HSSP; P80362; 1WTL.
DR   SMR; P01596; 1-107.
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DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Glycoprotein; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   CARBOHYD     28     28       N-linked (GlcNAc. . .).
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11704 MW;  E1BF0DF9844C3346 CRC64;

  Query Match             96.5%;  Score 83;  DB 1;  Length 107;
  Best Local Similarity   93.3%;  Pred. No. 1.2e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||:|||
Db         35 WYQQKPGKAPKVLIY 49


RESULT 12
KV1F_HUMAN
ID   KV1F_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01598;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region EU.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=71064023; PubMed=5489770;
RA   Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. VI. Amino
RT   acid sequence of the light chain.";
RL   Biochemistry 9:3155-3161(1970).
RN   [2]
RP   DISULFIDE BOND.
RX   MEDLINE=71064027; PubMed=4923144;
RA   Gall W.E., Edelman G.M.;
RT   "The covalent structure of a human gamma G-immunoglobulin. X.
RT   Intrachain disulfide bonds.";
RL   Biochemistry 9:3188-3196(1970).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A90562; K1HUEU.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01598; 1-107.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION       1     23       Framework-1.
FT   REGION      24     34       Complementarity-determining-1.
FT   REGION      35     49       Framework-2.
FT   REGION      50     56       Complementarity-determining-2.
FT   REGION      57     88       Framework-3.
FT   REGION      89     97       Complementarity-determining-3.
FT   REGION      98    107       Framework-4.
FT   DISULFID    23     88
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;  11788 MW;  9CD294F2F4D88823 CRC64;

  Query Match             96.5%;  Score 83;  DB 1;  Length 108;
  Best Local Similarity   93.3%;  Pred. No. 1.2e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||:|
Db         35 WYQQKPGKAPKLLMY 49


RESULT 13
KV1C_HUMAN
ID   KV1C_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01595;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Bi.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=73029807; PubMed=4563064;
RA   Braun M., Leibold W., Barnikol H.U., Hilschmann N.;
RT   "Principle of antibody structure. The primary structure of a
RT   monoclonal kappa I-type immunoglobulin L-chain (Bence Jones protein
RT   Bi). 3. The complete amino acid sequence and the genetic significance
RT   of the variability principles for the mechanism of antibody
RT   formation.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:1284-1306(1972).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A01863; K1HUBI.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01595; 1-108.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION       1     23       Framework-1.
FT   REGION      24     34       Complementarity-determining-1.
FT   REGION      35     49       Framework-2.
FT   REGION      50     56       Complementarity-determining-2.
FT   REGION      57     88       Framework-3.
FT   REGION      89     97       Complementarity-determining-3.
FT   REGION      98    107       Framework-4.
FT   DISULFID    23     88       By similarity.
FT   NON_TER    108    108
SQ   SEQUENCE   108 AA;  12026 MW;  7A83983986A431E7 CRC64;
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  Query Match             95.3%;  Score 82;  DB 1;  Length 108;
  Best Local Similarity   93.3%;  Pred. No. 1.7e-05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||| |||
Db         35 WYQQKPGKAPKFLIY 49


RESULT 14
KV5Q_MOUSE
ID   KV5Q_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01650;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-V region UPC 61.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=79195288; PubMed=109517;
RA   Vrana M., Rudikoff S., Potter M.;
RT   "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
RL   J. Immunol. 122:1905-1910(1979).
CC   -!- MISCELLANEOUS: This chain was isolated from myeloma proteins that
CC       bind beta(2-1)-fructofuranosyl moieties (inulin).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A92808; KVMS61.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01650; 1-108.
DR   Ensembl; ENSMUSG00000050218; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11809 MW;  FAE4DA36076F2AFE CRC64;

  Query Match             95.3%;  Score 82;  DB 1;  Length 108;
  Best Local Similarity   93.3%;  Pred. No. 1.7e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |:|||||||||||||
Db         35 WFQQKPGKAPKLLIY 49


RESULT 15
KV5R_MOUSE
ID   KV5R_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01651;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-V region EPC 109.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=79195288; PubMed=109517;
RA   Vrana M., Rudikoff S., Potter M.;
RT   "The structural basis of a hapten-inhibitable kappa-chain idiotype.";
RL   J. Immunol. 122:1905-1910(1979).
CC   -!- MISCELLANEOUS: This chain was isolated from myeloma proteins that
CC       bind beta(2-1)-fructofuranosyl moieties (inulin).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; B92808; KVMS09.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01651; 1-108.
DR   Ensembl; ENSMUSG00000050218; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11876 MW;  35C116BD60F79310 CRC64;

  Query Match             95.3%;  Score 82;  DB 1;  Length 108;
  Best Local Similarity   93.3%;  Pred. No. 1.7e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |:|||||||||||||
Db         35 WFQQKPGKAPKLLIY 49


RESULT 16
KV5S_MOUSE
ID   KV5S_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01652;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-V region J606.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=82099361; PubMed=6798111;
RA   Johnson N., Slankard J., Paul L., Hood L.;
RT   "The complete V domain amino acid sequences of two myeloma inulin-
RT   binding proteins.";
RL   J. Immunol. 128:302-307(1982).
CC   -!- MISCELLANEOUS: This chain was isolated from myeloma proteins that
```

```
CC       bind beta(2-1)-fructofuranosyl moieties (inulin).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A92811; KVMS06.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01652; 1-108.
DR   Ensembl; ENSMUSG00000050218; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11810 MW;  8DE4DD31076F2AFB CRC64;

  Query Match             95.3%;  Score 82;  DB 1;  Length 108;
  Best Local Similarity   93.3%;  Pred. No. 1.7e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |:|||||||||||||
Db         35 WFQQKPGKAPKLLIY 49


RESULT 17
KV5T_MOUSE
ID   KV5T_MOUSE     STANDARD;      PRT;   108 AA.
AC   P01653;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-V region W3082.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=82099361; PubMed=6798111;
RA   Johnson N., Slankard J., Paul L., Hood L.;
RT   "The complete V domain amino acid sequences of two myeloma inulin-
RT   binding proteins.";
RL   J. Immunol. 128:302-307(1982).
CC   -!- MISCELLANEOUS: This chain was isolated from myeloma proteins that
CC       bind beta(2-1)-fructofuranosyl moieties (inulin).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; B92811; KVMS82.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01653; 1-108.
DR   Ensembl; ENSMUSG00000050218; Mus musculus.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11850 MW;  C5C145DC376F30CD CRC64;

  Query Match             95.3%;  Score 82;  DB 1;  Length 108;
  Best Local Similarity   93.3%;  Pred. No. 1.7e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |:|||||||||||||
Db         35 WFQQKPGKAPKLLIY 49


RESULT 18
Q9UL79_HUMAN
ID   Q9UL79_HUMAN PRELIMINARY;      PRT;   108 AA.
AC   Q9UL79;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1601042;
RA   Huber C., Klobeck H.G., Zachau H.G.;
RT   "Ongoing V kappa-J kappa recombination after formation of a productive
RT   V kappa-J kappa coding joint.";
RL   Eur. J. Immunol. 22:1561-1565(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=8436174;
RA   Wagner S.D., Luzzatto L.;
RT   "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT   distributed over a large portion of the V kappa locus and do not show
RT   somatic mutation.";
RL   Eur. J. Immunol. 23:391-397(1993).
DR   EMBL; AF035035; AAD56271.1; -; mRNA.
DR   PIR; S23638; S23638.
DR   PIR; S30521; S30521.
DR   PIR; S34090; S34090.
DR   HSSP; P01607; 1BWW.
DR   SMR; Q9UL79; 1-108.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
```

```
SQ   SEQUENCE   108 AA;  11787 MW;  DB5845F19724FB4E CRC64;

  Query Match             95.3%;  Score 82;  DB 2;  Length 108;
  Best Local Similarity   93.3%;  Pred. No. 1.7e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||:||||
Db         35 WYQQKPGKAPELLIY 49


RESULT 19
KV1T_HUMAN
ID   KV1T_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01612;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Mev.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=83081018; PubMed=6816713;
RA   Eulitz M., Linke R.P.;
RT   "Primary structure of the variable part of an amyloidogenic Bence-
RT   Jones Protein (Mev). An unusual insertion in the third hypervariable
RT   region of a human kappa-immunoglobulin light chain.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 363:1347-1358(1982).
CC   -!- MISCELLANEOUS: Another form that lacked residues 1-3 was also
CC       found.
CC   -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01879; K1HUMV.
DR   HSSP; P80362; 1WTL.
DR   SMR; P01612; 1-109.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     98       Complementarity-determining-3.
FT   REGION       99    108       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11870 MW;  B6ABF4515D55F5A0 CRC64;

  Query Match             95.3%;  Score 82;  DB 1;  Length 109;
  Best Local Similarity   93.3%;  Pred. No. 1.8e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||:
Db         35 WYQQKPGKAPKLLIF 49


RESULT 20
Q569I7_HUMAN
ID   Q569I7_HUMAN PRELIMINARY;      PRT;   189 AA.
AC   Q569I7;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Glandular pool- thyroid;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Glandular pool- thyroid;
RG   NIH MGC Project;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC092455; AAH92455.1; -; mRNA.
DR   SMR; Q569I7; 23-186.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein; Immunoglobulin domain.
SQ   SEQUENCE   189 AA;  20668 MW;  CFFD14A19F6E3622 CRC64;

  Query Match             95.3%;  Score 82;  DB 2;  Length 189;
  Best Local Similarity   93.3%;  Pred. No. 3e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||:|||||||
Db         57 WYQQKPGQAPKLLIY 71


RESULT 21
Q569I9_HUMAN
ID   Q569I9_HUMAN PRELIMINARY;      PRT;   234 AA.
AC   Q569I9;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   IGKC protein.
GN   Name=IGKC;
OS   Homo sapiens (Human).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Glandular pool- thyroid;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Glandular pool- thyroid;
RG   NIH MGC Project;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC092453; AAH92453.1; -; mRNA.
SQ   SEQUENCE   234 AA;  25389 MW;  648949ECCE329BB9 CRC64;

  Query Match             95.3%;  Score 82;  DB 2;  Length 234;
  Best Local Similarity   93.3%;  Pred. No. 3.7e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||:|||||||
Db         56 WYQQKPGQAPKLLIY 70


RESULT 22
Q7Z473_HUMAN
ID   Q7Z473_HUMAN PRELIMINARY;      PRT;   234 AA.
AC   Q7Z473;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   IGKC protein.
GN   Name=IGKC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RG   NIH MGC Project;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC056256; AAH56256.1; -; mRNA.
DR   HSSP; P01834; 1HEZ.
DR   SMR; Q7Z473; 22-234.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   234 AA;  25674 MW;  1A2C259BAB51BC0F CRC64;

  Query Match             95.3%;  Score 82;  DB 2;  Length 234;
  Best Local Similarity   93.3%;  Pred. No. 3.7e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||:||||
Db         55 WYQQKPGKAPQLLIY 69


RESULT 23
Q65ZC8_HUMAN
ID   Q65ZC8_HUMAN PRELIMINARY;      PRT;   244 AA.
AC   Q65ZC8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Single-chain Fv (Fragment).
GN   Name=scFv;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97362799; PubMed=9219263; DOI=10.1038/nbt0797-629;
RA   Kontermann R.E., Wing M.G., Winter G.;
RT   "Complement recruitment using bispecific diabodies.";
RL   Nat. Biotechnol. 15:629-631(1997).
DR   EMBL; Y13057; CAA73500.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00406; IGv; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
FT   NON_TER       1     1
FT   NON_TER     244   244
SQ   SEQUENCE   244 AA;  26127 MW;  4B1F17868338F2BF CRC64;

  Query Match             95.3%;  Score 82;  DB 2;  Length 244;
  Best Local Similarity   93.3%;  Pred. No. 3.9e-05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
```

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Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||| |||
Db        171 WYQQKPGKAPKFLIY 185


RESULT 24
Q566X2_BRARE
ID   Q566X2_BRARE PRELIMINARY;      PRT;   266 AA.
AC   Q566X2;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Olfactory epithelium;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Olfactory epithelium;
RG   NIH MGC Project;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC093291; AAH93291.1; -; mRNA.
KW   Hypothetical protein.
FT   NON_TER       1      1
SQ   SEQUENCE   266 AA;  28895 MW;  5665F8442AC13812 CRC64;

  Query Match             95.3%;  Score 82;  DB 2;  Length 266;
  Best Local Similarity   93.3%;  Pred. No. 4.2e-05;
  Matches   14;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||:|||||||
Db         85 WYQQKPGEAPKLLIY 99


RESULT 25
Q9UL81_HUMAN
ID   Q9UL81_HUMAN PRELIMINARY;      PRT;   107 AA.
AC   Q9UL81;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035033; AAD56269.1; -; mRNA.
DR   HSSP; P01607; 1BWW.
DR   SMR; Q9UL81; 1-107.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     107    107
SQ   SEQUENCE   107 AA;  11501 MW;  070549FDE0754748 CRC64;

  Query Match             94.2%;  Score 81;  DB 2;  Length 107;
  Best Local Similarity   93.3%;  Pred. No. 2.5e-05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||| ||||
Db         35 WYQQKPGKAPNLLIY 49


RESULT 26
Q9UL77_HUMAN
ID   Q9UL77_HUMAN PRELIMINARY;      PRT;   108 AA.
AC   Q9UL77;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1516616;
RA   Victor K.D., Pascual V., Williams C.L., Lennon V.A., Capra J.D.;
RT   "Human monoclonal striational autoantibodies isolated from thymic B
RT   lymphocytes of patients with myasthenia gravis use VH and VL gene
RT   segments associated with the autoimmune repertoire.";
RL   Eur. J. Immunol. 22:2231-2236(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=8436174;
RA   Wagner S.D., Luzzatto L.;
RT   "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT   distributed over a large portion of the V kappa locus and do not show
RT   somatic mutation.";
RL   Eur. J. Immunol. 23:391-397(1993).
DR   EMBL; AF035037; AAD56273.1; -; mRNA.
DR   PIR; B49047; B49047.
DR   PIR; S34083; S34083.
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DR   HSSP; P01607; 1BWW.
DR   SMR; Q9UL77; 1-108.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11738 MW;  C06681716C4D16F3 CRC64;

  Query Match             94.2%;  Score 81;  DB 2;  Length 108;
  Best Local Similarity   93.3%;  Pred. No. 2.5e-05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||| ||||
Db         35 WYQQKPGKAPNLLIY 49


RESULT 27
Q6PIT5_HUMAN
ID   Q6PIT5_HUMAN PRELIMINARY;      PRT;   236 AA.
AC   Q6PIT5;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RA   Strausberg R.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC029444; AAH29444.1; -; mRNA.
DR   HSSP; P01607; 1AR2.
DR   SMR; Q6PIT5; 26-236.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   236 AA;  25741 MW;  BD50AF071FEEE351 CRC64;

  Query Match             94.2%;  Score 81;  DB 2;  Length 236;
  Best Local Similarity   93.3%;  Pred. No. 5.5e-05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||| ||||||
Db         57 WYQQKPGKPPKLLIY 71


RESULT 28
Q6PIH7_HUMAN
ID   Q6PIH7_HUMAN PRELIMINARY;      PRT;   236 AA.
AC   Q6PIH7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   IGKC protein.
GN   Name=IGKC;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RG   NIH MGC Project;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC034141; AAH34141.1; -; mRNA.
DR   HSSP; P01607; 1AR2.
DR   SMR; Q6PIH7; 23-236.
DR   Ensembl; ENSG00000163245; Homo sapiens.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF07654; C1-set; 1.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
```

```
SQ   SEQUENCE   236 AA;  25603 MW;  8BC561106861213F CRC64;

  Query Match             94.2%;  Score 81;  DB 2;  Length 236;
  Best Local Similarity   93.3%;  Pred. No. 5.5e-05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||| ||||
Db         57 WYQQKPGKAPNLLIY 71


RESULT 29
KV1O_HUMAN
ID   KV1O_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01607;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Rei.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=76023758; PubMed=809329;
RA   Palm W., Hilschmann N.;
RT   "The primary structure of a crystalline monoclonal immunoglobulin
RT   kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT   and characterization of the tryptic peptides; the complete amino acid
RT   sequence of the protein; a contribution to the elucidation of the
RT   three-dimensional structure of antibodies, in particular their
RT   combining site.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE=76039968; PubMed=1182131;
RA   Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT   "The molecular structure of a dimer composed of the variable portions
RT   of the Bence-Jones protein REI refined at 2.0-A resolution.";
RL   Biochemistry 14:4943-4952(1975).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC       marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A91663; K1HURE.
DR   PDB; 1AR2; X-ray; @=1-107.
DR   PDB; 1BWW; X-ray; A/B=1-107.
DR   PDB; 1REI; X-ray; A/B=1-107.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin domain; Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88
FT   NON_TER     108    108
FT   STRAND        4      7
FT   STRAND       10     13
FT   TURN         15     16
FT   STRAND       19     25
FT   TURN         30     31
FT   STRAND       33     38
FT   TURN         40     41
FT   STRAND       45     49
FT   TURN         50     52
FT   STRAND       53     54
FT   TURN         56     57
FT   TURN         60     61
FT   STRAND       62     67
FT   TURN         68     69
FT   STRAND       70     75
FT   HELIX        80     82
FT   STRAND       84     90
FT   STRAND       97     98
FT   STRAND      102    106
SQ   SEQUENCE   108 AA;  11902 MW;  9E8143E1188BCE2A CRC64;

  Query Match             93.0%;  Score 80;  DB 1;  Length 108;
  Best Local Similarity   93.3%;  Pred. No. 3.7e-05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||| ||||||||||
Db         35 WYQQTPGKAPKLLIY 49


RESULT 30
LV2K_HUMAN
ID   LV2K_HUMAN     STANDARD;      PRT;   112 AA.
AC   P04209;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig lambda chain V-II region NIG-84.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=85204383; PubMed=3922791; DOI=10.1016/0014-5793(85)80757-2;
RA   Tonoike H., Kametani F., Hoshi A., Shinoda T., Isobe T.;
RT   "Amino acid sequence of an amyloidogenic Bence Jones protein in
RT   myeloma-associated systemic amyloidosis.";
RL   FEBS Lett. 185:139-141(1985).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein isolated from an
CC       individual with myeloma-associated systemic amyloidosis.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A01971; L2HUNG.
DR   HSSP; P01709; 2MCG.
DR   SMR; P04209; 1-112.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Amyloid; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin domain; Immunoglobulin V region.
```

```
FT   DOMAIN        1    102       Ig-like.
FT   DISULFID     22     90       By similarity.
FT   NON_TER     112    112
SQ   SEQUENCE   112 AA;  11581 MW;  988FEF363AE1E4F3 CRC64;

  Query Match             93.0%;  Score 80;  DB 1;  Length 112;
  Best Local Similarity   93.3%;  Pred. No. 3.9e-05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||| ||||||||||
Db         37 WYQQHPGKAPKLLIY 51


RESULT 31
KV1X_HUMAN
ID   KV1X_HUMAN     STANDARD;      PRT;   129 AA.
AC   P04432;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Daudi precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=85014148; PubMed=6091049;
RA   Klobeck H.G., Combriato G., Zachau H.G.;
RT   "Immunoglobulin genes of the kappa light chain type from two human
RT   lymphoid cell lines are closely related.";
RL   Nucleic Acids Res. 12:6995-7006(1984).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X00966; CAA25478.1; ALT_TERM; Genomic_DNA.
DR   PIR; A01884; K1HUDI.
DR   HSSP; P80362; 1WTL.
DR   SMR; P04432; 23-129.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    129       Ig kappa chain V-I region Daudi.
FT   REGION       23     45       Framework-1.
FT   REGION       46     56       Complementarity-determining-1.
FT   REGION       57     71       Framework-2.
FT   REGION       72     78       Complementarity-determining-2.
FT   REGION       79    110       Framework-3.
FT   REGION      111    119       Complementarity-determining-3.
FT   REGION      120    129       Framework-4.
FT   DISULFID     45    110       By similarity.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14235 MW;  CAF076BC7E5574C8 CRC64;

  Query Match             93.0%;  Score 80;  DB 1;  Length 129;
  Best Local Similarity   93.3%;  Pred. No. 4.4e-05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||| ||||
Db         57 WYQQKPGKAPTLLIY 71


RESULT 32
Q5NV70_HUMAN
ID   Q5NV70_HUMAN PRELIMINARY;      PRT;    97 AA.
AC   Q5NV70;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   V1-11 protein (Fragment).
GN   Name=V1-11;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97228902; PubMed=9074928;
RA   Kawasaki K., Minoshima S., Nakato E., Shibuya K., Shintani A.,
RA   Schmeits J.L., Wang J., Shimizu N.;
RT   "One-megabase sequence analysis of the human immunoglobulin lambda
RT   gene locus.";
RL   Genome Res. 7:250-261(1997).
DR   EMBL; D87009; BAA20004.1; -; Genomic_DNA.
DR   SMR; Q5NV70; 1-97.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER      97     97
SQ   SEQUENCE   97 AA;  10333 MW;  2209F126C2869985 CRC64;

  Query Match             91.9%;  Score 79;  DB 2;  Length 97;
  Best Local Similarity   93.3%;  Pred. No. 4.9e-05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||| ||||||||||
Db         36 WYQQLPGKAPKLLIY 50


RESULT 33
Q5NV67_HUMAN
ID   Q5NV67_HUMAN PRELIMINARY;      PRT;    99 AA.
AC   Q5NV67;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE   V1-11 protein (Fragment).
GN   Name=IGLV1-36; Synonyms=V1-11;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97228902; PubMed=9074928;
RA   Kawasaki K., Minoshima S., Nakato E., Shibuya K., Shintani A.,
RA   Schmeits J.L., Wang J., Shimizu N.;
RT   "One-megabase sequence analysis of the human immunoglobulin lambda
RT   gene locus.";
RL   Genome Res. 7:250-261(1997).
DR   EMBL; D87010; BAA20897.1; -; Genomic_DNA.
DR   SMR; Q5NV67; 1-99.
DR   HGNC; HGNC:5876; IGLV1-36.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00406; IGv; 1.
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```
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER      99     99
SQ   SEQUENCE   99 AA;  10487 MW;  B8874209F126C286 CRC64;

  Query Match             91.9%;  Score 79;  DB 2;  Length 99;
  Best Local Similarity   93.3%;  Pred. No. 5e-05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||| ||||||||||
Db         36 WYQQLPGKAPKLLIY 50


RESULT 34
Q9JL74_MOUSE
ID   Q9JL74_MOUSE PRELIMINARY;      PRT;    99 AA.
AC   Q9JL74;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Anti-myosin immunoglobulin light chain variable region
DE   (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BALB/c;
RX   MEDLINE=20448942; PubMed=10992488;
RX   DOI=10.1128/IAI.68.10.5803-5808.2000;
RA   Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT   "T-Cell-dependent antibody response to the dominant epitope of
RT   streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT   with cardiac myosin.";
RL   Infect. Immun. 68:5803-5808(2000).
DR   EMBL; AF206032; AAF69330.1; -; mRNA.
DR   HSSP; P01634; 1IGC.
DR   SMR; Q9JL74; 1-99.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER      99     99
SQ   SEQUENCE   99 AA;  10939 MW;  3B25D0E784533324 CRC64;

  Query Match             91.9%;  Score 79;  DB 2;  Length 99;
  Best Local Similarity   86.7%;  Pred. No. 5e-05;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||::||||||
Db         27 WYQQKPGQSPKLLIY 41


RESULT 35
KV3C_HUMAN
ID   KV3C_HUMAN     STANDARD;      PRT;   100 AA.
AC   P01621;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-III region NG9 precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=84093600; PubMed=6419127;
RA   Bentley D.L.;
RT   "Most kappa immunoglobulin mRNA in human lymphocytes is homologous to
RT   a small family of germ-line V genes.";
RL   Nature 307:77-80(1984).
CC   -!- MISCELLANEOUS: This gene was isolated from the NG9/9.1 hybridoma.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A01894; K3HUNG.
DR   HSSP; P01625; 1EEQ.
DR   SMR; P01621; 6-99.
DR   Ensembl; ENSG00000169769; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hybridoma; Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL       <1      4
FT   CHAIN         5    100       Ig kappa chain V-III region NG9.
FT   DISULFID     27     93       By similarity.
FT   NON_TER       1      1
FT   NON_TER     100    100
SQ   SEQUENCE   100 AA;  10729 MW;  5D9AF363CC52632F CRC64;

  Query Match             91.9%;  Score 79;  DB 1;  Length 100;
  Best Local Similarity   86.7%;  Pred. No. 5.1e-05;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||:||:||||
Db         40 WYQQKPGQAPRLLIY 54


RESULT 36
KV1E_HUMAN
ID   KV1E_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01597;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region DEE.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=72053133; PubMed=5124396;
RA   Milstein C.P., Deverson E.V.;
RT   "The amino acid sequence of a human kappa light chain.";
RL   Biochem. J. 123:945-958(1971).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A01865; K1HUDE.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01597; 4-108.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
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DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11661 MW;  BDD6E350017F1E51 CRC64;

  Query Match             91.9%;  Score 79;  DB 1;  Length 108;
  Best Local Similarity   86.7%;  Pred. No. 5.5e-05;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||:||:
Db         35 WYQQKPGKAPKVLIF 49


RESULT 37
KV1G_HUMAN
ID   KV1G_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01599;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Gal.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=75059122; PubMed=4215718;
RA   Laure C.J., Watanabe S., Hilschmann N.;
RT   "The primary structure of a monoclonal IgM-immunoglobulin
RT   (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT   kappa-type, subgroup I.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 354:1503-1504(1973).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC       macroglobulin.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01867; K1HUGL.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01599; 1-107.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11814 MW;  C1AD3CB0F600FF73 CRC64;

  Query Match             91.9%;  Score 79;  DB 1;  Length 108;
  Best Local Similarity   93.3%;  Pred. No. 5.5e-05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||| |||
Db         35 WYQQKPGKAPKELIY 49


RESULT 38
KV1H_HUMAN
ID   KV1H_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01600;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-I region Hau.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=71032830; PubMed=4097974;
RA   Watanabe S., Hilschmann N.;
RT   "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT   chain of subgroup I (Bence-Jones Protein Hau): subdivision within
RT   subgroups.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01868; K1HUHU.
DR   PDB; 1F6L; X-ray; L=1-108.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   3D-structure; Bence-Jones protein; Direct protein sequencing;
KW   Immunoglobulin domain; Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11671 MW;  08D3A6160D8D0618 CRC64;

  Query Match             91.9%;  Score 79;  DB 1;  Length 108;
  Best Local Similarity   86.7%;  Pred. No. 5.5e-05;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||::|||
Db         35 WYQQKPGKAPQVLIY 49


RESULT 39
KV1M_HUMAN
ID   KV1M_HUMAN     STANDARD;      PRT;   108 AA.
AC   P01605;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Ig kappa chain V-I region Lay.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=77038198; PubMed=824717;
RA   Capra J.D., Klapper D.G.;
RT   "Complete amino acid sequence of the variable domains of two human IgM
RT   anti-gamma globulins (Lay/Pom) with shared idiotypic specificities.";
RL   Scand. J. Immunol. 5:677-684(1976).
RN   [2]
RP   PROTEIN SEQUENCE OF 1-104.
RX   MEDLINE=89215279; PubMed=2496160;
RA   Goni F.R., Chen P.P., McGinnis D., Arjonilla M.L., Fernandez J.,
RA   Carson D., Solomon A., Mendez E., Frangione B.;
RT   "Structural and idiotypic characterization of the L chains of human
RT   IgM autoantibodies with different specificities.";
RL   J. Immunol. 142:3158-3163(1989).
RN   [3]
RP   ERRATUM.
RA   Goni F.R., Chen P.P., McGinnis D., Arjonilla M.L., Fernandez J.,
RA   Carson D., Solomon A., Mendez E., Frangione B.;
RL   J. Immunol. 143:3864-3864(1989).
CC   -!- MISCELLANEOUS: The second and third hypervariable regions of this
CC       chain are identical with those of the human POM V-III kappa chain,
CC       with which it shares certain idiotypic determinants.
CC   -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC       globulin activity.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01871; K1HULY.
DR   HSSP; P01607; 1BWW.
DR   SMR; P01605; 1-108.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   REGION        1     23       Framework-1.
FT   REGION       24     34       Complementarity-determining-1.
FT   REGION       35     49       Framework-2.
FT   REGION       50     56       Complementarity-determining-2.
FT   REGION       57     88       Framework-3.
FT   REGION       89     97       Complementarity-determining-3.
FT   REGION       98    107       Framework-4.
FT   DISULFID     23     88       By similarity.
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11834 MW;  739993A95431434A CRC64;

  Query Match            91.9%;  Score 79;  DB 1;  Length 108;
  Best Local Similarity  93.3%;  Pred. No. 5.5e-05;
  Matches   14;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||| |||||||
Db         35 WYQQKPGLAPKLLIY 49


RESULT 40
Q9UL83_HUMAN
ID   Q9UL83_HUMAN PRELIMINARY;      PRT;   108 AA.
AC   Q9UL83;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=8436174;
RA   Wagner S.D., Luzzatto L.;
RT   "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT   distributed over a large portion of the V kappa locus and do not show
RT   somatic mutation.";
RL   Eur. J. Immunol. 23:391-397(1993).
DR   EMBL; AF035031; AAD56267.1; -; mRNA.
DR   PIR; B30609; B30609.
DR   PIR; C30609; C30609.
DR   PIR; D30609; D30609.
DR   PIR; S34098; S34098.
DR   PIR; S34099; S34099.
DR   HSSP; P01625; 1LVE.
DR   SMR; Q9UL83; 1-108.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     108    108
SQ   SEQUENCE   108 AA;  11834 MW;  9F9C5A92EBA96EEA CRC64;

  Query Match            91.9%;  Score 79;  DB 2;  Length 108;
  Best Local Similarity  86.7%;  Pred. No. 5.5e-05;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||:||:||||
Db         35 WYQQKPGQAPRLLIY 49


RESULT 41
KV3B_HUMAN
ID   KV3B_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01620;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-III region SIE.
OS   Homo sapiens (Human).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=82046598; PubMed=6794615;
RA   Andrews D.W., Capra J.D.;
RT   "Amino acid sequence of the variable regions of light chains from two
RT   idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT   group.";
RL   Biochemistry 20:5816-5822(1981).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC       globulin activity.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01892; K3HUSI.
DR   HSSP; P01625; 1LVE.
DR   SMR; P01620; 1-109.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11775 MW;  7689C3ECD646FFB4 CRC64;

  Query Match             91.9%;  Score 79;  DB 1;  Length 109;
  Best Local Similarity   86.7%;  Pred. No. 5.5e-05;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||:||:||||
Db         36 WYQQKPGQAPRLLIY 50


RESULT 42
KV3D_HUMAN
ID   KV3D_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01622;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-III region Ti.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=72188439; PubMed=5027703;
RA   Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT   "Rule of antibody structure. The primary structure of a monoclonal
RT   immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT   Ti). IV. The complete amino acid sequence and its significance for the
RT   mechanism of antibody production.";
RL   Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC   -!- MISCELLANEOUS: The C region of this chain has the INV (3) marker.
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01895; K3HUTI.
DR   HSSP; P01625; 1LVE.
DR   SMR; P01622; 1-109.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11788 MW;  8C35058CDC7749BC CRC64;

  Query Match             91.9%;  Score 79;  DB 1;  Length 109;
  Best Local Similarity   86.7%;  Pred. No. 5.5e-05;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||:||:||||
Db         36 WYQQKPGQAPRLLIY 50


RESULT 43
KV3E_HUMAN
ID   KV3E_HUMAN     STANDARD;      PRT;   109 AA.
AC   P01623;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-III region WOL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=82046598; PubMed=6794615;
RA   Andrews D.W., Capra J.D.;
RT   "Amino acid sequence of the variable regions of light chains from two
RT   idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT   group.";
RL   Biochemistry 20:5816-5822(1981).
CC   -!- MISCELLANEOUS: This chain was isolated from an IgM with anti-gamma
CC       globulin activity.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between  the Swiss Institute of Bioinformatics  and the  EMBL outstation -
CC   the European Bioinformatics Institute.  There are no  restrictions on  its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; A01896; K3HUWL.
DR   HSSP; P01625; 1LVE.
DR   SMR; P01623; 1-109.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Direct protein sequencing; Immunoglobulin domain;
KW   Immunoglobulin V region.
FT   DISULFID     23     89       By similarity.
FT   NON_TER     109    109
```

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SQ   SEQUENCE   109 AA;  11746 MW;  566C115E6B9CBEEE CRC64;

  Query Match             91.9%;  Score 79;  DB 1;  Length 109;
  Best Local Similarity   86.7%;  Pred. No. 5.5e-05;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||:||:||||
Db         36 WYQQKPGQAPRLLIY 50


RESULT 44
Q9UL85_HUMAN
ID   Q9UL85_HUMAN PRELIMINARY;      PRT;   109 AA.
AC   Q9UL85;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin kappa chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035029; AAD56265.1; -; mRNA.
DR   PIR; D30609; D30609.
DR   HSSP; P01625; 1EK3.
DR   SMR; Q9UL85; 1-109.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11761 MW;  FB1E43E7C7AFACCC CRC64;

  Query Match             91.9%;  Score 79;  DB 2;  Length 109;
  Best Local Similarity   86.7%;  Pred. No. 5.5e-05;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||:||:||||
Db         35 WYQQKPGQAPRLLIY 49


RESULT 45
Q9UL86_HUMAN
ID   Q9UL86_HUMAN PRELIMINARY;      PRT;   109 AA.
AC   Q9UL86;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Myosin-reactive immunoglobulin kappa chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
DR   EMBL; AF035028; AAD56264.1; -; mRNA.
DR   PIR; B30607; B30607.
DR   PIR; I30601; I30601.
DR   HSSP; P01625; 1EK3.
DR   SMR; Q9UL86; 1-109.
DR   Ensembl; ENSG00000169769; Homo sapiens.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11928 MW;  243325F72C7DAC83 CRC64;

  Query Match             91.9%;  Score 79;  DB 2;  Length 109;
  Best Local Similarity   86.7%;  Pred. No. 5.5e-05;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||:||:||||
Db         36 WYQQKPGQAPRLLIY 50


RESULT 46
Q9UL78_HUMAN
ID   Q9UL78_HUMAN PRELIMINARY;      PRT;   109 AA.
AC   Q9UL78;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Myosin-reactive immunoglobulin light chain variable region
DE   (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA   Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA   Young D.C.;
RT   "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT   fetus.";
RL   Clin. Immunol. Immunopathol. 87:184-192(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1373487;
RA   Zebedee S.L., Barbas C.F. 3rd, Hom Y.L., Caothien R.H., Graff R.,
RA   DeGraw J., Pyati J., LaPolla R., Burton D.R., Lerner R.A.;
RT   "Human combinatorial antibody libraries to hepatitis B surface
RT   antigen.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:3175-3179(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=8436174;
RA   Wagner S.D., Luzzatto L.;
RT   "V kappa gene segments rearranged in chronic lymphocytic leukemia are
RT   distributed over a large portion of the V kappa locus and do not show
RT   somatic mutation.";
RL   Eur. J. Immunol. 23:391-397(1993).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   PubMed=1552291;
RA   Martin T., Duffy S.F., Carson D.A., Kipps T.J.;
RT   "Evidence for somatic selection of natural autoantibodies.";
RL   J. Exp. Med. 175:983-991(1992).
DR   EMBL; AF035036; AAD56272.1; -; mRNA.
DR   PIR; A30601; A30601.
DR   PIR; A30608; A30608.
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DR   PIR; B30601; B30601.
DR   PIR; B30607; B30607.
DR   PIR; C30601; C30601.
DR   PIR; C30607; C30607.
DR   PIR; C30608; C30608.
DR   PIR; D30601; D30601.
DR   PIR; D30607; D30607.
DR   PIR; D30608; D30608.
DR   PIR; F30607; F30607.
DR   PIR; F30608; F30608.
DR   PIR; G30601; G30601.
DR   PIR; G30608; G30608.
DR   PIR; H30607; H30607.
DR   PIR; H30608; H30608.
DR   PIR; H44151; H44151.
DR   PIR; I30601; I30601.
DR   PIR; PH0963; PH0963.
DR   PIR; PH0964; PH0964.
DR   PIR; PH0965; PH0965.
DR   PIR; S33988; S33988.
DR   PIR; S34096; S34096.
DR   HSSP; P01625; 1EK3.
DR   SMR; Q9UL78; 1-109.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
FT   NON_TER       1      1
FT   NON_TER     109    109
SQ   SEQUENCE   109 AA;  11646 MW;  5F675C52EC7EE197 CRC64;

  Query Match             91.9%;  Score 79;  DB 2;  Length 109;
  Best Local Similarity   86.7%;  Pred. No. 5.5e-05;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||:||:||||
Db         36 WYQQKPGQAPRLLIY 50


RESULT 47
LV2B_HUMAN
ID   LV2B_HUMAN     STANDARD;      PRT;   111 AA.
AC   P01705;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig lambda chain V-II region NEI.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=72233223; PubMed=5043326;
RA   Garver F.A., Hilschmann N.;
RT   "The primary structure of a monoclonal human lambda-type
RT   immunoglobulin L-chain of subgroup II (Bence-Jones protein NEI).";
RL   Eur. J. Biochem. 26:10-32(1972).
CC   -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC   -!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   PIR; A01970; L2HUNI.
DR   HSSP; P01709; 2MCG.
DR   SMR; P01705; 1-110.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Bence-Jones protein; Direct protein sequencing; Glycoprotein;
KW   Immunoglobulin domain; Immunoglobulin V region;
KW   Pyrrolidone carboxylic acid.
FT   DOMAIN        1    106       Ig-like.
FT   MOD_RES       1      1       Pyrrolidone carboxylic acid.
FT   CARBOHYD     96     96       N-linked (GlcNAc. . .).
FT   DISULFID     22     90       By similarity.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  11591 MW;  AD6D156584D087EB CRC64;

  Query Match             91.9%;  Score 79;  DB 1;  Length 111;
  Best Local Similarity   86.7%;  Pred. No. 5.6e-05;
  Matches   13;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||| |||||||:||
Db         37 WYQQNPGKAPKLMIY 51


RESULT 48
KV3I_HUMAN
ID   KV3I_HUMAN     STANDARD;      PRT;   115 AA.
AC   P04433;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-III region VG precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=85087932; PubMed=6440122;
RA   Pech M., Zachau H.G.;
RT   "Immunoglobulin genes of different subgroups are interdigitated within
RT   the VK locus.";
RL   Nucleic Acids Res. 12:9229-9236(1984).
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; X01668; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR   PIR; A01900; K3HUVG.
DR   HSSP; P01625; 1EEQ.
DR   SMR; P04433; 21-115.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21   >115       Ig kappa chain V-III region VG.
FT   REGION       21     43       Framework-1.
FT   REGION       44     54       Complementarity-determining-1.
FT   REGION       55     69       Framework-2.
FT   REGION       70     76       Complementarity-determining-2.
FT   REGION       77    108       Framework-3.
FT   REGION      109    115       Complementarity-determining-3.
FT   DISULFID     43    108       By similarity.
```

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FT   NON_TER     115    115
SQ   SEQUENCE   115 AA;  12575 MW;  2DE47CDA3A17D555 CRC64;

  Query Match             91.9%;  Score 79;  DB 1;  Length 115;
  Best Local Similarity   86.7%;  Pred. No. 5.8e-05;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||:||:||||
Db         55 WYQQKPGQAPRLLIY 69


RESULT 49
KV3J_HUMAN
ID   KV3J_HUMAN     STANDARD;      PRT;   116 AA.
AC   P04434;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-III region VH precursor (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=85087932; PubMed=6440122;
RA   Pech M., Zachau H.G.;
RT   "Immunoglobulin genes of different subgroups are interdigitated within
RT   the VK locus.";
RL   Nucleic Acids Res. 12:9229-9236(1984).
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X02725; -; NOT_ANNOTATED_CDS; Genomic_DNA.
DR   PIR; A01901; K3HUVH.
DR   HSSP; P01625; 1LVE.
DR   SMR; P04434; 22-111.
DR   Ensembl; ENSG00000184817; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21   >116       Ig kappa chain V-III region VH.
FT   REGION       21     43       Framework-1.
FT   REGION       44     55       Complementarity-determining-1.
FT   REGION       56     70       Framework-2.
FT   REGION       71     77       Complementarity-determining-2.
FT   REGION       78    109       Framework-3.
FT   REGION      110    116       Complementarity-determining-3.
FT   DISULFID     43    109       By similarity.
FT   NON_TER     116    116
SQ   SEQUENCE   116 AA;  12757 MW;  51CD55BA53B21929 CRC64;

  Query Match             91.9%;  Score 79;  DB 1;  Length 116;
  Best Local Similarity   86.7%;  Pred. No. 5.9e-05;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||:||:||||
Db         56 WYQQKPGQAPRLLIY 70


RESULT 50
KV3L_HUMAN
ID   KV3L_HUMAN     STANDARD;      PRT;   129 AA.
AC   P18135;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ig kappa chain V-III region HAH precursor.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=88171307; PubMed=3127527; DOI=10.1084/jem.167.3.840;
RA   Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT   "Autoantibody-associated kappa light chain variable region gene
RT   expressed in chronic lymphocytic leukemia with little or no somatic
RT   mutation. Implications for etiology and immunotherapy.";
RL   J. Exp. Med. 167:840-852(1988).
CC   -!- DISEASE: The protein is one of the surface immunoglobulin M
CC       autoantibodies expressed in patients with chronic lymphocytic
CC       leukemia.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   PIR; PL0022; K3HUHA.
DR   HSSP; P01625; 1EEQ.
DR   SMR; P18135; 21-129.
DR   Ensembl; ENSG00000169769; Homo sapiens.
DR   GO; GO:0005576; C:extracellular region; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain; Immunoglobulin V region; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    129       Ig kappa chain V-III region HAH.
FT   REGION       21     43       Framework-1.
FT   REGION       44     55       Complementarity-determining-1.
FT   REGION       56     70       Framework-2.
FT   REGION       71     77       Complementarity-determining-2.
FT   REGION       78    109       Framework-3.
FT   REGION      110    118       Complementarity-determining-3.
FT   REGION      119    129       JK1 segment.
FT   DISULFID     43    109       By similarity.
FT   NON_TER     129    129
SQ   SEQUENCE   129 AA;  14073 MW;  D3C55292772774D0 CRC64;

  Query Match             91.9%;  Score 79;  DB 1;  Length 129;
  Best Local Similarity   86.7%;  Pred. No. 6.5e-05;
  Matches   13;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||:||:||||
Db         56 WYQQKPGQAPRLLIY 70


Search completed: March 23, 2006, 02:05:13
Job time : 148.184 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:05:22 ; Search time 32.4658 Seconds
(without alignments)
38.198 Million cell updates/sec

Title: US-10-755-382-27
Perfect score: 86
Sequence: 1 WYQQKPGKAPKLLIY 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	86	100.0	15	1	US-07-946-421-8	Sequence 8, Appli
2	86	100.0	15	1	US-08-137-117D-121	Sequence 121, App
3	86	100.0	15	1	US-08-137-117D-140	Sequence 140, App
4	86	100.0	15	1	US-08-436-717-121	Sequence 121, App
5	86	100.0	15	1	US-08-436-717-140	Sequence 140, App
6	86	100.0	15	1	US-08-553-501A-66	Sequence 66, Appl
7	86	100.0	15	1	US-08-553-501A-70	Sequence 70, Appl
8	86	100.0	15	1	US-08-318-157B-27	Sequence 27, Appl
9	86	100.0	15	1	US-08-765-783A-88	Sequence 88, Appl
10	86	100.0	15	1	US-08-470-139-11	Sequence 11, Appl
11	86	100.0	15	2	US-08-649-100-28	Sequence 28, Appl
12	86	100.0	15	2	US-09-205-231-66	Sequence 66, Appl
13	86	100.0	15	2	US-09-205-231-70	Sequence 70, Appl
14	86	100.0	15	2	US-08-569-147-38	Sequence 38, Appl
15	86	100.0	15	2	US-09-416-557-88	Sequence 88, Appl
16	86	100.0	15	2	US-09-347-061-11	Sequence 11, Appl
17	86	100.0	15	2	US-09-425-638A-85	Sequence 85, Appl
18	86	100.0	15	2	US-09-425-638A-86	Sequence 86, Appl
19	86	100.0	15	2	US-09-543-004-85	Sequence 85, Appl
20	86	100.0	15	2	US-09-543-004-86	Sequence 86, Appl
21	86	100.0	15	2	US-09-253-794-27	Sequence 27, Appl
22	86	100.0	15	2	US-09-647-468-126	Sequence 126, App
23	86	100.0	15	2	US-09-563-222C-75	Sequence 75, Appl
24	86	100.0	15	2	US-09-855-271-11	Sequence 11, Appl
25	86	100.0	40	2	US-08-812-586-40	Sequence 40, Appl
26	86	100.0	40	2	US-09-535-832A-37	Sequence 37, Appl
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29	86	100.0	70	2	US-08-925-339-9	Sequence 9, Appli
30	86	100.0	70	2	US-09-332-595-9	Sequence 9, Appli
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33	86	100.0	80	1	US-08-553-501A-85	Sequence 85, Appl
34	86	100.0	80	1	US-08-765-783A-104	Sequence 104, App
35	86	100.0	80	2	US-09-205-231-85	Sequence 85, Appl
36	86	100.0	80	2	US-09-416-557-104	Sequence 104, App
37	86	100.0	80	2	US-09-269-921-130	Sequence 130, App
38	86	100.0	80	2	US-09-269-921-131	Sequence 131, App
39	86	100.0	81	2	US-09-254-180C-160	Sequence 160, App
40	86	100.0	87	2	US-08-646-265A-112	Sequence 112, App
41	86	100.0	88	2	US-09-905-243-29	Sequence 29, Appl
42	86	100.0	88	2	US-09-905-243-31	Sequence 31, Appl
43	86	100.0	88	2	US-09-905-243-35	Sequence 35, Appl
44	86	100.0	88	2	US-09-905-243-36	Sequence 36, Appl
45	86	100.0	88	2	US-09-905-243-63	Sequence 63, Appl
46	86	100.0	90	2	US-09-199-149-15	Sequence 15, Appl
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63	86	100.0	95	2	US-10-194-975-72	Sequence 72, Appl
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72	86	100.0	102	2	US-09-199-149-10	Sequence 10, Appl
73	86	100.0	102	2	US-09-199-149-29	Sequence 29, Appl
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75	86	100.0	102	2	US-09-196-522-173	Sequence 173, App
76	86	100.0	104	1	US-08-276-852-106	Sequence 106, App
77	86	100.0	104	1	US-08-899-575-106	Sequence 106, App
78	86	100.0	104	1	US-08-899-575-106	Sequence 106, App
79	86	100.0	104	4	PCT-US95-08743-106	Sequence 106, App
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85	86	100.0	106	1	US-07-634-278-59	Sequence 59, Appl
86	86	100.0	106	1	US-08-477-728-7	Sequence 7, Appli
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92	86	100.0	106	1	US-08-487-200-7	Sequence 7, Appli
93	86	100.0	106	1	US-08-487-200-35	Sequence 35, Appl
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95	86	100.0	106	1	US-08-488-113B-165	Sequence 165, App
96	86	100.0	106	1	US-08-477-484B-165	Sequence 165, App
97	86	100.0	106	1	US-08-107-669D-51	Sequence 51, Appl
98	86	100.0	106	1	US-08-472-788A-84	Sequence 84, Appl
99	86	100.0	106	1	US-08-477-531B-51	Sequence 51, Appl
100	86	100.0	106	1	US-08-646-360-165	Sequence 165, App

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107	86	100.0	106	2	US-08-839-765-165	Sequence 165, App
108	86	100.0	106	2	US-09-136-389-165	Sequence 165, App
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120	86	100.0	106	2	US-09-771-415-25	Sequence 25, Appl
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131	86	100.0	106	2	US-09-996-288-46	Sequence 46, Appl
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143	86	100.0	106	2	US-09-996-288-70	Sequence 70, Appl
144	86	100.0	106	2	US-09-996-288-71	Sequence 71, Appl
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156	86	100.0	106	2	US-09-996-265-46	Sequence 46, Appl
157	86	100.0	106	2	US-09-996-265-49	Sequence 49, Appl
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174	86	100.0	107	1	US-08-477-728-103	Sequence 103, App
175	86	100.0	107	1	US-08-459-310-14	Sequence 14, Appl
176	86	100.0	107	1	US-08-276-852-104	Sequence 104, App
177	86	100.0	107	1	US-08-276-852-105	Sequence 105, App
178	86	100.0	107	1	US-08-276-852-107	Sequence 107, App
179	86	100.0	107	1	US-08-276-852-108	Sequence 108, App
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181	86	100.0	107	1	US-08-474-040-103	Sequence 103, App
182	86	100.0	107	1	US-08-487-200-103	Sequence 103, App
183	86	100.0	107	1	US-08-488-113B-149	Sequence 149, App
184	86	100.0	107	1	US-08-477-484B-149	Sequence 149, App
185	86	100.0	107	1	US-08-107-669D-13	Sequence 13, Appl
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187	86	100.0	107	1	US-08-899-575-104	Sequence 104, App
188	86	100.0	107	1	US-08-899-575-105	Sequence 105, App
189	86	100.0	107	1	US-08-899-575-107	Sequence 107, App
190	86	100.0	107	1	US-08-899-575-108	Sequence 108, App
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192	86	100.0	107	1	US-08-899-575-104	Sequence 104, App
193	86	100.0	107	1	US-08-899-575-105	Sequence 105, App
194	86	100.0	107	1	US-08-899-575-107	Sequence 107, App
195	86	100.0	107	1	US-08-899-575-108	Sequence 108, App
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203	86	100.0	107	1	US-08-652-558-36	Sequence 36, Appl
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206	86	100.0	107	1	US-08-378-939-14	Sequence 14, Appl
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208	86	100.0	107	2	US-08-437-642B-18	Sequence 18, Appl
209	86	100.0	107	2	US-08-437-642B-41	Sequence 41, Appl
210	86	100.0	107	2	US-08-437-642B-43	Sequence 43, Appl
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212	86	100.0	107	2	US-08-599-226-9	Sequence 9, Appli
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215	86	100.0	107	2	US-09-136-389-149	Sequence 149, App
216	86	100.0	107	2	US-08-484-537-103	Sequence 103, App
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229	86	100.0	107	2	US-09-240-274-176	Sequence 176, App
230	86	100.0	107	2	US-09-240-274-179	Sequence 179, App
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235	86	100.0	107	2	US-09-171-945-65	Sequence 65, Appl
236	86	100.0	107	2	US-09-610-838-149	Sequence 149, App
237	86	100.0	107	2	US-08-146-206C-17	Sequence 17, Appl
238	86	100.0	107	2	US-08-146-206C-18	Sequence 18, Appl
239	86	100.0	107	2	US-09-540-018-1	Sequence 1, Appli
240	86	100.0	107	2	US-09-540-018-9	Sequence 9, Appli
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244	86	100.0	107	2	US-09-705-686-18	Sequence 18, Appl
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246	86	100.0	107	2	US-09-253-794-6	Sequence 6, Appli

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259	86	100.0	107	2	US-09-848-798-39	Sequence 39, Appl
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262	86	100.0	107	2	US-09-848-798-156	Sequence 156, App
263	86	100.0	107	2	US-09-848-798-158	Sequence 158, App
264	86	100.0	107	2	US-09-848-798-175	Sequence 175, App
265	86	100.0	107	2	US-09-848-798-176	Sequence 176, App
266	86	100.0	107	2	US-09-848-798-179	Sequence 179, App
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271	86	100.0	107	2	US-09-910-059-65	Sequence 65, Appl
272	86	100.0	107	2	US-10-330-613A-26	Sequence 26, Appl
273	86	100.0	107	2	US-09-602-812A-3	Sequence 3, Appli
274	86	100.0	107	2	US-09-602-812A-5	Sequence 5, Appli
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278	86	100.0	107	4	PCT-US95-08743-105	Sequence 105, App
279	86	100.0	107	4	PCT-US95-08743-107	Sequence 107, App
280	86	100.0	107	4	PCT-US95-08743-108	Sequence 108, App
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282	86	100.0	107	4	PCT-US95-11235-66	Sequence 66, Appl
283	86	100.0	107	4	PCT-US96-09448-20	Sequence 20, Appl
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285	86	100.0	108	1	US-08-276-852-109	Sequence 109, App
286	86	100.0	108	1	US-08-899-575-102	Sequence 102, App
287	86	100.0	108	1	US-08-899-575-109	Sequence 109, App
288	86	100.0	108	1	US-08-899-575-102	Sequence 102, App
289	86	100.0	108	1	US-08-899-575-109	Sequence 109, App
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578	86	100.0	213	2	US-09-996-265-235	Sequence 235, App
579	86	100.0	213	2	US-09-996-265-237	Sequence 237, App
580	86	100.0	213	2	US-09-996-265-239	Sequence 239, App
581	86	100.0	213	2	US-09-996-265-241	Sequence 241, App
582	86	100.0	213	2	US-09-996-265-243	Sequence 243, App
583	86	100.0	213	2	US-09-996-265-245	Sequence 245, App
584	86	100.0	213	2	US-09-996-265-247	Sequence 247, App
585	86	100.0	213	2	US-09-996-265-251	Sequence 251, App
586	86	100.0	213	2	US-09-996-265-253	Sequence 253, App
587	86	100.0	213	2	US-09-996-265-255	Sequence 255, App
588	86	100.0	213	2	US-09-996-265-257	Sequence 257, App
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722	86	100.0	248	2	US-09-716-028-22	Sequence 22, Appl
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735	86	100.0	301	2	US-09-364-088-14	Sequence 14, Appl
736	86	100.0	301	2	US-09-102-716-14	Sequence 14, Appl
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776	83	96.5	107	1	US-08-477-484B-162	Sequence 162, App
777	83	96.5	107	1	US-08-107-669D-48	Sequence 48, Appl
778	83	96.5	107	1	US-08-472-788A-48	Sequence 48, Appl
779	83	96.5	107	1	US-08-477-531B-48	Sequence 48, Appl
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785	83	96.5	107	2	US-09-136-389-162	Sequence 162, App
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798	83	96.5	107	2	US-09-848-798-168	Sequence 168, App
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807	83	96.5	110	2	US-08-908-469-111	Sequence 111, App
808	83	96.5	110	2	US-08-908-469-113	Sequence 113, App
809	83	96.5	110	2	US-08-908-469-115	Sequence 115, App
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814	83	96.5	214	1	US-08-452-164A-5	Sequence 5, Appli
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818	82	95.3	15	2	US-09-543-004-89	Sequence 89, Appl
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821	82	95.3	95	2	US-10-194-975-70	Sequence 70, Appl
822	82	95.3	95	2	US-09-339-596A-42	Sequence 42, Appl
823	82	95.3	95	2	US-10-330-613A-63	Sequence 63, Appl
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828	82	95.3	105	1	US-08-899-575-89	Sequence 89, Appl
829	82	95.3	105	1	US-08-899-575-89	Sequence 89, Appl
830	82	95.3	105	4	PCT-US95-08743-89	Sequence 89, Appl

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835	82	95.3	106	2	US-08-964-690-26	Sequence 26, Appl
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843	82	95.3	107	2	US-09-240-274-169	Sequence 169, App
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845	82	95.3	107	2	US-09-848-798-164	Sequence 164, App
846	82	95.3	107	2	US-09-848-798-169	Sequence 169, App
847	82	95.3	107	4	PCT-US95-08743-84	Sequence 84, Appl
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853	82	95.3	109	2	US-09-543-004-41	Sequence 41, Appl
854	82	95.3	109	2	US-09-543-004-44	Sequence 44, Appl
855	82	95.3	109	2	US-09-905-243-67	Sequence 67, Appl
856	82	95.3	109	4	PCT-US95-11235-69	Sequence 69, Appl
857	82	95.3	111	1	US-07-634-278-55	Sequence 55, Appl
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859	82	95.3	111	1	US-08-477-728-55	Sequence 55, Appl
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862	82	95.3	111	1	US-08-474-040-71	Sequence 71, Appl
863	82	95.3	111	1	US-08-487-200-55	Sequence 55, Appl
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866	82	95.3	111	2	US-08-484-537-71	Sequence 71, Appl
867	82	95.3	134	2	US-09-472-087-23	Sequence 23, Appl
868	82	95.3	134	2	US-09-472-087-97	Sequence 97, Appl
869	81	94.2	40	2	US-08-812-586-39	Sequence 39, Appl
870	81	94.2	40	2	US-09-535-832A-36	Sequence 36, Appl
871	81	94.2	88	2	US-09-905-243-62	Sequence 62, Appl
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885	81	94.2	107	2	US-09-848-798-173	Sequence 173, App
886	81	94.2	107	2	US-09-848-798-174	Sequence 174, App
887	81	94.2	107	2	US-09-905-243-77	Sequence 77, Appl
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892	81	94.2	111	1	US-08-899-575-150	Sequence 150, App
893	81	94.2	111	4	PCT-US95-08743-150	Sequence 150, App
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899	81	94.2	374	2	US-08-812-586-15	Sequence 15, Appl
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903	80	93.0	15	2	US-08-454-899G-102	Sequence 102, App
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906	80	93.0	95	2	US-10-194-975-59	Sequence 59, Appl
907	80	93.0	95	2	US-10-330-613A-47	Sequence 47, Appl
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909	80	93.0	95	2	US-10-330-613A-51	Sequence 51, Appl
910	80	93.0	95	2	US-10-330-613A-52	Sequence 52, Appl
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916	80	93.0	106	2	US-09-240-274-159	Sequence 159, App
917	80	93.0	106	2	US-09-848-798-159	Sequence 159, App
918	80	93.0	106	4	PCT-US95-10053-31	Sequence 31, Appl
919	80	93.0	106	4	PCT-US96-09448-34	Sequence 34, Appl
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921	80	93.0	107	1	US-08-476-349A-86	Sequence 86, Appl
922	80	93.0	107	1	US-08-561-521-6	Sequence 6, Appli
923	80	93.0	107	1	US-08-652-558-2	Sequence 2, Appli
924	80	93.0	107	1	US-08-652-558-34	Sequence 34, Appl
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927	80	93.0	107	1	US-08-116-247-26	Sequence 26, Appl
928	80	93.0	107	2	US-09-240-274-29	Sequence 29, Appl
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932	80	93.0	107	2	US-09-999-021-15	Sequence 15, Appl
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934	80	93.0	107	2	US-09-348-224-26	Sequence 26, Appl
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939	80	93.0	107	2	US-09-910-059-71	Sequence 71, Appl
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949	80	93.0	108	1	US-08-116-247-9	Sequence 9, Appli
950	80	93.0	108	1	US-08-602-725-29	Sequence 29, Appl
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952	80	93.0	108	2	US-08-454-899G-100	Sequence 100, App
953	80	93.0	108	2	US-09-348-224-9	Sequence 9, Appli
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962	80	93.0	111	1	US-08-111-080-32	Sequence 32, Appl
963	80	93.0	111	1	US-08-275-053-14	Sequence 14, Appl
964	80	93.0	111	1	US-08-211-980-30	Sequence 30, Appl
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971	80	93.0	112	2	US-08-207-861-33	Sequence 33, Appl
972	80	93.0	112	2	US-08-859-648-25	Sequence 25, Appl
973	80	93.0	112	2	US-08-859-648-33	Sequence 33, Appl
974	80	93.0	113	2	US-09-155-107-20	Sequence 20, Appl
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976	80	93.0	113	2	US-09-025-203-9	Sequence 9, Appli

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979	80	93.0	113	2	US-09-999-021-9	Sequence 9, Appli
980	80	93.0	113	2	US-09-999-021-14	Sequence 14, Appl
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982	80	93.0	113	2	US-09-999-025-9	Sequence 9, Appli
983	80	93.0	113	2	US-09-999-025-14	Sequence 14, Appl
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985	80	93.0	113	2	US-10-040-997-9	Sequence 9, Appli
986	80	93.0	113	2	US-10-040-997-14	Sequence 14, Appl
987	80	93.0	113	2	US-09-999-040-8	Sequence 8, Appli
988	80	93.0	113	2	US-09-999-040-9	Sequence 9, Appli
989	80	93.0	113	2	US-09-999-040-14	Sequence 14, Appl
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991	80	93.0	113	2	US-09-998-817-9	Sequence 9, Appli
992	80	93.0	113	2	US-09-998-817-14	Sequence 14, Appl
993	80	93.0	114	2	US-09-217-268B-35	Sequence 35, Appl
994	80	93.0	126	1	US-08-656-586-6	Sequence 6, Appli
995	80	93.0	150	2	US-09-472-087-24	Sequence 24, Appl
996	80	93.0	150	2	US-09-472-087-98	Sequence 98, Appl
997	80	93.0	213	2	US-08-397-411-12	Sequence 12, Appl
998	80	93.0	235	2	US-09-171-945-99	Sequence 99, Appl
999	80	93.0	235	2	US-09-910-059-99	Sequence 99, Appl
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ALIGNMENTS

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RESULT 1
US-07-946-421-8
; Sequence 8, Application US/07946421
; Patent No. 5558864
;  GENERAL INFORMATION:
;    APPLICANT:  Bendig, Mary M.
;    APPLICANT:  Kettleborough, Catherine A.
;    APPLICANT:  Saldanha, Jose
;    TITLE OF INVENTION:  Humanized and Chimeric Monoclonal
;    TITLE OF INVENTION:  Antibodies
;    NUMBER OF SEQUENCES:  42
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Millen, White, Zelano & Branigan, P.C.
;      STREET:  2200 Clarendon Boulevard, Suite 1400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/946,421
;      FILING DATE:  06-NOV-1992
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/EP92/00480
;      FILING DATE:  04-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 911933892
;      FILING DATE:  06-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hamlet-King, Diana
;      REGISTRATION NUMBER:  33,302
;      REFERENCE/DOCKET NUMBER:  Merck 1430
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703-243-6333
;      TELEFAX:  703-243-6410
;      TELEX:  64191
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-07-946-421-8

  Query Match             100.0%;  Score 86;  DB 1;  Length 15;
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Db          1 WYQQKPGKAPKLLIY 15


RESULT 2
US-08-137-117D-121
; Sequence 121, Application US/08137117D
; Patent No. 5795965
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  BENDIG, Mary
;    APPLICANT:  JONES, Steven
;    APPLICANT:  SALDANHA, Jose
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6 RECEPTOR
;    NUMBER OF SEQUENCES:  158
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,117D
;      FILING DATE:  20-DEC-1993
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP92/00544
;      FILING DATE:  24-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 4-32084
;      FILING DATE:  19-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 3-95476
;      FILING DATE:  25-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/126/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  121:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-137-117D-121

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Db          1 WYQQKPGKAPKLLIY 15


RESULT 3
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; Sequence 140, Application US/08137117D
; Patent No. 5795965
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  BENDIG, Mary
;    APPLICANT:  JONES, Steven
;    APPLICANT:  SALDANHA, Jose
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6 RECEPTOR
;    NUMBER OF SEQUENCES:  158
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,117D
;      FILING DATE:  20-DEC-1993
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP92/00544
;      FILING DATE:  24-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 4-32084
;      FILING DATE:  19-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 3-95476
;      FILING DATE:  25-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/126/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  140:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-137-117D-140

  Query Match             100.0%;  Score 86;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
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Db          1 WYQQKPGKAPKLLIY 15


RESULT 4
US-08-436-717-121
; Sequence 121, Application US/08436717
; Patent No. 5817790
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  BENDIG, Mary
;    APPLICANT:  JONES, Steven
;    APPLICANT:  SALDANHA, Jose
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6 RECEPTOR
;    NUMBER OF SEQUENCES:  158
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/436,717
;      FILING DATE:
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/137,117
;      FILING DATE:  20-DEC-1993
;      APPLICATION NUMBER:  WO PCT/JP92/00544
;      FILING DATE:  24-APR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 4-32084
;      FILING DATE:  19-FEB-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 3-95476
;      FILING DATE:  25-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/126/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  121:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-436-717-121

  Query Match             100.0%;  Score 86;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 5
US-08-436-717-140
; Sequence 140, Application US/08436717
; Patent No. 5817790
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  BENDIG, Mary
;    APPLICANT:  JONES, Steven
;    APPLICANT:  SALDANHA, Jose
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6 RECEPTOR
;    NUMBER OF SEQUENCES:  158
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
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;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;      FILING DATE:
;      CLASSIFICATION:  536
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;      APPLICATION NUMBER:  US/08/137,117
;      FILING DATE:  20-DEC-1993
;      APPLICATION NUMBER:  WO PCT/JP92/00544
;      FILING DATE:  24-APR-1992
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;      APPLICATION NUMBER:  JP 4-32084
;      FILING DATE:  19-FEB-1992
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;      APPLICATION NUMBER:  JP 3-95476
;      FILING DATE:  25-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/126/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  140:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-436-717-140

  Query Match             100.0%;  Score 86;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 6
US-08-553-501A-66
; Sequence 66, Application US/08553501A
; Patent No. 5856135
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  HIRATA, Yuichi
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,501A
;      FILING DATE:  20-FEB-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/00859
;      FILING DATE:  30-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-129787
;      FILING DATE:  31-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/177/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  66:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-553-501A-66

  Query Match             100.0%;  Score 86;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 7
US-08-553-501A-70
; Sequence 70, Application US/08553501A
; Patent No. 5856135
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  HIRATA, Yuichi
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,501A
;      FILING DATE:  20-FEB-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/00859
;      FILING DATE:  30-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-129787
;      FILING DATE:  31-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/177/AAOK
;    TELECOMMUNICATION INFORMATION:
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;       TELEPHONE:  (202)672-5300
;       TELEFAX:  (202)672-5399
;       TELEX:  904136
;   INFORMATION FOR SEQ ID NO:  70:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  15 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-553-501A-70

  Query Match             100.0%;  Score 86;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 8
US-08-318-157B-27
; Sequence 27, Application US/08318157B
; Patent No. 5874540
;  GENERAL INFORMATION:
;    APPLICANT:  HANSEN, Hans J.
;    APPLICANT:  ARMOUR, Kathryn L.
;    TITLE OF INVENTION:  CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;    TITLE OF INVENTION:  MOUSE MONOCLONAL ANTIBODIES
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,157B
;      FILING DATE:  05-OCT-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SAXE, Bernhard D.
;      REGISTRATION NUMBER:  28,665
;      REFERENCE/DOCKET NUMBER:  18733/464
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-157B-27

  Query Match             100.0%;  Score 86;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 9
US-08-765-783A-88
; Sequence 88, Application US/08765783A
; Patent No. 5994524
;  GENERAL INFORMATION:
;    APPLICANT:  Matsushima, Kouji
;    APPLICANT:  Matsumoto, Yoshihiro
;    APPLICANT:  Yamada, Yoshiki
;    APPLICANT:  Sato, Koh
;    APPLICANT:  Tsuchiya, Masayuki
;    APPLICANT:  Yamazaki, Tatsumi
;    TITLE OF INVENTION:  Reshaped Human Antibody to
;    TITLE OF INVENTION:  Interleukin-8
;    NUMBER OF SEQUENCES:  105
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/765,783A
;      FILING DATE:  07-MAR-1997
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  35029-20001.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-822-0168
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  88:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-765-783A-88

  Query Match             100.0%;  Score 86;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 10
US-08-470-139-11
; Sequence 11, Application US/08470139
; Patent No. 5998586
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Interleukin-5 specific recombinant antibodies
;    NUMBER OF SEQUENCES:  28
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,139
;      FILING DATE:  06 JUNE-1995
```

```
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  TRUJILLO, DOREEN YATKO
;      REGISTRATION NUMBER:  35,719
;      REFERENCE/DOCKET NUMBER:  CARP-0044
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-470-139-11

  Query Match             100.0%;  Score 86;  DB 1;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 11
US-08-649-100-28
; Sequence 28, Application US/08649100
; Patent No. 6114507
;  GENERAL INFORMATION:
;    APPLICANT:  SHIRAKAWA, KAMON
;    APPLICANT:  MATUSUE, TOMOKAZU
;    APPLICANT:  NAGATA, SHIGEKAZU
;    APPLICANT:  CO, MAN SUNG
;    APPLICANT:  VASQUEZ, MAXIMILIANO
;    TITLE OF INVENTION:  ANTI-FAS LIGAND ANTIBODY AND ASSAY
;    TITLE OF INVENTION:  METHOD USING THE ANTI-FAS LIGAND ANTIBODY
;    NUMBER OF SEQUENCES:  41
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BIRCH, STEWART, KOLASCH AND BIRCH
;      STREET:  PO BOX 747
;      CITY:  FALLS CHURCH
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22040-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/649,100
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MURPHY JR, GERALD M
;      REGISTRATION NUMBER:  28,977
;      REFERENCE/DOCKET NUMBER:  1110-160
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-649-100-28

  Query Match             100.0%;  Score 86;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 12
US-09-205-231-66
; Sequence 66, Application US/09205231
; Patent No. 6121423
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  HIRATA, Yuichi
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/205,231
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,501
;      FILING DATE:  20-FEB-1996
;      APPLICATION NUMBER:  WO PCT/JP94/00859
;      FILING DATE:  30-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-129787
;      FILING DATE:  31-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/177/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  66:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-205-231-66

  Query Match             100.0%;  Score 86;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 13
US-09-205-231-70
; Sequence 70, Application US/09205231
; Patent No. 6121423
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  HIRATA, Yuichi
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
```

```
;    TITLE OF INVENTION:  INTERLEUKIN-6
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/205,231
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,501
;      FILING DATE:  20-FEB-1996
;      APPLICATION NUMBER:  WO PCT/JP94/00859
;      FILING DATE:  30-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-129787
;      FILING DATE:  31-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/177/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  70:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-205-231-70

  Query Match             100.0%;  Score 86;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 14
US-08-569-147-38
; Sequence 38, Application US/08569147
; Patent No. 6180377
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  HUMANISED ANTIBODIES
;    NUMBER OF SEQUENCES:  95
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz &
;      ADDRESSEE:  No. 6180377ris, LLP
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  U.S.A.
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/569,147
;      FILING DATE:  25-March-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Trujillo, Doreen Yatko
;      REGISTRATION NUMBER:  35,719
;      REFERENCE/DOCKET NUMBER:  CARP-0047
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  38:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-569-147-38

  Query Match             100.0%;  Score 86;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 15
US-09-416-557-88
; Sequence 88, Application US/09416557
; Patent No. 6245894
;  GENERAL INFORMATION:
;    APPLICANT:  Matsushima, Kouji
;    APPLICANT:  Matsumoto, Yoshihiro
;    APPLICANT:  Yamada, Yoshiki
;    APPLICANT:  Sato, Koh
;    APPLICANT:  Tsuchiya, Masayuki
;    APPLICANT:  Yamazaki, Tatsumi
;    TITLE OF INVENTION:  Reshaped Human Antibody to
;    TITLE OF INVENTION:  Interleukin-8
;    NUMBER OF SEQUENCES:  105
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORRISON & FOERSTER
;      STREET:  2000 Pennsylvania Avenue, NW, suite 5500
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20006-1888
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/416,557
;      FILING DATE:  12-October-1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/765,783
;      FILING DATE:  7-March-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murashige, Kate H
;      REGISTRATION NUMBER:  29,959
;      REFERENCE/DOCKET NUMBER:  35029-20001.10
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-887-1500
;      TELEFAX:  202-822-0168
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  88:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 amino acids
;      TYPE:  amino acid
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-416-557-88

  Query Match             100.0%;  Score 86;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 16
US-09-347-061-11
; Sequence 11, Application US/09347061
; Patent No. 6316227
; GENERAL INFORMATION:
;  APPLICANT:  Bodmer, Mark
;  APPLICANT:  Athwal, Diljeet Singh
;  APPLICANT:  Emtage, John Spencer
;  TITLE OF INVENTION:   Interleukin-5 Specific Recombinant Antibodies
;  FILE REFERENCE:   CARP-0071
;  CURRENT APPLICATION NUMBER: US/09/347,061
;  CURRENT FILING DATE:  1999-07-02
;  NUMBER OF SEQ ID NOS:   28
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 11
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Consensus
US-09-347-061-11

  Query Match             100.0%;  Score 86;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 17
US-09-425-638A-85
; Sequence 85, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
;  APPLICANT:      Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
;  APPLICANT:  Lloyd J. Old
;  TITLE OF INVENTION:      A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO
;  FILE REFERENCE:      LUD 5630
;  CURRENT APPLICATION NUMBER: US/09/425,638A
;  CURRENT FILING DATE:  1999-10-22
;  NUMBER OF SEQ ID NOS:      129
; SEQ ID NO 85
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-425-638A-85

  Query Match             100.0%;  Score 86;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 18
US-09-425-638A-86
; Sequence 86, Application US/09425638A
; Patent No. 6342587
; GENERAL INFORMATION:
;  APPLICANT:      Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
;  APPLICANT:  Lloyd J. Old
;  TITLE OF INVENTION:      A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO
;  FILE REFERENCE:      LUD 5630
;  CURRENT APPLICATION NUMBER: US/09/425,638A
;  CURRENT FILING DATE:  1999-10-22
;  NUMBER OF SEQ ID NOS:      129
; SEQ ID NO 86
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-425-638A-86

  Query Match             100.0%;  Score 86;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 19
US-09-543-004-85
; Sequence 85, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
;  APPLICANT:      Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
;  APPLICANT:  Lloyd J. Old
;  TITLE OF INVENTION:      A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO
;  FILE REFERENCE:      LUD 5630.1
;  CURRENT APPLICATION NUMBER: US/09/543,004
;  CURRENT FILING DATE:  2000-04-04
;  PRIOR APPLICATION NUMBER:      09/425,638
;  PRIOR FILING DATE:      1999-10-22
;  NUMBER OF SEQ ID NOS:      129
; SEQ ID NO 85
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-543-004-85

  Query Match             100.0%;  Score 86;  DB 2;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 20
US-09-543-004-86
; Sequence 86, Application US/09543004
; Patent No. 6346249
; GENERAL INFORMATION:
;  APPLICANT:      Carlos F. Barbas III, Christoph Rader, Gerd Ritter, Sydney Welt and
;  APPLICANT:  Lloyd J. Old
;  TITLE OF INVENTION:      A33 ANTIGEN SPECIFIC IMMUNOGLOBULIN PRODUCTS AND USES THEREO
;  FILE REFERENCE:      LUD 5630.1
;  CURRENT APPLICATION NUMBER: US/09/543,004
;  CURRENT FILING DATE:  2000-04-04
;  PRIOR APPLICATION NUMBER:      09/425,638
;  PRIOR FILING DATE:      1999-10-22
;  NUMBER OF SEQ ID NOS:      129
; SEQ ID NO 86
```

; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-543-004-86

Query Match 100.0%; Score 86; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 21
US-09-253-794-27
; Sequence 27, Application US/09253794
; Patent No. 6676924
; GENERAL INFORMATION:
; APPLICANT: HANSEN, Hans J.
; ARMOUR, Kathryn L.
; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
; MOUSE MONOCLONAL ANTIBODIES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,794
; FILING DATE: 22-Feb-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,157
; FILING DATE: 05-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 18733/464
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-253-794-27

Query Match 100.0%; Score 86; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 22
US-09-647-468-126
; Sequence 126, Application US/09647468
; Patent No. 6677436
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: ADACHI, HIDEKI
; APPLICANT: YABUTA, NAOHIRO
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
; TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0289
; CURRENT APPLICATION NUMBER: US/09/647,468
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: PCT/JP99/01768
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: JP 10-91850
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 183
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
; OTHER INFORMATION: of FR2 of versions "a", "b" and "c" of humanized L
; OTHER INFORMATION: chain V region
US-09-647-468-126

Query Match 100.0%; Score 86; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 23
US-09-563-222C-75
; Sequence 75, Application US/09563222C
; Patent No. 6696620
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-563-222C-75

Query Match 100.0%; Score 86; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 1 WYQQKPGKAPKLLIY 15

RESULT 24
US-09-855-271-11
; Sequence 11, Application US/09855271
; Patent No. 6734286

```
; GENERAL INFORMATION:
;  APPLICANT: Bodmer, Mark W
;  APPLICANT:  Athwal, Diljeet Singh
;  APPLICANT:  Emtage, John Spencer
;  TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
;  FILE REFERENCE: CARP-0088
;  CURRENT APPLICATION NUMBER: US/09/855,271
;  CURRENT FILING DATE:  2001-05-15
;  PRIOR APPLICATION NUMBER: 09/347,061
;  PRIOR FILING DATE: 1999-07-02
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Consensus
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Consensus
US-09-855-271-11

  Query Match           100.0%;  Score 86;  DB 2;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 25
US-08-812-586-40
; Sequence 40, Application US/08812586
; Patent No. 6048704
;  GENERAL INFORMATION:
;    APPLICANT:  Martin David Tilson
;    TITLE OF INVENTION:  PURIFIED AND RECOMBINANT ANTIGENIC
;    TITLE OF INVENTION:  PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYM (AAA)
;    TITLE OF INVENTION:  DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
;    NUMBER OF SEQUENCES:  61
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/812,586
;      FILING DATE:  07-MAR-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  0575/53862-A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  40:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  40 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-812-586-40

  Query Match           100.0%;  Score 86;  DB 2;  Length 40;
  Best Local Similarity  100.0%;  Pred. No. 1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 26
US-09-535-832A-37
; Sequence 37, Application US/09535832A
; Patent No. 6537769
; GENERAL INFORMATION:
;  APPLICANT:  Tilson, Martin David
;  TITLE OF INVENTION:  Purified and Recombinant Antigenic Proteins Associated
;  TITLE OF INVENTION:  with Abdominal Aortic Aneurysm (AAA) Disease, and
;  TITLE OF INVENTION:  Diagnostic and Therapeutic use Thereof
;  FILE REFERENCE:  53862-AZ
;  CURRENT APPLICATION NUMBER: US/09/535,832A
;  CURRENT FILING DATE:  2000-03-28
;  NUMBER OF SEQ ID NOS:  57
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 37
;   LENGTH: 40
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Source:
;   OTHER INFORMATION: Synthesized
US-09-535-832A-37

  Query Match           100.0%;  Score 86;  DB 2;  Length 40;
  Best Local Similarity  100.0%;  Pred. No. 1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 27
US-08-765-179B-10
; Sequence 10, Application US/08765179B
; Patent No. 5854027
;  GENERAL INFORMATION:
;    APPLICANT:  STEIPE, Boris
;    APPLICANT:  STEINBACHER, Stefan
;    TITLE OF INVENTION:  PROCESS FOR MODIFYING THE STABILITY
;    TITLE OF INVENTION:  OF ANTIBODIES
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Nikaido, Marmelstein, Murray & Oram LLP
;      STREET:  655 Fifteenth Street N.W. Suite 330
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-5701
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/765,179B
;      FILING DATE:  14-JAN-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/02626
;      FILING DATE:  06-JUL-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  DE P 44 25 115.7
;      FILING DATE:  15-JUL-1994
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;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  64 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-765-179B-10

  Query Match             100.0%;  Score 86;  DB 1;  Length 64;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          4 WYQQKPGKAPKLLIY 18


RESULT 28
US-08-554-840-9
; Sequence 9, Application US/08554840
; Patent No. 6001358
;  GENERAL INFORMATION:
;    APPLICANT:  BLACK, Amelia
;    APPLICANT:  HANNA, Nabil
;    APPLICANT:  PADLAN, Eduardo A.
;    APPLICANT:  NEWMAN, Roland A.
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES TO HUMAN gp39,
;    TITLE OF INVENTION:  COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/554,840
;      FILING DATE:  07-NOV-1995
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-127
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  70 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-554-840-9

  Query Match             100.0%;  Score 86;  DB 2;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 29
US-08-925-339-9
; Sequence 9, Application US/08925339
; Patent No. 6440418
;  GENERAL INFORMATION:
;    APPLICANT:  BLACK, Amelia
;    APPLICANT:  HANNA, Nabil
;    APPLICANT:  PADLAN, Eduardo A.
;    APPLICANT:  NEWMAN, Roland A.
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES TO HUMAN gp39,
;    TITLE OF INVENTION:  COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/925,339
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/554,840
;      FILING DATE:  07-NOV-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-127
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  70 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-925-339-9

  Query Match             100.0%;  Score 86;  DB 2;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 30
US-09-332-595-9
; Sequence 9, Application US/09332595
; Patent No. 6506383
;  GENERAL INFORMATION:
;    APPLICANT:  BLACK, Amelia
;    APPLICANT:  HANNA, Nabil
;    APPLICANT:  PADLAN, Eduardo A.
;    APPLICANT:  NEWMAN, Roland A.
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES TO HUMAN gp39,
;    TITLE OF INVENTION:  COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
```

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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/332,595
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/554,840
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-127
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  70 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-332-595-9

  Query Match             100.0%;  Score 86;  DB 2;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 31
US-08-851-362D-20
; Sequence 20, Application US/08851362D
; Patent No. 6235883
; GENERAL INFORMATION:
;  APPLICANT:  Jakobovits, Aya
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Gallo, Michael
;  APPLICANT:  Jia, Xiao-Chi
;  TITLE OF INVENTION:  Human Monoclonal Antibodies to Epidermal
;  TITLE OF INVENTION:  Growth Factor Receptor
;  FILE REFERENCE:  Cell 4.20
;  CURRENT APPLICATION NUMBER: US/08/851,362D
;  CURRENT FILING DATE:  1997-05-05
;  NUMBER OF SEQ ID NOS:  49
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 76
;   TYPE: PRT
;   ORGANISM: human
US-08-851-362D-20

  Query Match             100.0%;  Score 86;  DB 2;  Length 76;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         16 WYQQKPGKAPKLLIY 30


RESULT 32
US-08-851-362D-21
; Sequence 21, Application US/08851362D
; Patent No. 6235883
; GENERAL INFORMATION:
;  APPLICANT:  Jakobovits, Aya
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Gallo, Michael
;  APPLICANT:  Jia, Xiao-Chi
;  TITLE OF INVENTION:  Human Monoclonal Antibodies to Epidermal
;  TITLE OF INVENTION:  Growth Factor Receptor
;  FILE REFERENCE:  Cell 4.20
;  CURRENT APPLICATION NUMBER: US/08/851,362D
;  CURRENT FILING DATE:  1997-05-05
;  NUMBER OF SEQ ID NOS:  49
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 76
;   TYPE: PRT
;   ORGANISM: human
US-08-851-362D-21

  Query Match             100.0%;  Score 86;  DB 2;  Length 76;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         16 WYQQKPGKAPKLLIY 30


RESULT 33
US-08-553-501A-85
; Sequence 85, Application US/08553501A
; Patent No. 5856135
;  GENERAL INFORMATION:
;    APPLICANT:  TSUCHIYA, Masayuki
;    APPLICANT:  SATO, Koh
;    APPLICANT:  HIRATA, Yuichi
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  INTERLEUKIN-6
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/553,501A
;      FILING DATE:  20-FEB-1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/00859
;      FILING DATE:  30-MAY-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-129787
;      FILING DATE:  31-MAY-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/177/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  85:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  80 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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US-08-553-501A-85

Query Match 100.0%; Score 86; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38
```

RESULT 34
US-08-765-783A-104
; Sequence 104, Application US/08765783A
; Patent No. 5994524
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,783A
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX:
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-765-783A-104

Query Match 100.0%; Score 86; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38
```

RESULT 35
US-09-205-231-85
; Sequence 85, Application US/09205231
; Patent No. 6121423
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, Masayuki
; APPLICANT: SATO, Koh
; APPLICANT: HIRATA, Yuichi
; TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/205,231
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/553,501
; FILING DATE: 20-FEB-1996
; APPLICATION NUMBER: WO PCT/JP94/00859
; FILING DATE: 30-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-129787
; FILING DATE: 31-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/177/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 80 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-205-231-85

Query Match 100.0%; Score 86; DB 2; Length 80;
Best Local Similarity 100.0%; Pred. No. 2e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38
```

RESULT 36
US-09-416-557-104
; Sequence 104, Application US/09416557
; Patent No. 6245894
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; APPLICANT: Matsumoto, Yoshihiro
; APPLICANT: Yamada, Yoshiki
; APPLICANT: Sato, Koh
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; TITLE OF INVENTION: Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500

```
;       CITY:  Washington
;       STATE:  DC
;       COUNTRY:  USA
;       ZIP:  20006-1888
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/416,557
;       FILING DATE:  12-October-1999
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/765,783
;       FILING DATE:  7-March-1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Murashige, Kate H
;       REGISTRATION NUMBER:  29,959
;       REFERENCE/DOCKET NUMBER:  35029-20001.10
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  202-887-1500
;       TELEFAX:  202-822-0168
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  104:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  80 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-09-416-557-104

  Query Match             100.0%;  Score 86;  DB 2;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 2e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 37
US-09-269-921-130
; Sequence 130, Application US/09269921
; Patent No. 6699974
; GENERAL INFORMATION:
;  APPLICANT: Ono, Koichiro
;  APPLICANT: Ohtomo, Toshihiko
;  APPLICANT: Tsuchiya, Masayuki
;  APPLICANT: Yoshimura, Yasushi
;  APPLICANT: Koishihara, Yasuo
;  TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
;  FILE REFERENCE: 35029-20007.00
;  CURRENT APPLICATION NUMBER: US/09/269,921
;  CURRENT FILING DATE: 1999-04-01
;  EARLIER APPLICATION NUMBER: PCT/JP97/03553
;  EARLIER FILING DATE: 1997-10-03
;  EARLIER APPLICATION NUMBER: JP 8-264756
;  EARLIER FILING DATE: 1996-10-04
;  NUMBER OF SEQ ID NOS: 137
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
;   LENGTH: 80
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: HuSGI
;  PUBLICATION INFORMATION:
;   AUTHORS: Kabat, E.A. et al.
;   JOURNAL: SEQUENCE OF PROTEINS OF IMMUNOLOGICAL INTEREST, U.S. DEPT.
;   DATE: 1991
US-09-269-921-130

  Query Match             100.0%;  Score 86;  DB 2;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 2e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 38
US-09-269-921-131
; Sequence 131, Application US/09269921
; Patent No. 6699974
; GENERAL INFORMATION:
;  APPLICANT: Ono, Koichiro
;  APPLICANT: Ohtomo, Toshihiko
;  APPLICANT: Tsuchiya, Masayuki
;  APPLICANT: Yoshimura, Yasushi
;  APPLICANT: Koishihara, Yasuo
;  TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
;  FILE REFERENCE: 35029-20007.00
;  CURRENT APPLICATION NUMBER: US/09/269,921
;  CURRENT FILING DATE: 1999-04-01
;  EARLIER APPLICATION NUMBER: PCT/JP97/03553
;  EARLIER FILING DATE: 1997-10-03
;  EARLIER APPLICATION NUMBER: JP 8-264756
;  EARLIER FILING DATE: 1996-10-04
;  NUMBER OF SEQ ID NOS: 137
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
;   LENGTH: 80
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: REI
;  PUBLICATION INFORMATION:
;   AUTHORS: Recchmann, L. et al.
;   JOURNAL: NATURE
;   VOLUME: 322
;   PAGES: 21-25
;   DATE: 1998
US-09-269-921-131

  Query Match             100.0%;  Score 86;  DB 2;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 2e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 39
US-09-254-180C-160
; Sequence 160, Application US/09254180C
; Patent No. 6777540
; GENERAL INFORMATION:
;  APPLICANT: OKUMURA, Ko
;  APPLICANT:  EDA, Yasuyuki
;  APPLICANT:  MAEDA, Hiroaki
;  APPLICANT:  USHIO, Yoshitaka
;  APPLICANT:  HIGUCHI, Hirofumi
;  APPLICANT:  NAKATA, Motomi
;  TITLE OF INVENTION: Humanized Immunoglobulins Specifically Reactive to Fas Ligand or F
;  TITLE OF INVENTION:  Fragments Thereof, and Apoptosis-Induced Site From Fas Ligand
;  FILE REFERENCE: 050006-0055
;  CURRENT APPLICATION NUMBER: US/09/254,180C
;  CURRENT FILING DATE:  1999-04-15
;  PRIOR APPLICATION NUMBER: PCT/JP97/02983
;  PRIOR FILING DATE: 1997-08-27
;  PRIOR APPLICATION NUMBER: 271546/1996
;  PRIOR FILING DATE: 1996-09-20
;  PRIOR APPLICATION NUMBER: 231472/1996
```

```
;  PRIOR FILING DATE: 1996-09-02
;  NUMBER OF SEQ ID NOS: 183
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 160
;   LENGTH: 81
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-09-254-180C-160

  Query Match            100.0%;  Score 86;  DB 2;  Length 81;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 40
US-08-646-265A-112
; Sequence 112, Application US/08646265A
; Patent No. 6214973
;  GENERAL INFORMATION:
;    APPLICANT:  OHTOMO, Toshihiko
;    APPLICANT:  SATO, Koh
;    APPLICANT:  TSUCHIYA, Masayuki
;    TITLE OF INVENTION:  RESHAPED HUMAN ANTIBODY TO HUMAN
;    TITLE OF INVENTION:  MEDULLOBLASTOMA CELLS
;    NUMBER OF SEQUENCES:  132
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/646,265A
;      FILING DATE:  09-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/JP94/01763
;      FILING DATE:  19-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 5-291078
;      FILING DATE:  19-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/184
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  112:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  87 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-646-265A-112

  Query Match            100.0%;  Score 86;  DB 2;  Length 87;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 41
US-09-905-243-29
; Sequence 29, Application US/09905243
; Patent No. 6936698
; GENERAL INFORMATION:
;  APPLICANT: Taylor, Alexander H
;  TITLE OF INVENTION: Monoclonal Antibodies with Reduced
;  TITLE OF INVENTION:  Immunogenicity
;  FILE REFERENCE: P50770
;  CURRENT APPLICATION NUMBER: US/09/905,243
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 09/300,970
;  PRIOR FILING DATE: 1999-04-28
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
;   LENGTH: 88
;   TYPE: PRT
;   ORGANISM: Pan troglodytes
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (24)...(34)
;   OTHER INFORMATION: CDRI
;   NAME/KEY: DOMAIN
;   LOCATION: (50)...(66)
;   OTHER INFORMATION: CDRII
US-09-905-243-29

  Query Match            100.0%;  Score 86;  DB 2;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 42
US-09-905-243-31
; Sequence 31, Application US/09905243
; Patent No. 6936698
; GENERAL INFORMATION:
;  APPLICANT: Taylor, Alexander H
;  TITLE OF INVENTION: Monoclonal Antibodies with Reduced
;  TITLE OF INVENTION:  Immunogenicity
;  FILE REFERENCE: P50770
;  CURRENT APPLICATION NUMBER: US/09/905,243
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 09/300,970
;  PRIOR FILING DATE: 1999-04-28
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 31
;   LENGTH: 88
;   TYPE: PRT
;   ORGANISM: Pan troglodytes
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (24)...(34)
;   OTHER INFORMATION: CDRI
;   NAME/KEY: DOMAIN
;   LOCATION: (50)...(66)
;   OTHER INFORMATION: CDRII
US-09-905-243-31

  Query Match            100.0%;  Score 86;  DB 2;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 43
US-09-905-243-35
; Sequence 35, Application US/09905243
; Patent No. 6936698
; GENERAL INFORMATION:
;  APPLICANT: Taylor, Alexander H
;  TITLE OF INVENTION: Monoclonal Antibodies with Reduced
;  TITLE OF INVENTION:  Immunogenicity
;  FILE REFERENCE: P50770
;  CURRENT APPLICATION NUMBER: US/09/905,243
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 09/300,970
;  PRIOR FILING DATE: 1999-04-28
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
;   LENGTH: 88
;   TYPE: PRT
;   ORGANISM: Pan troglodytes
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (24)...(34)
;   OTHER INFORMATION: CDRI
;   NAME/KEY: DOMAIN
;   LOCATION: (50)...(66)
;   OTHER INFORMATION: CDRII
US-09-905-243-35

  Query Match             100.0%;  Score 86;  DB 2;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 44
US-09-905-243-36
; Sequence 36, Application US/09905243
; Patent No. 6936698
; GENERAL INFORMATION:
;  APPLICANT: Taylor, Alexander H
;  TITLE OF INVENTION: Monoclonal Antibodies with Reduced
;  TITLE OF INVENTION:  Immunogenicity
;  FILE REFERENCE: P50770
;  CURRENT APPLICATION NUMBER: US/09/905,243
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 09/300,970
;  PRIOR FILING DATE: 1999-04-28
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
;   LENGTH: 88
;   TYPE: PRT
;   ORGANISM: Pan troglodytes
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (24)...(34)
;   OTHER INFORMATION: CDRI
;   NAME/KEY: DOMAIN
;   LOCATION: (50)...(66)
;   OTHER INFORMATION: CDRII
US-09-905-243-36

  Query Match             100.0%;  Score 86;  DB 2;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 45
US-09-905-243-63
; Sequence 63, Application US/09905243
; Patent No. 6936698
; GENERAL INFORMATION:
;  APPLICANT: Taylor, Alexander H
;  TITLE OF INVENTION: Monoclonal Antibodies with Reduced
;  TITLE OF INVENTION:  Immunogenicity
;  FILE REFERENCE: P50770
;  CURRENT APPLICATION NUMBER: US/09/905,243
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 09/300,970
;  PRIOR FILING DATE: 1999-04-28
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 63
;   LENGTH: 88
;   TYPE: PRT
;   ORGANISM: Macaca cynomolgus
;   FEATURE:
;   NAME/KEY: DOMAIN
;   LOCATION: (24)...(34)
;   OTHER INFORMATION: CDRI
;   NAME/KEY: DOMAIN
;   LOCATION: (50)...(56)
;   OTHER INFORMATION: CDRII
US-09-905-243-63

  Query Match             100.0%;  Score 86;  DB 2;  Length 88;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 46
US-09-199-149-15
; Sequence 15, Application US/09199149
; Patent No. 6160099
; GENERAL INFORMATION:
;  APPLICANT: Jonak, Zdenka L.
;  APPLICANT: Taylor, Alexander H.
;  APPLICANT: Trulli Jr., Stephen H.
;  APPLICANT: Johanson, Kyung O.
;  TITLE OF INVENTION: Humanized Monoclonal Antibodies
;  FILE REFERENCE: P50860
;  CURRENT APPLICATION NUMBER: US/09/199,149
;  CURRENT FILING DATE: 1998-11-24
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 90
;   TYPE: PRT
;   ORGANISM: human and murine cells
US-09-199-149-15

  Query Match             100.0%;  Score 86;  DB 2;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49
```

```
RESULT 47
US-10-330-613A-60
; Sequence 60, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
;  FILE REFERENCE: ABGENIX.022A
;  CURRENT APPLICATION NUMBER: US/10/330,613A
;  CURRENT FILING DATE:  2002-12-26
;  PRIOR APPLICATION NUMBER: 60/346299
;  PRIOR FILING DATE: 2001-12-18
;  NUMBER OF SEQ ID NOS: 90
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 60
;   LENGTH: 92
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-330-613A-60

  Query Match             100.0%;  Score 86;  DB 2;  Length 92;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         34 WYQQKPGKAPKLLIY 48


RESULT 48
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; Sequence 44, Application US/10330613A
; Patent No. 6924360
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  TITLE OF INVENTION: ANTIBODIES AGAINST THE MUC18 ANTIGEN
;  FILE REFERENCE: ABGENIX.022A
;  CURRENT APPLICATION NUMBER: US/10/330,613A
;  CURRENT FILING DATE:  2002-12-26
;  PRIOR APPLICATION NUMBER: 60/346299
;  PRIOR FILING DATE: 2001-12-18
;  NUMBER OF SEQ ID NOS: 90
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 44
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-330-613A-44

  Query Match             100.0%;  Score 86;  DB 2;  Length 93;
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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
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RESULT 49
US-08-290-592E-19
; Sequence 19, Application US/08290592E
; Patent No. 5824307
;  GENERAL INFORMATION:
;    APPLICANT:  JOHNSON, L.
;    TITLE OF INVENTION:  Human Murine Chimeric Antibodies Against
;    TITLE OF INVENTION:  Respiratory Syncytical Virus
;    NUMBER OF SEQUENCES:  49
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART &
;      ADDRESSEE:  OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/290,592E
;      FILING DATE:  August 15, 1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/813,372
;      FILING DATE:  December 23, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  469201-257
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  95 AMINO ACIDS
;      TYPE:  AMINO ACID
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  PROTEIN
US-08-290-592E-19

  Query Match             100.0%;  Score 86;  DB 1;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
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RESULT 50
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; Sequence 33, Application US/08290592E
; Patent No. 5824307
;  GENERAL INFORMATION:
;    APPLICANT:  JOHNSON, L.
;    TITLE OF INVENTION:  Human Murine Chimeric Antibodies Against
;    TITLE OF INVENTION:  Respiratory Syncytical Virus
;    NUMBER OF SEQUENCES:  49
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART &
;      ADDRESSEE:  OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/290,592E
;      FILING DATE:  August 15, 1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/813,372
;      FILING DATE:  December 23, 1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  469201-257
;    TELECOMMUNICATION INFORMATION:
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; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 95 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-290-592E-33

Query Match 100.0%; Score 86; DB 1; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db         35 WYQQKPGKAPKLLIY 49
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Job time : 35.4658 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:42:16 ; Search time 105.205 Seconds
(without alignments)
59.573 Million cell updates/sec

Title: US-10-755-382-27
Perfect score: 86
Sequence: 1 W¥QQKPGKAPKLLIY 15

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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472	86	100.0	107	4	US-10-302-356A-9	Sequence 9, Appli
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841	86	100.0	127	4	US-10-462-062-180	Sequence 180, App
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846	86	100.0	127	4	US-10-472-905A-120	Sequence 120, App
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999	86	100.0	213	5	US-10-900-230-233	Sequence 233, App
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ALIGNMENTS

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RESULT 1
US-09-253-794-27
; Sequence 27, Application US/09253794
; Patent No. US20020018750A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 27:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-253-794-27

  Query Match           100.0%;  Score 86;  DB 3;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-06;
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Db          1 WYQQKPGKAPKLLIY 15


RESULT 2
US-09-855-271-11
; Sequence 11, Application US/09855271
; Patent No. US20020042089A1
; GENERAL INFORMATION:
;  APPLICANT: Bodmer, Mark W
;  APPLICANT:  Athwal, Diljeet Singh
;  APPLICANT:  Emtage, John Spencer
;  TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
;  FILE REFERENCE: CARP-0088
;  CURRENT APPLICATION NUMBER: US/09/855,271
;  CURRENT FILING DATE:  2001-05-15
;  PRIOR APPLICATION NUMBER: 09/347,061
;  PRIOR FILING DATE: 1999-07-02
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
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;   OTHER INFORMATION: Consensus
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US-09-855-271-11

  Query Match           100.0%;  Score 86;  DB 3;  Length 15;
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Db          1 WYQQKPGKAPKLLIY 15


RESULT 3
US-09-730-857-88
; Sequence 88, Application US/09730857
; Patent No. US20020082396A1
;   GENERAL INFORMATION:
;        APPLICANT: Matsushima, Kouji
;                   Matsumoto, Yoshihiro
;                   Yamada, Yoshiki
;                   Sato, Koh
;                   Tsuchiya, Masayuki
;                   Yamazaki, Tatsumi
;        TITLE OF INVENTION: Reshaped Human Antibody to
;                            Interleukin-8
;        NUMBER OF SEQUENCES: 105
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORRISON & FOERSTER
;             STREET: 2000 Pennsylvania Avenue, NW, suite 5500
;             CITY: Washington
;             STATE: DC
;             COUNTRY: USA
;             ZIP: 20006-1888
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
```

```
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/730,857
;            FILING DATE: 07-Dec-2000
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/416,557
;            FILING DATE: 1999-10-12
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Murashige, Kate H
;            REGISTRATION NUMBER: 29,959
;            REFERENCE/DOCKET NUMBER: 35029-20001.10
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-887-1500
;            TELEFAX: 202-822-0168
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 88:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 15 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-09-730-857-88

  Query Match           100.0%;  Score 86;  DB 3;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 4
US-09-949-559-89
; Sequence 89, Application US/09949559
; Patent No. US20020151682A1
; GENERAL INFORMATION:
;  APPLICANT: Athwal, Diljeet Singh
;  APPLICANT:  Brown, Derek Thomas
;  APPLICANT:  Weir, Andrew Neil Charles
;  APPLICANT:  Popplewell, Andrew George
;  APPLICANT:  Chapman, Andrew Paul
;  APPLICANT:  King, David John
;  TITLE OF INVENTION: Biological Products
;  FILE REFERENCE: Carp-0095
;  CURRENT APPLICATION NUMBER: US/09/949,559
;  CURRENT FILING DATE:  2001-12-20
;  PRIOR APPLICATION NUMBER: 0013810.7GB
;  PRIOR FILING DATE: 2000-06-06
;  PRIOR APPLICATION NUMBER: 09/875,221
;  PRIOR FILING DATE: 2001-06-06
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Human group 1 consensus framework L2
US-09-949-559-89

  Query Match           100.0%;  Score 86;  DB 3;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 5
US-09-875-221A-89
; Sequence 89, Application US/09875221A
; Publication No. US20030026805A1
; GENERAL INFORMATION:
;  APPLICANT: Athwal, Diljeet Singh
;  APPLICANT:  Brown, Derek Thomas
;  APPLICANT:  Weir, Andrew Neil Charles
;  APPLICANT:  Popplewell, Andrew George
;  APPLICANT:  Chapman, Andrew Paul
;  APPLICANT:  King, David John
;  TITLE OF INVENTION: Biological Products
;  FILE REFERENCE: Carp-0089
;  CURRENT APPLICATION NUMBER: US/09/875,221A
;  CURRENT FILING DATE:  2001-06-06
;  PRIOR APPLICATION NUMBER: GB0013810.7
;  PRIOR FILING DATE: 2000-06-06
;  NUMBER OF SEQ ID NOS: 130
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Human group 1 consensus framework L2
US-09-875-221A-89

  Query Match           100.0%;  Score 86;  DB 3;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 6
US-09-563-222-75
; Sequence 75, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
;  APPLICANT:  Hiatt, Andrew
;  APPLICANT:  Hein, Mich B.
;  TITLE OF INVENTION:  IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
;  TITLE OF INVENTION:  EUKARYOTIC CELLS
;  FILE REFERENCE:  310098.406
;  CURRENT APPLICATION NUMBER: US/09/563,222
;  CURRENT FILING DATE:  2000-05-02
;  NUMBER OF SEQ ID NOS:  197
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 75
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-09-563-222-75

  Query Match           100.0%;  Score 86;  DB 3;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 7
US-10-462-062-126
; Sequence 126, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
;  APPLICANT: SATO, KOH
;  APPLICANT:  ADACHI, HIDEKI
;  TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
;  TITLE OF INVENTION:  AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
;  FILE REFERENCE: 053466-0360
```

```
;  CURRENT APPLICATION NUMBER: US/10/462,062
;  CURRENT FILING DATE:  2003-06-16
;  PRIOR APPLICATION NUMBER: PCT/JP99/01768
;  PRIOR FILING DATE: 1999-04-02
;  PRIOR APPLICATION NUMBER: JP 10-91850
;  PRIOR FILING DATE: 1998-04-03
;  NUMBER OF SEQ ID NOS: 183
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 126
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of
;   OTHER INFORMATION: FR2 of versions "a", "b" and "c" of humanized L chain V region
US-10-462-062-126

  Query Match           100.0%;  Score 86;  DB 4;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 8
US-10-307-276B-39
; Sequence 39, Application US/10307276B
; Publication No. US20040101904A1
;   GENERAL INFORMATION:
;        APPLICANT: William M. Pardridge
;                   Ruben J. Boado
;        TITLE OF INVENTION: Delivery Of Pharmaceutical Agents
;                            Via The Human Insulin Receptor
;        NUMBER OF SEQUENCES: 50
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Shapiro & Dupont LLP
;             STREET: 233 Wilshire Boulevard, Suite 700
;             CITY: Santa Monica
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 90067
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy Disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 2000
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/307,276B
;             FILING DATE: 27-Nov-2002
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Oldenkamp, David J.
;             REGISTRATION NUMBER: 29,421
;             REFERENCE/DOCKET NUMBER: 0180.0038
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (310) 319-5411
;             TELEFAX: (310) 319-5401
;   INFORMATION FOR SEQ ID NO: 39:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: polypeptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 39
US-10-307-276B-39

  Query Match           100.0%;  Score 86;  DB 4;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 9
US-10-632-706-246
; Sequence 246, Application US/10632706
; Publication No. US20040175385A1
; GENERAL INFORMATION:
;  APPLICANT: MARKS, JAMES D.
;  APPLICANT:  AMERSDORFER, PETER
;  TITLE OF INVENTION: THERAPEUTIC MONOCLONAL ANTIBODIES THAT NEUTRALIZE BOTULINUM
;  TITLE OF INVENTION:  NEUROTOXINS
;  FILE REFERENCE: 407T-895120US
;  CURRENT APPLICATION NUMBER: US/10/632,706
;  CURRENT FILING DATE:  2003-08-01
;  PRIOR APPLICATION NUMBER: US 60/400,721
;  PRIOR FILING DATE: 2002-08-01
;  PRIOR APPLICATION NUMBER: US 09/144,806
;  PRIOR FILING DATE: 1998-08-31
;  NUMBER OF SEQ ID NOS: 278
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 246
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: single chain antibody fragment
US-10-632-706-246

  Query Match           100.0%;  Score 86;  DB 4;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 10
US-10-783-950-75
; Sequence 75, Application US/10783950
; Publication No. US20040199945A1
; GENERAL INFORMATION:
;  APPLICANT: EPICYTE PHARMACEUTICALS, INC.
;  APPLICANT:  HIATT, ANDREW C.
;  APPLICANT:  HEIN, MICH B.
;  TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
;  FILE REFERENCE: 068904-0501
;  CURRENT APPLICATION NUMBER: US/10/783,950
;  CURRENT FILING DATE:  2004-02-19
;  PRIOR APPLICATION NUMBER: US/09/563,222
;  PRIOR FILING DATE: 2000-05-02
;  PRIOR APPLICATION NUMBER: PCT/US01/14349
;  PRIOR FILING DATE: 2001-05-02
;  PRIOR APPLICATION NUMBER: 09/563,222
;  PRIOR FILING DATE: 2000-05-02
;  NUMBER OF SEQ ID NOS: 182
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-783-950-75

  Query Match           100.0%;  Score 86;  DB 4;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15
```

```
RESULT 11
US-10-823-253-40
; Sequence 40, Application US/10823253
; Publication No. US20050002934A1
; GENERAL INFORMATION:
;  APPLICANT: Reed, Jennifer
;  TITLE OF INVENTION: RECOMBINANT IL-9 ANTIBODIES AND USES THEREOF
;  FILE REFERENCE: 10271-112-999
;  CURRENT APPLICATION NUMBER: US/10/823,253
;  CURRENT FILING DATE:  2004-04-12
;  PRIOR APPLICATION NUMBER: 60/462,259
;  PRIOR FILING DATE: 2003-04-11
;  PRIOR APPLICATION NUMBER: 60/477,797
;  PRIOR FILING DATE: 2003-06-10
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-823-253-40

  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 12
US-10-728-420B-85
; Sequence 85, Application US/10728420B
; Publication No. US20050042219A1
; GENERAL INFORMATION:
;  APPLICANT: WOULFE, SUSAN L.
;  APPLICANT:  JAIN, RITA
;  APPLICANT:  BURR, AIMEE
;  TITLE OF INVENTION: ENGINEERED FAB' FRAGMENT ANTI-TUMOR
;  TITLE OF INVENTION:  NECROSIS FACTOR ALPHA IN COMBINATION WITH DISEASE MODIFYING
;  TITLE OF INVENTION:  ANTI-RHEUMATIC DRUGS
;  FILE REFERENCE: 122294-1010
;  CURRENT APPLICATION NUMBER: US/10/728,420B
;  CURRENT FILING DATE:  2003-12-05
;  PRIOR APPLICATION NUMBER: US 60/431,053
;  PRIOR FILING DATE: 2002-12-05
;  NUMBER OF SEQ ID NOS: 117
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 85
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: human group 1 consensus framework L2
US-10-728-420B-85

  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 13
US-10-923-068-62
; Sequence 62, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-62

  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 14
US-10-923-068-65
; Sequence 65, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-65

  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 15
US-10-923-068-77
; Sequence 77, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 77
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-77
```

```
  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 16
US-10-923-068-80
; Sequence 80, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-80

  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 17
US-10-923-068-101
; Sequence 101, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 101
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-101

  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 18
US-10-923-068-104
; Sequence 104, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 104
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-104

  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 19
US-10-923-068-110
; Sequence 110, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 110
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-110

  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 20
US-10-923-068-113
; Sequence 113, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 113
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-113

  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
```

```
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 21
US-10-923-068-122
; Sequence 122, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 122
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-122

  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 22
US-10-923-068-128
; Sequence 128, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 128
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-128

  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 23
US-10-923-068-131
; Sequence 131, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 131
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-131

  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 24
US-10-923-068-137
; Sequence 137, Application US/10923068
; Publication No. US20050042664A1
; GENERAL INFORMATION:
;  APPLICANT: Wu, Herren
;  APPLICANT:  Dall'Acqua, William
;  APPLICANT:  Damschroder, Melissa
;  TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
;  FILE REFERENCE: AE600US
;  CURRENT APPLICATION NUMBER: US/10/923,068
;  CURRENT FILING DATE:  2004-08-20
;  NUMBER OF SEQ ID NOS: 518
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 137
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-923-068-137

  Query Match             100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 25
US-10-914-015-85
; Sequence 85, Application US/10914015
; Publication No. US20050048056A1
; GENERAL INFORMATION:
;  APPLICANT: PHARMACIA CORPORATION
;  TITLE OF INVENTION: METHOD FOR THE PREPARATION OF MOLECULES HAVING ANTIBODY ACTIVITY
;  FILE REFERENCE: PHA-01686/1
;  CURRENT APPLICATION NUMBER: US/10/914,015
;  CURRENT FILING DATE:  2004-08-06
;  PRIOR APPLICATION NUMBER: US 60/493,740
;  PRIOR FILING DATE: 2003-08-08
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 85
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:human group 1 consensus framewo
US-10-914-015-85
```

```
  Query Match           100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 26
US-10-755-382-27
; Sequence 27, Application US/10755382
; Publication No. US20050089538A1
;   GENERAL INFORMATION:
;        APPLICANT: HANSEN, Hans J.
;                   ARMOUR, Kathryn L.
;        TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;                            MOUSE MONOCLONAL ANTIBODIES
;        NUMBER OF SEQUENCES: 58
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/755,382
;             FILING DATE: 13-Jan-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/253,794
;             FILING DATE: 22-Feb-1999
;             APPLICATION NUMBER: US 08/318,157
;             FILING DATE: 05-OCT-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: SAXE, Bernhard D.
;             REGISTRATION NUMBER: 28,665
;             REFERENCE/DOCKET NUMBER: 18733/464
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 27:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-10-755-382-27

  Query Match           100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 27
US-10-823-810-40
; Sequence 40, Application US/10823810
; Publication No. US20050147607A1
; GENERAL INFORMATION:
;  APPLICANT: Reed, Jennifer
;  TITLE OF INVENTION: METHODS OF PREVENTING OR TREATING RESPIRATORY CONDITIONS
;  FILE REFERENCE: 10271-113-999
;  CURRENT APPLICATION NUMBER: US/10/823,810
;  CURRENT FILING DATE:  2004-04-12
;  PRIOR APPLICATION NUMBER: 60/462,307
;  PRIOR FILING DATE: 2003-04-11
;  PRIOR APPLICATION NUMBER: 60/477,801
;  PRIOR FILING DATE: 2003-06-10
;  NUMBER OF SEQ ID NOS: 63
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-823-810-40

  Query Match           100.0%;  Score 86;  DB 5;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 28
US-11-061-956-39
; Sequence 39, Application US/11061956
; Publication No. US20050142141A1
;   GENERAL INFORMATION:
;        APPLICANT: William M. Pardridge
;        TITLE OF INVENTION: Delivery Of Enzymes To The Brain
;        NUMBER OF SEQUENCES: 50
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Shapiro & Dupont LLP
;             STREET: 233 Wilshire Boulevard, Suite 700
;             CITY: Santa Monica
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 90067
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy Disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 2000
;             SOFTWARE: MS Word
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/11/061,956
;             FILING DATE: 17-Feb-2005
;             CLASSIFICATION: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Oldenkamp, David J.
;             REGISTRATION NUMBER: 29,421
;             REFERENCE/DOCKET NUMBER: 0180.0086
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (310) 319-5411
;             TELEFAX: (310) 319-5401
;   INFORMATION FOR SEQ ID NO: 39:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: polypeptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 39
US-11-061-956-39

  Query Match           100.0%;  Score 86;  DB 6;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15
```

```
RESULT 29
US-09-874-141-11
; Sequence 11, Application US/09874141
; Publication No. US20030012781A1
; GENERAL INFORMATION:
;  APPLICANT: ANDERSON, DARRELL
;  APPLICANT:  PAN, LI-ZHEN
;  APPLICANT:  HANNA, NABIL
;  APPLICANT:  RASTETTER, WILLIAM H.
;  APPLICANT:  KLOETZER, WILLIAM S.
;  TITLE OF INVENTION: NON-AGONISTIC ANTIBODIES TO HUMAN GP39, COMPOSITIONS
;  TITLE OF INVENTION:  CONTAINING, AND THERAPEUTIC USE THEREOF
;  FILE REFERENCE: 037003-0280632
;  CURRENT APPLICATION NUMBER: US/09/874,141
;  CURRENT FILING DATE:  2001-06-06
;  PRIOR APPLICATION NUMBER: 60/209,584
;  PRIOR FILING DATE: 2000-06-06
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 38
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-874-141-11

  Query Match             100.0%;  Score 86;  DB 3;  Length 38;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 30
US-10-171-681-9
; Sequence 9, Application US/10171681
; Publication No. US20030170233A1
;  GENERAL INFORMATION:
;    APPLICANT:  BLACK, Amelia
;    APPLICANT:  HANNA, Nabil
;    APPLICANT:  PADLAN, Eduardo A.
;    APPLICANT:  NEWMAN, Roland A.
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES TO HUMAN gp39,
;    TITLE OF INVENTION:  COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/171,681
;      FILING DATE:  17-JUNE-2001
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/925,339
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/554,840
;      FILING DATE:  07-NOV-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-127
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  70 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-10-171-681-9

  Query Match             100.0%;  Score 86;  DB 4;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 31
US-10-171-680-9
; Sequence 9, Application US/10171680
; Publication No. US20030175269A1
;  GENERAL INFORMATION:
;    APPLICANT:  BLACK, Amelia
;    APPLICANT:  HANNA, Nabil
;    APPLICANT:  PADLAN, Eduardo A.
;    APPLICANT:  NEWMAN, Roland A.
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES TO HUMAN gp39,
;    TITLE OF INVENTION:  COMPOSITIONS CONTAINING AND THERAPEUTIC USE THEREOF
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Burns, Doane, Swecker & Mathis
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/10/171,680
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/332,595
;      FILING DATE:
;      APPLICATION NUMBER:  US/08/554,840
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Teskin, Robin L.
;      REGISTRATION NUMBER:  35,030
;      REFERENCE/DOCKET NUMBER:  012712-127
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  70 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-10-171-680-9

  Query Match             100.0%;  Score 86;  DB 4;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 32
US-10-428-408A-17
; Sequence 17, Application US/10428408A
; Publication No. US20030235869A1
; GENERAL INFORMATION:
;  APPLICANT: Celltech R&D Limited
;  TITLE OF INVENTION: BIOLOGICAL PRODUCTS
;  FILE REFERENCE: CARP0004-100
;  CURRENT APPLICATION NUMBER: US/10/428,408A
;  CURRENT FILING DATE:  2003-05-02
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 17
;   LENGTH: 70
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: DOMAIN
;   OTHER INFORMATION: DPK9 HUMAN ACCEPTOR FRAMEWORK
US-10-428-408A-17

  Query Match             100.0%;  Score 86;  DB 4;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 33
US-10-428-894-17
; Sequence 17, Application US/10428894
; Publication No. US20040082764A1
; GENERAL INFORMATION:
;  APPLICANT: WYETH HOLDINGS CORPORATION.; KUNZ, ARTHUR ET AL.
;  TITLE OF INVENTION: CALICHEAMICIN DERIVATIVE-CARRIER CONJUGATES
;  FILE REFERENCE: AM100788
;  CURRENT APPLICATION NUMBER: US/10/428,894
;  CURRENT FILING DATE:  2003-05-02
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 17
;   LENGTH: 70
;   TYPE: PRT
;   ORGANISM: Homo sapien
;   FEATURE:
;   OTHER INFORMATION: DPK9
;   FEATURE:
;   NAME/KEY:
US-10-428-894-17

  Query Match             100.0%;  Score 86;  DB 4;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 34
US-10-699-874-17
; Sequence 17, Application US/10699874
; Publication No. US20040192900A1
; GENERAL INFORMATION:
;  APPLICANT: WYETH HOLDING CORPORATION.; KUNZ, ARTHUR ET AL.
;  TITLE OF INVENTION: CALICHEAMICIN DERIVATIVE-CARRIER CONJUGATES
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/699,874
;  CURRENT FILING DATE:  2003-11-03
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 17
;   LENGTH: 70
;   TYPE: PRT
;   ORGANISM: Homo sapien
;   FEATURE:
;   OTHER INFORMATION: DPK9
;   FEATURE:
;   NAME/KEY:
US-10-699-874-17

  Query Match             100.0%;  Score 86;  DB 4;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 35
US-10-078-958-13
; Sequence 13, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
;  APPLICANT: JAKOBOVITS, AYA
;  APPLICANT:  KUCHERLAPATI, RAJU
;  APPLICANT:  KLAPHOLZ, SUSAN
;  APPLICANT:  MENDEZ, MICHAEL J.
;  APPLICANT:  GREEN, LARRY
;  TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
;  TITLE OF INVENTION:  PLURAL Vh AND Vk REGIONS AND ANTIBODIES PRODUCED
;  TITLE OF INVENTION:  THEREFROM
;  FILE REFERENCE: CELL 4.18 CON
;  CURRENT APPLICATION NUMBER: US/10/078,958
;  CURRENT FILING DATE:  2002-02-19
;  PRIOR APPLICATION NUMBER: 08/759,620
;  PRIOR FILING DATE: 1996-12-03
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 73
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-078-958-13

  Query Match             100.0%;  Score 86;  DB 4;  Length 73;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         14 WYQQKPGKAPKLLIY 28


RESULT 36
US-10-078-958-25
; Sequence 25, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
;  APPLICANT: JAKOBOVITS, AYA
;  APPLICANT:  KUCHERLAPATI, RAJU
;  APPLICANT:  KLAPHOLZ, SUSAN
;  APPLICANT:  MENDEZ, MICHAEL J.
;  APPLICANT:  GREEN, LARRY
;  TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
;  TITLE OF INVENTION:  PLURAL Vh AND Vk REGIONS AND ANTIBODIES PRODUCED
;  TITLE OF INVENTION:  THEREFROM
```

```
;  FILE REFERENCE: CELL 4.18 CON
;  CURRENT APPLICATION NUMBER: US/10/078,958
;  CURRENT FILING DATE:  2002-02-19
;  PRIOR APPLICATION NUMBER: 08/759,620
;  PRIOR FILING DATE: 1996-12-03
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
;   LENGTH: 75
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-078-958-25

  Query Match             100.0%;  Score 86;  DB 4;  Length 75;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         16 WYQQKPGKAPKLLIY 30


RESULT 37
US-09-187-693-36
; Sequence 36, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
;  APPLICANT: Jakobovits, Aya
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Gallo, Michael
;  APPLICANT:  Jia, Xiao-Chi
;  TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
;  TITLE OF INVENTION:  Growth Factor Receptor
;  FILE REFERENCE: Cell 4.20 CIP2
;  CURRENT APPLICATION NUMBER: US/09/187,693
;  CURRENT FILING DATE:  1998-11-05
;  PRIOR APPLICATION NUMBER: 09/162,280
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 08/851,362
;  PRIOR FILING DATE: 1997-05-05
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
;   LENGTH: 76
;   TYPE: PRT
;   ORGANISM: human
US-09-187-693-36

  Query Match             100.0%;  Score 86;  DB 3;  Length 76;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         16 WYQQKPGKAPKLLIY 30


RESULT 38
US-09-187-693-37
; Sequence 37, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
;  APPLICANT: Jakobovits, Aya
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Gallo, Michael
;  APPLICANT:  Jia, Xiao-Chi
;  TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
;  TITLE OF INVENTION:  Growth Factor Receptor
;  FILE REFERENCE: Cell 4.20 CIP2
;  CURRENT APPLICATION NUMBER: US/09/187,693
;  CURRENT FILING DATE:  1998-11-05
;  PRIOR APPLICATION NUMBER: 09/162,280
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 08/851,362
;  PRIOR FILING DATE: 1997-05-05
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
;   LENGTH: 76
;   TYPE: PRT
;   ORGANISM: human
US-09-187-693-37

  Query Match             100.0%;  Score 86;  DB 3;  Length 76;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         16 WYQQKPGKAPKLLIY 30


RESULT 39
US-10-078-958-10
; Sequence 10, Application US/10078958
; Publication No. US20030070185A1
; GENERAL INFORMATION:
;  APPLICANT: JAKOBOVITS, AYA
;  APPLICANT:  KUCHERLAPATI, RAJU
;  APPLICANT:  KLAPHOLZ, SUSAN
;  APPLICANT:  MENDEZ, MICHAEL J.
;  APPLICANT:  GREEN, LARRY
;  TITLE OF INVENTION: TRANSGENIC MAMMALS HAVING HUMAN Ig LOCI INCLUDING
;  TITLE OF INVENTION:  PLURAL Vh AND Vk REGIONS AND ANTIBODIES PRODUCED
;  TITLE OF INVENTION:  THEREFROM
;  FILE REFERENCE: CELL 4.18 CON
;  CURRENT APPLICATION NUMBER: US/10/078,958
;  CURRENT FILING DATE:  2002-02-19
;  PRIOR APPLICATION NUMBER: 08/759,620
;  PRIOR FILING DATE: 1996-12-03
;  NUMBER OF SEQ ID NOS: 79
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 76
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-078-958-10

  Query Match             100.0%;  Score 86;  DB 4;  Length 76;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         16 WYQQKPGKAPKLLIY 30


RESULT 40
US-11-021-795-36
; Sequence 36, Application US/11021795
; Publication No. US20050100546A1
; GENERAL INFORMATION:
;  APPLICANT: Jakobovits, Aya
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Gallo, Michael
;  APPLICANT:  Jia, Xiao-Chi
;  TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
;  TITLE OF INVENTION:  Growth Factor Receptor
;  FILE REFERENCE: Cell 4.20 CIP2
;  CURRENT APPLICATION NUMBER: US/11/021,795
;  CURRENT FILING DATE:  2004-12-22
;  PRIOR APPLICATION NUMBER: US/09/187,693
;  PRIOR FILING DATE: 1998-11-05
;  PRIOR APPLICATION NUMBER: 09/162,280
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 08/851,362
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;  PRIOR FILING DATE: 1997-05-05
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 36
;   LENGTH: 76
;   TYPE: PRT
;   ORGANISM: human
US-11-021-795-36

  Query Match            100.0%;  Score 86;  DB 6;  Length 76;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         16 WYQQKPGKAPKLLIY 30


RESULT 41
US-11-021-795-37
; Sequence 37, Application US/11021795
; Publication No. US20050100546A1
; GENERAL INFORMATION:
;  APPLICANT: Jakobovits, Aya
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Gallo, Michael
;  APPLICANT:  Jia, Xiao-Chi
;  TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
;  TITLE OF INVENTION:  Growth Factor Receptor
;  FILE REFERENCE: Cell 4.20 CIP2
;  CURRENT APPLICATION NUMBER: US/11/021,795
;  CURRENT FILING DATE:  2004-12-22
;  PRIOR APPLICATION NUMBER: US/09/187,693
;  PRIOR FILING DATE: 1998-11-05
;  PRIOR APPLICATION NUMBER: 09/162,280
;  PRIOR FILING DATE: 1998-09-29
;  PRIOR APPLICATION NUMBER: 08/851,362
;  PRIOR FILING DATE: 1997-05-05
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
;   LENGTH: 76
;   TYPE: PRT
;   ORGANISM: human
US-11-021-795-37

  Query Match            100.0%;  Score 86;  DB 6;  Length 76;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         16 WYQQKPGKAPKLLIY 30


RESULT 42
US-09-730-857-104
; Sequence 104, Application US/09730857
; Patent No. US20020082396A1
;   GENERAL INFORMATION:
;        APPLICANT: Matsushima, Kouji
;                   Matsumoto, Yoshihiro
;                   Yamada, Yoshiki
;                   Sato, Koh
;                   Tsuchiya, Masayuki
;                   Yamazaki, Tatsumi
;        TITLE OF INVENTION: Reshaped Human Antibody to
;                            Interleukin-8
;        NUMBER OF SEQUENCES: 105
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORRISON & FOERSTER
;             STREET: 2000 Pennsylvania Avenue, NW, suite 5500
;             CITY: Washington
;             STATE: DC
;             COUNTRY: USA
;             ZIP: 20006-1888
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/730,857
;             FILING DATE: 07-Dec-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/416,557
;             FILING DATE: 1999-10-12
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Murashige, Kate H
;             REGISTRATION NUMBER: 29,959
;             REFERENCE/DOCKET NUMBER: 35029-20001.10
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-887-1500
;             TELEFAX: 202-822-0168
;             TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 104:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 80 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-09-730-857-104

  Query Match            100.0%;  Score 86;  DB 3;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 43
US-09-269-921-130
; Sequence 130, Application US/09269921
; Publication No. US20030045691A1
; GENERAL INFORMATION:
;  APPLICANT: Ono, Koichiro
;  APPLICANT: Ohtomo, Toshihiko
;  APPLICANT: Tsuchiya, Masayuki
;  APPLICANT: Yoshimura, Yasushi
;  APPLICANT: Koishihara, Yasuo
;  TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
;  FILE REFERENCE: 35029-20007.00
;  CURRENT APPLICATION NUMBER: US/09/269,921
;  CURRENT FILING DATE: 1999-04-01
;  EARLIER APPLICATION NUMBER: PCT/JP97/03553
;  EARLIER FILING DATE: 1997-10-03
;  EARLIER APPLICATION NUMBER: JP 8-264756
;  EARLIER FILING DATE: 1996-10-04
;  NUMBER OF SEQ ID NOS: 137
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
;   LENGTH: 80
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: HuSGI
;  PUBLICATION INFORMATION:
;   AUTHORS: Kabat, E.A. et al.
;   JOURNAL: SEQUENCE OF PROTEINS OF IMMUNOLOGICAL INTEREST, U.S. DEPT.
;   DATE: 1991
US-09-269-921-130
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Query Match 100.0%; Score 86; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 24 WYQQKPGKAPKLLIY 38

RESULT 44
US-09-269-921-131
; Sequence 131, Application US/09269921
; Publication No. US20030045691A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/09/269,921
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: PCT/JP97/03553
; EARLIER FILING DATE: 1997-10-03
; EARLIER APPLICATION NUMBER: JP 8-264756
; EARLIER FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: REI
; PUBLICATION INFORMATION:
; AUTHORS: Recchmann, L. et al.
; JOURNAL: NATURE
; VOLUME: 322
; PAGES: 21-25
; DATE: 1998
US-09-269-921-131

Query Match 100.0%; Score 86; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 24 WYQQKPGKAPKLLIY 38

RESULT 45
US-09-509-098-131
; Sequence 131, Application US/09509098
; Publication No. US20030103970A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0274
; CURRENT APPLICATION NUMBER: US/09/509,098
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/JP98/04469
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: JP 9-271726
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 131
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of the L chain V region of HuSG I
US-09-509-098-131

Query Match 100.0%; Score 86; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 24 WYQQKPGKAPKLLIY 38

RESULT 46
US-09-509-098-132
; Sequence 132, Application US/09509098
; Publication No. US20030103970A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0274
; CURRENT APPLICATION NUMBER: US/09/509,098
; CURRENT FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/JP98/04469
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: JP 9-271726
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of the L chain V region of REI
US-09-509-098-132

Query Match 100.0%; Score 86; DB 3; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WYQQKPGKAPKLLIY 15
||||||||||||||||
Db 24 WYQQKPGKAPKLLIY 38

RESULT 47
US-10-218-253-130
; Sequence 130, Application US/10218253
; Publication No. US20030129185A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasushi
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/10/218,253
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/09/269,921
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: PCT/JP97/03553
; PRIOR FILING DATE: 1997-10-03
; PRIOR APPLICATION NUMBER: JP 8-264756
; PRIOR FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Unknown

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;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: HuSGI
;  PUBLICATION INFORMATION:
;   AUTHORS: Kabat, E.A. et al.
;   JOURNAL: SEQUENCE OF PROTEINS OF IMMUNOLOGICAL INTEREST, U.S. DEPT.
;   DATE: 1991
US-10-218-253-130

  Query Match             100.0%;  Score 86;  DB 4;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 48
US-10-218-253-131
; Sequence 131, Application US/10218253
; Publication No. US20030129185A1
; GENERAL INFORMATION:
;  APPLICANT: Ono, Koichiro
;  APPLICANT:  Ohtomo, Toshihiko
;  APPLICANT:  Tsuchiya, Masayuki
;  APPLICANT:  Yoshimura, Yasushi
;  APPLICANT:  Koishihara, Yasuo
;  TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
;  FILE REFERENCE: 35029-20007.00
;  CURRENT APPLICATION NUMBER: US/10/218,253
;  CURRENT FILING DATE:  2002-11-21
;  PRIOR APPLICATION NUMBER: US/09/269,921
;  PRIOR FILING DATE: 1999-04-01
;  PRIOR APPLICATION NUMBER: PCT/JP97/03553
;  PRIOR FILING DATE: 1997-10-03
;  PRIOR APPLICATION NUMBER: JP 8-264756
;  PRIOR FILING DATE: 1996-10-04
;  NUMBER OF SEQ ID NOS: 137
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 131
;   LENGTH: 80
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: REI
;  PUBLICATION INFORMATION:
;   AUTHORS: Recchmann, L. et al.
;   JOURNAL: NATURE
;   VOLUME: 322
;   PAGES: 21-25
;   DATE: 1998
US-10-218-253-131

  Query Match             100.0%;  Score 86;  DB 4;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 49
US-10-230-880-155
; Sequence 155, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
;  APPLICANT: WONG, HING C.
;  APPLICANT:  STINSON, JEFFREY L.
;  APPLICANT:  MOSQUERA, LUIS A.
;  TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
;  FILE REFERENCE: 71758/58066
;  CURRENT APPLICATION NUMBER: US/10/230,880
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 09/990,586
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/343,306
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: 09/293,854
;  PRIOR FILING DATE: 1999-04-16
;  NUMBER OF SEQ ID NOS: 174
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
;   LENGTH: 80
;   TYPE: PRT
;   ORGANISM: Unknown Organism
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: CEA4-8A
US-10-230-880-155

  Query Match             100.0%;  Score 86;  DB 4;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 50
US-10-230-880-163
; Sequence 163, Application US/10230880
; Publication No. US20030190705A1
; GENERAL INFORMATION:
;  APPLICANT: WONG, HING C.
;  APPLICANT:  STINSON, JEFFREY L.
;  APPLICANT:  MOSQUERA, LUIS A.
;  TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
;  FILE REFERENCE: 71758/58066
;  CURRENT APPLICATION NUMBER: US/10/230,880
;  CURRENT FILING DATE:  2002-12-23
;  PRIOR APPLICATION NUMBER: 09/990,586
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: 60/343,306
;  PRIOR FILING DATE: 2001-10-29
;  PRIOR APPLICATION NUMBER: 09/293,854
;  PRIOR FILING DATE: 1999-04-16
;  NUMBER OF SEQ ID NOS: 174
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 163
;   LENGTH: 80
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Illustrative
;   OTHER INFORMATION: Framework peptide
US-10-230-880-163

  Query Match             100.0%;  Score 86;  DB 4;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-05;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


Search completed: March 23, 2006, 02:52:51
Job time : 109.348 secs
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OM protein - protein search, using sw model

Run on: March 23, 2006, 02:44:01 ; Search time 12.7397 Seconds
(without alignments)
33.701 Million cell updates/sec

Title: US-10-755-382-27
Perfect score: 86
Sequence: 1 WYQQKPGKAPKLLIY 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	86	100.0	15	7	US-11-105-268-40	Sequence 40, Appl
2	86	100.0	49	6	US-10-925-366A-307	Sequence 307, App
3	86	100.0	49	6	US-10-925-366A-327	Sequence 327, App
4	86	100.0	74	6	US-10-925-366A-295	Sequence 295, App
5	86	100.0	76	6	US-10-925-366A-319	Sequence 319, App
6	86	100.0	76	6	US-10-925-366A-322	Sequence 322, App
7	86	100.0	77	6	US-10-925-366A-305	Sequence 305, App
8	86	100.0	78	6	US-10-925-366A-302	Sequence 302, App
9	86	100.0	78	6	US-10-925-366A-311	Sequence 311, App
10	86	100.0	78	6	US-10-925-366A-314	Sequence 314, App
11	86	100.0	80	7	US-11-226-325-131	Sequence 131, App
12	86	100.0	80	7	US-11-226-325-132	Sequence 132, App
13	86	100.0	87	6	US-10-839-799-112	Sequence 112, App
14	86	100.0	90	7	US-11-173-071-23	Sequence 23, Appl
15	86	100.0	93	6	US-10-999-866-10	Sequence 10, Appl
16	86	100.0	93	6	US-10-935-005B-40	Sequence 40, Appl
17	86	100.0	93	7	US-11-061-821-10	Sequence 10, Appl
18	86	100.0	95	6	US-10-993-543-274	Sequence 274, App
19	86	100.0	95	6	US-10-993-543-276	Sequence 276, App
20	86	100.0	95	6	US-10-993-543-278	Sequence 278, App
21	86	100.0	95	6	US-10-993-543-283	Sequence 283, App
22	86	100.0	95	7	US-11-054-669-54	Sequence 54, Appl
23	86	100.0	95	7	US-11-054-669-55	Sequence 55, Appl
24	86	100.0	95	7	US-11-054-669-56	Sequence 56, Appl
25	86	100.0	95	7	US-11-054-669-57	Sequence 57, Appl
26	86	100.0	95	7	US-11-054-669-63	Sequence 63, Appl
27	86	100.0	95	7	US-11-054-669-64	Sequence 64, Appl
28	86	100.0	95	7	US-11-054-669-65	Sequence 65, Appl
29	86	100.0	95	7	US-11-054-669-66	Sequence 66, Appl
30	86	100.0	95	7	US-11-054-669-67	Sequence 67, Appl
31	86	100.0	95	7	US-11-054-669-69	Sequence 69, Appl
32	86	100.0	95	7	US-11-054-669-71	Sequence 71, Appl
33	86	100.0	95	7	US-11-054-669-72	Sequence 72, Appl
34	86	100.0	95	7	US-11-084-554-123	Sequence 123, App
35	86	100.0	95	7	US-11-084-554-124	Sequence 124, App
36	86	100.0	95	7	US-11-084-554-128	Sequence 128, App
37	86	100.0	95	7	US-11-084-554-129	Sequence 129, App
38	86	100.0	95	7	US-11-084-554-136	Sequence 136, App
39	86	100.0	95	7	US-11-084-554-137	Sequence 137, App
40	86	100.0	95	7	US-11-084-554-139	Sequence 139, App
41	86	100.0	95	7	US-11-084-554-140	Sequence 140, App
42	86	100.0	95	7	US-11-084-554-143	Sequence 143, App
43	86	100.0	95	7	US-11-084-554-145	Sequence 145, App
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328	86	100.0	114	6	US-10-923-327-2	Sequence 2, Appli
329	86	100.0	114	6	US-10-923-327-3	Sequence 3, Appli
330	86	100.0	114	6	US-10-925-366A-12	Sequence 12, Appl
331	86	100.0	116	6	US-10-981-356A-3	Sequence 3, Appli
332	86	100.0	116	7	US-11-096-046-3	Sequence 3, Appli
333	86	100.0	118	6	US-10-993-543-6	Sequence 6, Appli
334	86	100.0	119	6	US-10-993-543-170	Sequence 170, App
335	86	100.0	120	6	US-10-993-543-62	Sequence 62, Appl
336	86	100.0	120	6	US-10-993-543-78	Sequence 78, Appl
337	86	100.0	120	6	US-10-993-543-162	Sequence 162, App
338	86	100.0	121	6	US-10-993-543-30	Sequence 30, Appl
339	86	100.0	126	6	US-10-839-799-43	Sequence 43, Appl
340	86	100.0	126	6	US-10-839-799-47	Sequence 47, Appl
341	86	100.0	126	6	US-10-839-799-51	Sequence 51, Appl
342	86	100.0	126	6	US-10-839-799-53	Sequence 53, Appl
343	86	100.0	126	6	US-10-839-799-57	Sequence 57, Appl
344	86	100.0	126	6	US-10-839-799-59	Sequence 59, Appl
345	86	100.0	126	6	US-10-839-799-63	Sequence 63, Appl
346	86	100.0	126	6	US-10-839-799-65	Sequence 65, Appl
347	86	100.0	126	6	US-10-839-799-75	Sequence 75, Appl
348	86	100.0	126	7	US-11-226-325-12	Sequence 12, Appl
349	86	100.0	126	7	US-11-226-325-14	Sequence 14, Appl
350	86	100.0	126	7	US-11-250-411-94	Sequence 94, Appl
351	86	100.0	126	7	US-11-250-411-96	Sequence 96, Appl
352	86	100.0	127	7	US-11-193-512-71	Sequence 71, Appl
353	86	100.0	127	7	US-11-176-525-2	Sequence 2, Appli
354	86	100.0	128	7	US-11-096-074-20	Sequence 20, Appl
355	86	100.0	128	7	US-11-096-074-22	Sequence 22, Appl
356	86	100.0	128	7	US-11-096-074-24	Sequence 24, Appl
357	86	100.0	128	7	US-11-095-822-20	Sequence 20, Appl
358	86	100.0	128	7	US-11-095-822-22	Sequence 22, Appl
359	86	100.0	128	7	US-11-095-822-24	Sequence 24, Appl
360	86	100.0	128	7	US-11-250-411-92	Sequence 92, Appl
361	86	100.0	139	7	US-11-128-900-22	Sequence 22, Appl
362	86	100.0	139	7	US-11-128-900-96	Sequence 96, Appl
363	86	100.0	213	7	US-11-102-621-118	Sequence 118, App
364	86	100.0	213	7	US-11-158-505-34	Sequence 34, Appl
365	86	100.0	214	7	US-11-025-712-11	Sequence 11, Appl
366	86	100.0	214	7	US-11-094-625-9	Sequence 9, Appli
367	86	100.0	214	7	US-11-102-621-129	Sequence 129, App
368	86	100.0	214	7	US-11-128-900-71	Sequence 71, Appl
369	86	100.0	214	7	US-11-154-337-14	Sequence 14, Appl
370	86	100.0	214	7	US-11-154-337-16	Sequence 16, Appl
371	86	100.0	214	7	US-11-182-908-13	Sequence 13, Appl
372	86	100.0	214	7	US-11-182-908-15	Sequence 15, Appl
373	86	100.0	214	7	US-11-183-205-55	Sequence 55, Appl
374	86	100.0	217	7	US-11-182-908-23	Sequence 23, Appl
375	86	100.0	218	6	US-10-923-327-8	Sequence 8, Appli
376	86	100.0	218	6	US-10-923-327-10	Sequence 10, Appl
377	86	100.0	218	6	US-10-923-327-12	Sequence 12, Appl
378	86	100.0	218	6	US-10-923-327-17	Sequence 17, Appl
379	86	100.0	218	7	US-11-084-554-11	Sequence 11, Appl
380	86	100.0	218	7	US-11-136-250-11	Sequence 11, Appl
381	86	100.0	233	7	US-11-182-908-17	Sequence 17, Appl
382	86	100.0	235	7	US-11-166-994-2	Sequence 2, Appli
383	86	100.0	239	7	US-11-054-515-1882	Sequence 1882, Ap
384	86	100.0	239	7	US-11-054-515-1922	Sequence 1922, Ap
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386	86	100.0	240	6	US-10-902-546-12	Sequence 12, Appl
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392	86	100.0	241	7	US-11-054-515-2054	Sequence 2054, Ap
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394	86	100.0	241	7	US-11-190-364-14	Sequence 14, Appl
395	86	100.0	241	7	US-11-147-780-14	Sequence 14, Appl
396	86	100.0	243	7	US-11-054-515-1883	Sequence 1883, Ap
397	86	100.0	243	7	US-11-054-515-1935	Sequence 1935, Ap
398	86	100.0	243	7	US-11-054-515-1943	Sequence 1943, Ap
399	86	100.0	243	7	US-11-054-515-1945	Sequence 1945, Ap
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401	86	100.0	243	7	US-11-054-515-2064	Sequence 2064, Ap
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403	86	100.0	244	7	US-11-054-515-164	Sequence 164, App
404	86	100.0	244	7	US-11-054-515-261	Sequence 261, App
405	86	100.0	244	7	US-11-054-515-280	Sequence 280, App
406	86	100.0	244	7	US-11-054-515-1881	Sequence 1881, Ap
407	86	100.0	245	7	US-11-054-515-1900	Sequence 1900, Ap
408	86	100.0	245	7	US-11-054-515-1902	Sequence 1902, Ap
409	86	100.0	246	7	US-11-054-515-1920	Sequence 1920, Ap
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411	86	100.0	247	7	US-11-054-515-969	Sequence 969, App
412	86	100.0	247	7	US-11-054-515-1177	Sequence 1177, Ap
413	86	100.0	247	7	US-11-054-515-3242	Sequence 3242, Ap
414	86	100.0	248	6	US-10-923-327-15	Sequence 15, Appl
415	86	100.0	248	6	US-10-923-327-16	Sequence 16, Appl
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418	86	100.0	248	7	US-11-054-515-1421	Sequence 1421, Ap
419	86	100.0	248	7	US-11-054-515-1700	Sequence 1700, Ap
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421	86	100.0	248	7	US-11-054-515-1778	Sequence 1778, Ap
422	86	100.0	249	7	US-11-054-515-918	Sequence 918, App
423	86	100.0	249	7	US-11-054-515-919	Sequence 919, App
424	86	100.0	249	7	US-11-054-515-926	Sequence 926, App
425	86	100.0	249	7	US-11-054-515-1188	Sequence 1188, Ap
426	86	100.0	249	7	US-11-054-515-1635	Sequence 1635, Ap
427	86	100.0	250	7	US-11-054-515-932	Sequence 932, App
428	86	100.0	250	7	US-11-054-515-1174	Sequence 1174, Ap
429	86	100.0	251	7	US-11-054-515-922	Sequence 922, App
430	86	100.0	251	7	US-11-054-515-1310	Sequence 1310, Ap
431	86	100.0	251	7	US-11-054-515-1320	Sequence 1320, Ap
432	86	100.0	253	7	US-11-054-515-936	Sequence 936, App
433	86	100.0	255	7	US-11-054-515-1603	Sequence 1603, Ap
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435	86	100.0	276	7	US-11-038-901-19	Sequence 19, Appl
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437	86	100.0	277	6	US-10-996-007B-14	Sequence 14, Appl
438	86	100.0	277	6	US-10-996-007B-16	Sequence 16, Appl
439	86	100.0	313	7	US-11-000-463-427	Sequence 427, App
440	86	100.0	363	7	US-11-000-463-335	Sequence 335, App
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442	86	100.0	666	6	US-10-981-356A-25	Sequence 25, Appl
443	86	100.0	666	6	US-10-981-356A-27	Sequence 27, Appl
444	86	100.0	666	6	US-10-981-356A-28	Sequence 28, Appl
445	86	100.0	666	6	US-10-981-356A-30	Sequence 30, Appl
446	86	100.0	666	7	US-11-096-046-27	Sequence 27, Appl
447	86	100.0	667	7	US-11-096-046-25	Sequence 25, Appl
448	86	100.0	667	7	US-11-096-046-28	Sequence 28, Appl
449	86	100.0	667	7	US-11-096-046-30	Sequence 30, Appl
450	86	100.0	692	6	US-10-981-356A-26	Sequence 26, Appl
451	86	100.0	695	7	US-11-096-046-26	Sequence 26, Appl
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453	85	98.8	247	7	US-11-054-515-1923	Sequence 1923, Ap
454	84	97.7	112	7	US-11-049-536-312	Sequence 312, App
455	83	96.5	102	7	US-11-049-536-46	Sequence 46, Appl
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458	83	96.5	103	6	US-10-771-257-111	Sequence 111, App
459	83	96.5	103	6	US-10-771-257-113	Sequence 113, App
460	83	96.5	105	7	US-11-155-775-16	Sequence 16, Appl
461	83	96.5	106	7	US-11-155-775-8	Sequence 8, Appli
462	83	96.5	106	7	US-11-041-471-4	Sequence 4, Appli
463	83	96.5	107	7	US-11-064-174-168	Sequence 168, App
464	83	96.5	108	6	US-10-925-366A-147	Sequence 147, App
465	83	96.5	108	6	US-10-925-366A-162	Sequence 162, App
466	83	96.5	108	6	US-10-925-366A-193	Sequence 193, App
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468	83	96.5	108	7	US-11-049-536-244	Sequence 244, App
469	83	96.5	108	7	US-11-049-536-280	Sequence 280, App
470	83	96.5	108	7	US-11-049-536-452	Sequence 452, App
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474	83	96.5	109	7	US-11-040-159-11	Sequence 11, Appl
475	83	96.5	109	7	US-11-040-159-13	Sequence 13, Appl
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477	83	96.5	110	6	US-10-648-816-2	Sequence 2, Appli
478	83	96.5	110	6	US-10-648-816-3	Sequence 3, Appli
479	83	96.5	110	6	US-10-648-816-4	Sequence 4, Appli
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481	83	96.5	110	6	US-10-648-816-6	Sequence 6, Appli
482	83	96.5	110	6	US-10-648-816-7	Sequence 7, Appli
483	83	96.5	110	6	US-10-648-816-8	Sequence 8, Appli
484	83	96.5	110	7	US-11-049-536-468	Sequence 468, App
485	83	96.5	119	6	US-10-993-543-130	Sequence 130, App
486	83	96.5	120	6	US-10-993-543-126	Sequence 126, App
487	83	96.5	121	6	US-10-993-543-154	Sequence 154, App
488	83	96.5	242	7	US-11-054-515-1915	Sequence 1915, Ap
489	83	96.5	247	7	US-11-054-515-3240	Sequence 3240, Ap
490	83	96.5	248	7	US-11-054-515-1446	Sequence 1446, Ap
491	83	96.5	251	7	US-11-054-515-1921	Sequence 1921, Ap
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493	82	95.3	80	6	US-10-982-357-49	Sequence 49, Appl
494	82	95.3	95	6	US-10-993-543-281	Sequence 281, App
495	82	95.3	95	7	US-11-054-669-58	Sequence 58, Appl
496	82	95.3	95	7	US-11-054-669-70	Sequence 70, Appl
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498	82	95.3	95	7	US-11-084-554-134	Sequence 134, App
499	82	95.3	95	7	US-11-061-848-47	Sequence 47, Appl
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501	82	95.3	95	7	US-11-061-848-71	Sequence 71, Appl
502	82	95.3	95	7	US-11-004-590-57	Sequence 57, Appl
503	82	95.3	95	7	US-11-004-590-67	Sequence 67, Appl
504	82	95.3	95	7	US-11-136-250-111	Sequence 111, App
505	82	95.3	95	7	US-11-136-250-134	Sequence 134, App
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507	82	95.3	105	7	US-11-155-775-44	Sequence 44, Appl
508	82	95.3	106	7	US-11-157-494-29	Sequence 29, Appl
509	82	95.3	107	6	US-10-982-357-44	Sequence 44, Appl
510	82	95.3	107	6	US-10-982-357-50	Sequence 50, Appl
511	82	95.3	107	7	US-11-064-174-164	Sequence 164, App
512	82	95.3	107	7	US-11-064-174-169	Sequence 169, App
513	82	95.3	107	7	US-11-051-453-31	Sequence 31, Appl
514	82	95.3	107	7	US-11-049-536-116	Sequence 116, App
515	82	95.3	107	7	US-11-049-536-159	Sequence 159, App
516	82	95.3	107	7	US-11-157-494-30	Sequence 30, Appl
517	82	95.3	108	6	US-10-771-257-33	Sequence 33, Appl
518	82	95.3	108	6	US-10-771-257-80	Sequence 80, Appl
519	82	95.3	108	7	US-11-127-677-33	Sequence 33, Appl
520	82	95.3	108	7	US-11-127-677-78	Sequence 78, Appl
521	82	95.3	108	7	US-11-061-848-13	Sequence 13, Appl
522	82	95.3	108	7	US-11-049-536-248	Sequence 248, App
523	82	95.3	108	7	US-11-049-536-316	Sequence 316, App
524	82	95.3	108	7	US-11-049-536-480	Sequence 480, App
525	82	95.3	108	7	US-11-049-536-604	Sequence 604, App
526	82	95.3	119	6	US-10-993-543-122	Sequence 122, App
527	82	95.3	129	7	US-11-051-453-45	Sequence 45, Appl
528	82	95.3	134	7	US-11-128-900-23	Sequence 23, Appl
529	82	95.3	134	7	US-11-128-900-97	Sequence 97, Appl
530	82	95.3	214	7	US-11-049-536-700	Sequence 700, App
531	82	95.3	236	7	US-11-086-289-8	Sequence 8, Appli
532	82	95.3	236	7	US-11-086-289-20	Sequence 20, Appl
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534	81	94.2	92	7	US-11-144-222-18	Sequence 18, Appl
535	81	94.2	92	7	US-11-182-343-18	Sequence 18, Appl
536	81	94.2	107	7	US-11-064-174-45	Sequence 45, Appl

537	81	94.2	107	7	US-11-064-174-172	Sequence 172, App
538	81	94.2	107	7	US-11-064-174-173	Sequence 173, App
539	81	94.2	107	7	US-11-064-174-174	Sequence 174, App
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541	81	94.2	107	7	US-11-051-453-32	Sequence 32, Appl
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543	81	94.2	107	7	US-11-112-304A-8	Sequence 8, Appli
544	81	94.2	108	6	US-10-771-257-40	Sequence 40, Appl
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546	81	94.2	108	7	US-11-173-071-18	Sequence 18, Appl
547	81	94.2	108	7	US-11-173-071-20	Sequence 20, Appl
548	81	94.2	108	7	US-11-173-071-22	Sequence 22, Appl
549	81	94.2	108	7	US-11-127-677-40	Sequence 40, Appl
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552	81	94.2	109	7	US-11-049-536-324	Sequence 324, App
553	81	94.2	109	7	US-11-049-536-588	Sequence 588, App
554	81	94.2	109	7	US-11-049-536-620	Sequence 620, App
555	81	94.2	109	7	US-11-049-536-684	Sequence 684, App
556	81	94.2	129	7	US-11-051-453-43	Sequence 43, Appl
557	81	94.2	129	7	US-11-051-453-46	Sequence 46, Appl
558	80	93.0	95	7	US-11-054-669-59	Sequence 59, Appl
559	80	93.0	95	7	US-11-084-554-116	Sequence 116, App
560	80	93.0	95	7	US-11-061-848-38	Sequence 38, Appl
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562	80	93.0	95	7	US-11-004-590-65	Sequence 65, Appl
563	80	93.0	95	7	US-11-136-250-116	Sequence 116, App
564	80	93.0	96	7	US-11-144-248-40	Sequence 40, Appl
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566	80	93.0	96	7	US-11-182-343-40	Sequence 40, Appl
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569	80	93.0	100	7	US-11-182-343-10	Sequence 10, Appl
570	80	93.0	105	7	US-11-155-775-48	Sequence 48, Appl
571	80	93.0	106	7	US-11-064-174-159	Sequence 159, App
572	80	93.0	106	7	US-11-004-590-390	Sequence 390, App
573	80	93.0	106	7	US-11-004-590-392	Sequence 392, App
574	80	93.0	106	7	US-11-004-590-393	Sequence 393, App
575	80	93.0	106	7	US-11-004-590-394	Sequence 394, App
576	80	93.0	106	7	US-11-004-590-395	Sequence 395, App
577	80	93.0	106	7	US-11-004-590-396	Sequence 396, App
578	80	93.0	106	7	US-11-004-590-397	Sequence 397, App
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587	80	93.0	106	7	US-11-004-590-406	Sequence 406, App
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589	80	93.0	106	7	US-11-004-590-408	Sequence 408, App
590	80	93.0	106	7	US-11-004-590-409	Sequence 409, App
591	80	93.0	106	7	US-11-004-590-410	Sequence 410, App
592	80	93.0	106	7	US-11-004-590-411	Sequence 411, App
593	80	93.0	106	7	US-11-004-590-456	Sequence 456, App
594	80	93.0	106	7	US-11-183-205-38	Sequence 38, Appl
595	80	93.0	107	6	US-10-925-366A-153	Sequence 153, App
596	80	93.0	107	7	US-11-144-248-6	Sequence 6, Appli
597	80	93.0	107	7	US-11-084-554-6	Sequence 6, Appli
598	80	93.0	107	7	US-11-096-074-54	Sequence 54, Appl
599	80	93.0	107	7	US-11-064-174-29	Sequence 29, Appl
600	80	93.0	107	7	US-11-144-222-6	Sequence 6, Appli
601	80	93.0	107	7	US-11-095-822-54	Sequence 54, Appl
602	80	93.0	107	7	US-11-221-900-8	Sequence 8, Appli
603	80	93.0	107	7	US-11-102-424-16	Sequence 16, Appl
604	80	93.0	107	7	US-11-102-424-17	Sequence 17, Appl
605	80	93.0	107	7	US-11-136-250-6	Sequence 6, Appli
606	80	93.0	107	7	US-11-182-343-6	Sequence 6, Appli
607	80	93.0	108	6	US-10-925-366A-148	Sequence 148, App
608	80	93.0	108	6	US-10-925-366A-201	Sequence 201, App
609	80	93.0	108	6	US-10-771-257-39	Sequence 39, Appl
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854	79	91.9	111	7	US-11-049-536-168	Sequence 168, App
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892	79	91.9	131	7	US-11-226-325-2	Sequence 2, Appli
893	79	91.9	132	6	US-10-504-389A-53	Sequence 53, Appl
894	79	91.9	139	7	US-11-128-900-16	Sequence 16, Appl
895	79	91.9	139	7	US-11-128-900-90	Sequence 90, Appl
896	79	91.9	141	7	US-11-128-900-89	Sequence 89, Appl
897	79	91.9	142	7	US-11-128-900-19	Sequence 19, Appl
898	79	91.9	142	7	US-11-128-900-92	Sequence 92, Appl
899	79	91.9	142	7	US-11-079-907-1	Sequence 1, Appli
900	79	91.9	146	7	US-11-128-900-21	Sequence 21, Appl
901	79	91.9	146	7	US-11-128-900-93	Sequence 93, Appl
902	79	91.9	213	7	US-11-172-320-4	Sequence 4, Appli
903	79	91.9	213	7	US-11-120-338-13	Sequence 13, Appl
904	79	91.9	213	7	US-11-120-338-16	Sequence 16, Appl
905	79	91.9	213	7	US-11-173-969-4	Sequence 4, Appli
906	79	91.9	213	7	US-11-107-028-31	Sequence 31, Appl
907	79	91.9	213	7	US-11-107-028-44	Sequence 44, Appl
908	79	91.9	213	7	US-11-106-820-24	Sequence 24, Appl
909	79	91.9	213	7	US-11-106-820-29	Sequence 29, Appl
910	79	91.9	213	7	US-11-106-820-44	Sequence 44, Appl
911	79	91.9	213	7	US-11-143-077-13	Sequence 13, Appl
912	79	91.9	213	7	US-11-143-077-16	Sequence 16, Appl
913	79	91.9	213	7	US-11-143-386-13	Sequence 13, Appl
914	79	91.9	213	7	US-11-143-386-16	Sequence 16, Appl
915	79	91.9	232	7	US-11-106-820-23	Sequence 23, Appl
916	79	91.9	232	7	US-11-190-364-21	Sequence 21, Appl
917	79	91.9	232	7	US-11-147-780-21	Sequence 21, Appl
918	79	91.9	233	7	US-11-128-900-15	Sequence 15, Appl
919	79	91.9	233	7	US-11-128-900-67	Sequence 67, Appl
920	79	91.9	239	6	US-10-952-535A-6	Sequence 6, Appli
921	79	91.9	245	7	US-11-054-515-1972	Sequence 1972, Ap
922	79	91.9	246	7	US-11-054-515-1264	Sequence 1264, Ap
923	79	91.9	246	7	US-11-054-515-1268	Sequence 1268, Ap
924	79	91.9	247	7	US-11-056-825-8	Sequence 8, Appli
925	79	91.9	249	7	US-11-054-515-1035	Sequence 1035, Ap
926	79	91.9	249	7	US-11-056-825-4	Sequence 4, Appli
927	79	91.9	250	7	US-11-054-515-1952	Sequence 1952, Ap
928	79	91.9	251	7	US-11-054-515-110	Sequence 110, App
929	79	91.9	251	7	US-11-054-515-1049	Sequence 1049, Ap
930	79	91.9	251	7	US-11-054-515-1219	Sequence 1219, Ap
931	79	91.9	252	7	US-11-054-515-1495	Sequence 1495, Ap
932	79	91.9	252	7	US-11-054-515-1534	Sequence 1534, Ap
933	79	91.9	253	7	US-11-054-515-1499	Sequence 1499, Ap
934	79	91.9	259	6	US-10-512-184-31	Sequence 31, Appl
935	79	91.9	259	6	US-10-512-184-33	Sequence 33, Appl
936	79	91.9	269	6	US-10-839-799-109	Sequence 109, App
937	79	91.9	291	7	US-11-041-095-60	Sequence 60, Appl
938	79	91.9	293	7	US-11-116-939-10	Sequence 10, Appl
939	79	91.9	307	7	US-11-000-463-332	Sequence 332, App
940	79	91.9	312	7	US-11-000-463-334	Sequence 334, App
941	79	91.9	328	7	US-11-079-907-4	Sequence 4, Appli
942	79	91.9	329	6	US-10-512-184-68	Sequence 68, Appl
943	79	91.9	329	6	US-10-512-184-70	Sequence 70, Appl
944	79	91.9	384	7	US-11-000-463-804	Sequence 804, App
945	79	91.9	384	7	US-11-000-463-805	Sequence 805, App
946	79	91.9	384	7	US-11-000-463-806	Sequence 806, App
947	79	91.9	384	7	US-11-000-463-807	Sequence 807, App
948	79	91.9	412	7	US-11-116-939-12	Sequence 12, Appl
949	79	91.9	666	6	US-10-981-356A-29	Sequence 29, Appl
950	79	91.9	667	7	US-11-096-046-29	Sequence 29, Appl
951	79	91.9	824	7	US-11-116-939-11	Sequence 11, Appl
952	78	90.7	95	7	US-11-004-590-70	Sequence 70, Appl
953	78	90.7	95	7	US-11-004-590-71	Sequence 71, Appl
954	78	90.7	96	6	US-10-993-543-275	Sequence 275, App
955	78	90.7	96	6	US-10-993-543-279	Sequence 279, App
956	78	90.7	96	6	US-10-993-543-285	Sequence 285, App
957	78	90.7	96	7	US-11-084-554-144	Sequence 144, App
958	78	90.7	96	7	US-11-084-554-147	Sequence 147, App
959	78	90.7	96	7	US-11-136-250-144	Sequence 144, App
960	78	90.7	96	7	US-11-136-250-147	Sequence 147, App
961	78	90.7	99	6	US-10-999-866-18	Sequence 18, Appl
962	78	90.7	99	6	US-10-935-005B-49	Sequence 49, Appl
963	78	90.7	99	7	US-11-084-554-201	Sequence 201, App
964	78	90.7	99	7	US-11-084-554-204	Sequence 204, App
965	78	90.7	99	7	US-11-084-554-205	Sequence 205, App
966	78	90.7	99	7	US-11-084-554-207	Sequence 207, App
967	78	90.7	99	7	US-11-061-821-18	Sequence 18, Appl
968	78	90.7	99	7	US-11-136-250-201	Sequence 201, App
969	78	90.7	99	7	US-11-136-250-204	Sequence 204, App
970	78	90.7	99	7	US-11-136-250-205	Sequence 205, App
971	78	90.7	99	7	US-11-136-250-207	Sequence 207, App
972	78	90.7	101	7	US-11-049-536-10	Sequence 10, Appl
973	78	90.7	106	7	US-11-174-186-7	Sequence 7, Appli
974	78	90.7	107	7	US-11-102-621-8	Sequence 8, Appli

975	78	90.7	107	7	US-11-064-174-154	Sequence 154, App
976	78	90.7	107	7	US-11-064-174-162	Sequence 162, App
977	78	90.7	108	6	US-10-925-366A-169	Sequence 169, App
978	78	90.7	108	6	US-10-982-440-32	Sequence 32, Appl
979	78	90.7	108	6	US-10-982-440-36	Sequence 36, Appl
980	78	90.7	108	7	US-11-049-536-288	Sequence 288, App
981	78	90.7	109	6	US-10-771-257-29	Sequence 29, Appl
982	78	90.7	109	7	US-11-127-677-29	Sequence 29, Appl
983	78	90.7	110	6	US-10-834-397-33	Sequence 33, Appl
984	78	90.7	110	6	US-10-834-397-53	Sequence 53, Appl
985	78	90.7	110	7	US-11-112-240-28	Sequence 28, Appl
986	78	90.7	110	7	US-11-112-304A-28	Sequence 28, Appl
987	78	90.7	110	7	US-11-049-536-256	Sequence 256, App
988	78	90.7	110	7	US-11-049-536-272	Sequence 272, App
989	78	90.7	110	7	US-11-049-536-404	Sequence 404, App
990	78	90.7	110	7	US-11-049-536-444	Sequence 444, App
991	78	90.7	110	7	US-11-049-536-456	Sequence 456, App
992	78	90.7	110	7	US-11-049-536-460	Sequence 460, App
993	78	90.7	110	7	US-11-049-536-520	Sequence 520, App
994	78	90.7	110	7	US-11-049-536-526	Sequence 526, App
995	78	90.7	110	7	US-11-049-536-676	Sequence 676, App
996	78	90.7	112	6	US-10-834-397-19	Sequence 19, Appl
997	78	90.7	112	7	US-11-049-536-412	Sequence 412, App
998	78	90.7	112	7	US-11-049-536-552	Sequence 552, App
999	78	90.7	121	6	US-10-993-543-10	Sequence 10, Appl
1000	78	90.7	122	6	US-10-993-543-138	Sequence 138, App

ALIGNMENTS

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RESULT 1
US-11-105-268-40
; Sequence 40, Application US/11105268
; Publication No. US20050260204A1
; GENERAL INFORMATION:
;  APPLICANT: Allan, Christian
;  TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF
;  FILE REFERENCE: 10271-126-999
;  CURRENT APPLICATION NUMBER: US/11/105,268
;  CURRENT FILING DATE:  2005-04-12
;  PRIOR APPLICATION NUMBER: 60/561,845
;  PRIOR FILING DATE: 2004-04-12
;  NUMBER OF SEQ ID NOS: 60
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
;   LENGTH: 15
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-105-268-40

  Query Match            100.0%;  Score 86;  DB 7;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 6.2e-07;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 2
US-10-925-366A-307
; Sequence 307, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
;  APPLICANT: Ignatovich, Olga
;  APPLICANT:  DeWildt, Rudolph M.T.
;  APPLICANT:  Benjamin, Woolven
;  APPLICANT:  Grant, Steven
;  APPLICANT:  Jones, Philip
;  APPLICANT:  Basran, Amrik
;  APPLICANT:  Brewis, Neil
;  TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
;  FILE REFERENCE: 8039/2105
;  CURRENT APPLICATION NUMBER: US/10/925,366A
;  CURRENT FILING DATE:  2004-08-24
;  PRIOR APPLICATION NUMBER: US 10/744,774
;  PRIOR FILING DATE: 2003-12-23
;  PRIOR APPLICATION NUMBER: PCT/GB2003/002804
;  PRIOR FILING DATE: 2003-06-30
;  PRIOR APPLICATION NUMBER: PCT/GB2002/03014
;  PRIOR FILING DATE: 2002-06-28
;  PRIOR APPLICATION NUMBER: GB 0230202.4
;  PRIOR FILING DATE: 2002-12-27
;  PRIOR APPLICATION NUMBER: GB 115841.9
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: PCT/GB2004/002829
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/535,076
;  PRIOR FILING DATE: 2004-01-08
;  PRIOR APPLICATION NUMBER: PCT/GB2003/005646
;  PRIOR FILING DATE: 2003-12-24
;  PRIOR APPLICATION NUMBER: GB 0327706.8
;  PRIOR FILING DATE: 2003-11-28
;  PRIOR APPLICATION NUMBER: US 60/509,613
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 368
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 307
;   LENGTH: 49
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Amino Acid Sequence of Domain Antibody
US-10-925-366A-307

  Query Match            100.0%;  Score 86;  DB 6;  Length 49;
  Best Local Similarity  100.0%;  Pred. No. 1.7e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 3
US-10-925-366A-327
; Sequence 327, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
;  APPLICANT: Ignatovich, Olga
;  APPLICANT:  DeWildt, Rudolph M.T.
;  APPLICANT:  Benjamin, Woolven
;  APPLICANT:  Grant, Steven
;  APPLICANT:  Jones, Philip
;  APPLICANT:  Basran, Amrik
;  APPLICANT:  Brewis, Neil
;  TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
;  FILE REFERENCE: 8039/2105
;  CURRENT APPLICATION NUMBER: US/10/925,366A
;  CURRENT FILING DATE:  2004-08-24
;  PRIOR APPLICATION NUMBER: US 10/744,774
;  PRIOR FILING DATE: 2003-12-23
;  PRIOR APPLICATION NUMBER: PCT/GB2003/002804
;  PRIOR FILING DATE: 2003-06-30
;  PRIOR APPLICATION NUMBER: PCT/GB2002/03014
;  PRIOR FILING DATE: 2002-06-28
;  PRIOR APPLICATION NUMBER: GB 0230202.4
;  PRIOR FILING DATE: 2002-12-27
;  PRIOR APPLICATION NUMBER: GB 115841.9
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: PCT/GB2004/002829
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/535,076
;  PRIOR FILING DATE: 2004-01-08
;  PRIOR APPLICATION NUMBER: PCT/GB2003/005646
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;  PRIOR FILING DATE: 2003-12-24
;  PRIOR APPLICATION NUMBER: GB 0327706.8
;  PRIOR FILING DATE: 2003-11-28
;  PRIOR APPLICATION NUMBER: US 60/509,613
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 368
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 327
;   LENGTH: 49
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Amino Acid Sequence of Domain Antibody
US-10-925-366A-327

  Query Match             100.0%;  Score 86;  DB 6;  Length 49;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 4
US-10-925-366A-295
; Sequence 295, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
;  APPLICANT: Ignatovich, Olga
;  APPLICANT:  DeWildt, Rudolph M.T.
;  APPLICANT:  Benjamin, Woolven
;  APPLICANT:  Grant, Steven
;  APPLICANT:  Jones, Philip
;  APPLICANT:  Basran, Amrik
;  APPLICANT:  Brewis, Neil
;  TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
;  FILE REFERENCE: 8039/2105
;  CURRENT APPLICATION NUMBER: US/10/925,366A
;  CURRENT FILING DATE:  2004-08-24
;  PRIOR APPLICATION NUMBER: US 10/744,774
;  PRIOR FILING DATE: 2003-12-23
;  PRIOR APPLICATION NUMBER: PCT/GB2003/002804
;  PRIOR FILING DATE: 2003-06-30
;  PRIOR APPLICATION NUMBER: PCT/GB2002/03014
;  PRIOR FILING DATE: 2002-06-28
;  PRIOR APPLICATION NUMBER: GB 0230202.4
;  PRIOR FILING DATE: 2002-12-27
;  PRIOR APPLICATION NUMBER: GB 115841.9
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: PCT/GB2004/002829
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/535,076
;  PRIOR FILING DATE: 2004-01-08
;  PRIOR APPLICATION NUMBER: PCT/GB2003/005646
;  PRIOR FILING DATE: 2003-12-24
;  PRIOR APPLICATION NUMBER: GB 0327706.8
;  PRIOR FILING DATE: 2003-11-28
;  PRIOR APPLICATION NUMBER: US 60/509,613
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 368
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 295
;   LENGTH: 74
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-295

  Query Match             100.0%;  Score 86;  DB 6;  Length 74;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          1 WYQQKPGKAPKLLIY 15


RESULT 5
US-10-925-366A-319
; Sequence 319, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
;  APPLICANT: Ignatovich, Olga
;  APPLICANT:  DeWildt, Rudolph M.T.
;  APPLICANT:  Benjamin, Woolven
;  APPLICANT:  Grant, Steven
;  APPLICANT:  Jones, Philip
;  APPLICANT:  Basran, Amrik
;  APPLICANT:  Brewis, Neil
;  TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
;  FILE REFERENCE: 8039/2105
;  CURRENT APPLICATION NUMBER: US/10/925,366A
;  CURRENT FILING DATE:  2004-08-24
;  PRIOR APPLICATION NUMBER: US 10/744,774
;  PRIOR FILING DATE: 2003-12-23
;  PRIOR APPLICATION NUMBER: PCT/GB2003/002804
;  PRIOR FILING DATE: 2003-06-30
;  PRIOR APPLICATION NUMBER: PCT/GB2002/03014
;  PRIOR FILING DATE: 2002-06-28
;  PRIOR APPLICATION NUMBER: GB 0230202.4
;  PRIOR FILING DATE: 2002-12-27
;  PRIOR APPLICATION NUMBER: GB 115841.9
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: PCT/GB2004/002829
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/535,076
;  PRIOR FILING DATE: 2004-01-08
;  PRIOR APPLICATION NUMBER: PCT/GB2003/005646
;  PRIOR FILING DATE: 2003-12-24
;  PRIOR APPLICATION NUMBER: GB 0327706.8
;  PRIOR FILING DATE: 2003-11-28
;  PRIOR APPLICATION NUMBER: US 60/509,613
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 368
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 319
;   LENGTH: 76
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-319

  Query Match             100.0%;  Score 86;  DB 6;  Length 76;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          3 WYQQKPGKAPKLLIY 17


RESULT 6
US-10-925-366A-322
; Sequence 322, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
;  APPLICANT: Ignatovich, Olga
;  APPLICANT:  DeWildt, Rudolph M.T.
;  APPLICANT:  Benjamin, Woolven
;  APPLICANT:  Grant, Steven
;  APPLICANT:  Jones, Philip
;  APPLICANT:  Basran, Amrik
;  APPLICANT:  Brewis, Neil
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;  TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
;  FILE REFERENCE: 8039/2105
;  CURRENT APPLICATION NUMBER: US/10/925,366A
;  CURRENT FILING DATE:  2004-08-24
;  PRIOR APPLICATION NUMBER: US 10/744,774
;  PRIOR FILING DATE: 2003-12-23
;  PRIOR APPLICATION NUMBER: PCT/GB2003/002804
;  PRIOR FILING DATE: 2003-06-30
;  PRIOR APPLICATION NUMBER: PCT/GB2002/03014
;  PRIOR FILING DATE: 2002-06-28
;  PRIOR APPLICATION NUMBER: GB 0230202.4
;  PRIOR FILING DATE: 2002-12-27
;  PRIOR APPLICATION NUMBER: GB 115841.9
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: PCT/GB2004/002829
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/535,076
;  PRIOR FILING DATE: 2004-01-08
;  PRIOR APPLICATION NUMBER: PCT/GB2003/005646
;  PRIOR FILING DATE: 2003-12-24
;  PRIOR APPLICATION NUMBER: GB 0327706.8
;  PRIOR FILING DATE: 2003-11-28
;  PRIOR APPLICATION NUMBER: US 60/509,613
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 368
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 322
;   LENGTH: 76
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-322

  Query Match             100.0%;  Score 86;  DB 6;  Length 76;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          3 WYQQKPGKAPKLLIY 17


RESULT 7
US-10-925-366A-305
; Sequence 305, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
;  APPLICANT: Ignatovich, Olga
;  APPLICANT:  DeWildt, Rudolph M.T.
;  APPLICANT:  Benjamin, Woolven
;  APPLICANT:  Grant, Steven
;  APPLICANT:  Jones, Philip
;  APPLICANT:  Basran, Amrik
;  APPLICANT:  Brewis, Neil
;  TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
;  FILE REFERENCE: 8039/2105
;  CURRENT APPLICATION NUMBER: US/10/925,366A
;  CURRENT FILING DATE:  2004-08-24
;  PRIOR APPLICATION NUMBER: US 10/744,774
;  PRIOR FILING DATE: 2003-12-23
;  PRIOR APPLICATION NUMBER: PCT/GB2003/002804
;  PRIOR FILING DATE: 2003-06-30
;  PRIOR APPLICATION NUMBER: PCT/GB2002/03014
;  PRIOR FILING DATE: 2002-06-28
;  PRIOR APPLICATION NUMBER: GB 0230202.4
;  PRIOR FILING DATE: 2002-12-27
;  PRIOR APPLICATION NUMBER: GB 115841.9
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: PCT/GB2004/002829
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/535,076
;  PRIOR FILING DATE: 2004-01-08
;  PRIOR APPLICATION NUMBER: PCT/GB2003/005646
;  PRIOR FILING DATE: 2003-12-24
;  PRIOR APPLICATION NUMBER: GB 0327706.8
;  PRIOR FILING DATE: 2003-11-28
;  PRIOR APPLICATION NUMBER: US 60/509,613
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 368
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 305
;   LENGTH: 77
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-305

  Query Match             100.0%;  Score 86;  DB 6;  Length 77;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db          4 WYQQKPGKAPKLLIY 18


RESULT 8
US-10-925-366A-302
; Sequence 302, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
;  APPLICANT: Ignatovich, Olga
;  APPLICANT:  DeWildt, Rudolph M.T.
;  APPLICANT:  Benjamin, Woolven
;  APPLICANT:  Grant, Steven
;  APPLICANT:  Jones, Philip
;  APPLICANT:  Basran, Amrik
;  APPLICANT:  Brewis, Neil
;  TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
;  FILE REFERENCE: 8039/2105
;  CURRENT APPLICATION NUMBER: US/10/925,366A
;  CURRENT FILING DATE:  2004-08-24
;  PRIOR APPLICATION NUMBER: US 10/744,774
;  PRIOR FILING DATE: 2003-12-23
;  PRIOR APPLICATION NUMBER: PCT/GB2003/002804
;  PRIOR FILING DATE: 2003-06-30
;  PRIOR APPLICATION NUMBER: PCT/GB2002/03014
;  PRIOR FILING DATE: 2002-06-28
;  PRIOR APPLICATION NUMBER: GB 0230202.4
;  PRIOR FILING DATE: 2002-12-27
;  PRIOR APPLICATION NUMBER: GB 115841.9
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: PCT/GB2004/002829
;  PRIOR FILING DATE: 2004-06-30
;  PRIOR APPLICATION NUMBER: US 60/535,076
;  PRIOR FILING DATE: 2004-01-08
;  PRIOR APPLICATION NUMBER: PCT/GB2003/005646
;  PRIOR FILING DATE: 2003-12-24
;  PRIOR APPLICATION NUMBER: GB 0327706.8
;  PRIOR FILING DATE: 2003-11-28
;  PRIOR APPLICATION NUMBER: US 60/509,613
;  PRIOR FILING DATE: 2003-10-08
;  NUMBER OF SEQ ID NOS: 368
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 302
;   LENGTH: 78
;   TYPE: PRT
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-302

  Query Match             100.0%;  Score 86;  DB 6;  Length 78;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-06;
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db          5 WYQQKPGKAPKLLIY 19
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RESULT 9
US-10-925-366A-311
; Sequence 311, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: DeWildt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Basran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 311
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-311

Query Match 100.0%; Score 86; DB 6; Length 78;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db          5 WYQQKPGKAPKLLIY 19
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RESULT 10
US-10-925-366A-314
; Sequence 314, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: DeWildt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Basran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 314
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Domain antibody amino acid sequence
US-10-925-366A-314

Query Match 100.0%; Score 86; DB 6; Length 78;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db          5 WYQQKPGKAPKLLIY 19
```

RESULT 11
US-11-226-325-131
; Sequence 131, Application US/11226325
; Publication No. US20060008456A1
; GENERAL INFORMATION:
; APPLICANT: TSUCHIYA, MASAYUKI
; TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
; FILE REFERENCE: 053466/0274
; CURRENT APPLICATION NUMBER: US/11/226,325
; CURRENT FILING DATE: 2005-09-15
; PRIOR APPLICATION NUMBER: US/09/509,098
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: PCT/JP98/04469
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: JP 9-271726
; PRIOR FILING DATE: 1997-10-03
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 131
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of the L chain V region of HuSG I
US-11-226-325-131

Query Match 100.0%; Score 86; DB 7; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;

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  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 12
US-11-226-325-132
; Sequence 132, Application US/11226325
; Publication No. US20060008456A1
; GENERAL INFORMATION:
;  APPLICANT: TSUCHIYA, MASAYUKI
;  TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY
;  FILE REFERENCE: 053466/0274
;  CURRENT APPLICATION NUMBER: US/11/226,325
;  CURRENT FILING DATE:  2005-09-15
;  PRIOR APPLICATION NUMBER: US/09/509,098
;  PRIOR FILING DATE: 2000-03-22
;  PRIOR APPLICATION NUMBER: PCT/JP98/04469
;  PRIOR FILING DATE: 1998-10-02
;  PRIOR APPLICATION NUMBER: JP 9-271726
;  PRIOR FILING DATE: 1997-10-03
;  NUMBER OF SEQ ID NOS: 203
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 132
;   LENGTH: 80
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Amino acid
;   OTHER INFORMATION: sequence of the L chain V region of REI
US-11-226-325-132

  Query Match             100.0%;  Score 86;  DB 7;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 13
US-10-839-799-112
; Sequence 112, Application US/10839799
; Publication No. US20050249726A1
;   GENERAL INFORMATION:
;        APPLICANT: OHTOMO, Toshihiko
;                   SATO, Koh
;                   TSUCHIYA, Masayuki
;        TITLE OF INVENTION: RESHAPED HUMAN ANTIBODY TO HUMAN
;                            MEDULLOBLASTOMA CELLS
;        NUMBER OF SEQUENCES: 132
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Foley & Lardner
;             STREET: 3000 K Street, N.W., Suite 500
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20007-5109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/839,799
;             FILING DATE: 06-May-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/646,265
;             FILING DATE: 09-SEP-1996
;             APPLICATION NUMBER: WO PCT/JP94/01763
;             FILING DATE: 19-OCT-1994
;             APPLICATION NUMBER: JP 5-291078
;             FILING DATE: 19-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: WEGNER, Harold C.
;             REGISTRATION NUMBER: 25,258
;             REFERENCE/DOCKET NUMBER: 53466/184
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)672-5300
;             TELEFAX: (202)672-5399
;             TELEX: 904136
;   INFORMATION FOR SEQ ID NO: 112:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 87 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-839-799-112

  Query Match             100.0%;  Score 86;  DB 6;  Length 87;
  Best Local Similarity   100.0%;  Pred. No. 2.8e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         24 WYQQKPGKAPKLLIY 38


RESULT 14
US-11-173-071-23
; Sequence 23, Application US/11173071
; Publication No. US20050244409A1
; GENERAL INFORMATION:
;  APPLICANT: ERICKSON-MILLER, CONNIE
;  APPLICANT:  HOLMES, STEPHEN D.
;  APPLICANT:  TAYLOR, ALEXANDER H.
;  APPLICANT:  YOUNG, PETER R.
;  TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR ANTIBODIES
;  FILE REFERENCE: P50911
;  CURRENT APPLICATION NUMBER: US/11/173,071
;  CURRENT FILING DATE:  2005-07-01
;  PRIOR APPLICATION NUMBER: US/09/958,620
;  PRIOR FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: PCT/US00/10284
;  PRIOR FILING DATE: 2000-04-14
;  PRIOR APPLICATION NUMBER: 60/129,263
;  PRIOR FILING DATE: 1999-04-14
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 23
;   LENGTH: 90
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Derivative of human light chain REI, REI-con
US-11-173-071-23

  Query Match             100.0%;  Score 86;  DB 7;  Length 90;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 15
US-10-999-866-10
; Sequence 10, Application US/10999866
; Publication No. US20050266004A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann
;  TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS AN
;  FILE REFERENCE: CEN5042NP
;  CURRENT APPLICATION NUMBER: US/10/999,866
;  CURRENT FILING DATE:  2004-11-30
;  PRIOR APPLICATION NUMBER: 60/527,794
;  PRIOR FILING DATE: 2003-12-08
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(93)
;   OTHER INFORMATION: Kappa1_4 light chain variable region
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(24)
;   OTHER INFORMATION: framework 1
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (25)..(25)
;   OTHER INFORMATION: complementarity determinng region 1 (CDR1), X is 10-30 (17) of
;   OTHER INFORMATION: any amino acids.
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (26)..(40)
;   OTHER INFORMATION: framework 2
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (41)..(41)
;   OTHER INFORMATION: complementarity determinng region 2 (CDR2), X is 3-20 (7) of any
;   OTHER INFORMATION: amino acids.
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (42)..(73)
;   OTHER INFORMATION: framework 3
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (74)..(74)
;   OTHER INFORMATION: complementarity determinng region 3 (CDR3), X is 20-40 (30) of
;   OTHER INFORMATION: any amino acids.
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (75)..(93)
;   OTHER INFORMATION: framework 4
US-10-999-866-10

  Query Match            100.0%;  Score 86;  DB 6;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         26 WYQQKPGKAPKLLIY 40


RESULT 16
US-10-935-005B-40
; Sequence 40, Application US/10935005B
; Publication No. US20060051844A1
; GENERAL INFORMATION:
;  APPLICANT: HEAVNER, George A.; KNIGHT, David; GHRAYEB, John; SCALLON, Bernard;
;  APPLICANT:  NESSPOR, Thomas; HUANG, Chichang
;  TITLE OF INVENTION: HUMAN EPO MIMETIC HINGE CORE MIMETIBODIES,
;  FILE REFERENCE: CEN5039NP
;  CURRENT APPLICATION NUMBER: US/10/935,005B
;  CURRENT FILING DATE:  2004-09-03
;  NUMBER OF SEQ ID NOS: 89
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(93)
;   OTHER INFORMATION: Kappa 1_4 light chain variable region
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(24)
;   OTHER INFORMATION: framework 1
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (25)..(25)
;   OTHER INFORMATION: complementarity determinng region 1 (CDR1), X is 10-30 (17) of
;   OTHER INFORMATION: any amino acids.
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (26)..(40)
;   OTHER INFORMATION: framework 2
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (41)..(41)
;   OTHER INFORMATION: complementarity determinng region 2 (CDR2), X is 3-20 (7) of any
;   OTHER INFORMATION: amino acids.
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (42)..(73)
;   OTHER INFORMATION: framework 3
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (74)..(74)
;   OTHER INFORMATION: complementarity determinng region 3 (CDR3), X is 20-40 (30) of
;   OTHER INFORMATION: any amino acids.
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (75)..(93)
;   OTHER INFORMATION: framework 4
US-10-935-005B-40

  Query Match            100.0%;  Score 86;  DB 6;  Length 93;
  Best Local Similarity   100.0%;  Pred. No. 3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         26 WYQQKPGKAPKLLIY 40


RESULT 17
US-11-061-821-10
; Sequence 10, Application US/11061821
; Publication No. US20050266005A1
; GENERAL INFORMATION:
;  APPLICANT: Heavner, George; Li, Li; Oneil, Karyn
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING IL-13 RELATED PATHOLOGIES
;  FILE REFERENCE: CEN5048 NP
;  CURRENT APPLICATION NUMBER: US/11/061,821
;  CURRENT FILING DATE:  2005-02-18
;  PRIOR APPLICATION NUMBER: 60/548,648
;  PRIOR FILING DATE: 2004-02-27
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver 3.3
; SEQ ID NO 10
;   LENGTH: 93
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (1)..(93)
;   OTHER INFORMATION: Kappa1_4 light chain variable region
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
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;   LOCATION: (1)..(24)
;   OTHER INFORMATION: framework 1
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (25)..(25)
;   OTHER INFORMATION: complementarity determinng region 1 (CDR1), X is any amino acid.
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (26)..(40)
;   OTHER INFORMATION: framework 2
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (41)..(41)
;   OTHER INFORMATION: complementarity determinng region 2 (CDR2), X is any amino acid.
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (42)..(73)
;   OTHER INFORMATION: framework 3
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (74)..(74)
;   OTHER INFORMATION: complementarity determinng region 3 (CDR3), X is any amino acid.
;   FEATURE:
;   NAME/KEY: MISC_FEATURE
;   LOCATION: (75)..(93)
;   OTHER INFORMATION: framework 4
US-11-061-821-10

  Query Match            100.0%;  Score 86;  DB 7;  Length 93;
  Best Local Similarity  100.0%;  Pred. No. 3e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         26 WYQQKPGKAPKLLIY 40


RESULT 18
US-10-993-543-274
; Sequence 274, Application US/10993543
; Publication No. US20060036076A1
; GENERAL INFORMATION:
;  APPLICANT: Dransfield, Daniel T.
;  APPLICANT:  Rookey, Kristin
;  APPLICANT:  Ladner, Robert C.
;  TITLE OF INVENTION: Metalloproteinase-Binding Proteins
;  FILE REFERENCE: 10280-088001
;  CURRENT APPLICATION NUMBER: US/10/993,543
;  CURRENT FILING DATE:  2004-11-19
;  PRIOR APPLICATION NUMBER: US 60/523,745
;  PRIOR FILING DATE: 2003-11-19
;  NUMBER OF SEQ ID NOS: 299
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 274
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-993-543-274

  Query Match            100.0%;  Score 86;  DB 6;  Length 95;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 19
US-10-993-543-276
; Sequence 276, Application US/10993543
; Publication No. US20060036076A1
; GENERAL INFORMATION:
;  APPLICANT: Dransfield, Daniel T.
;  APPLICANT:  Rookey, Kristin
;  APPLICANT:  Ladner, Robert C.
;  TITLE OF INVENTION: Metalloproteinase-Binding Proteins
;  FILE REFERENCE: 10280-088001
;  CURRENT APPLICATION NUMBER: US/10/993,543
;  CURRENT FILING DATE:  2004-11-19
;  PRIOR APPLICATION NUMBER: US 60/523,745
;  PRIOR FILING DATE: 2003-11-19
;  NUMBER OF SEQ ID NOS: 299
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 276
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-993-543-276

  Query Match            100.0%;  Score 86;  DB 6;  Length 95;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 20
US-10-993-543-278
; Sequence 278, Application US/10993543
; Publication No. US20060036076A1
; GENERAL INFORMATION:
;  APPLICANT: Dransfield, Daniel T.
;  APPLICANT:  Rookey, Kristin
;  APPLICANT:  Ladner, Robert C.
;  TITLE OF INVENTION: Metalloproteinase-Binding Proteins
;  FILE REFERENCE: 10280-088001
;  CURRENT APPLICATION NUMBER: US/10/993,543
;  CURRENT FILING DATE:  2004-11-19
;  PRIOR APPLICATION NUMBER: US 60/523,745
;  PRIOR FILING DATE: 2003-11-19
;  NUMBER OF SEQ ID NOS: 299
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 278
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-993-543-278

  Query Match            100.0%;  Score 86;  DB 6;  Length 95;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 21
US-10-993-543-283
; Sequence 283, Application US/10993543
; Publication No. US20060036076A1
; GENERAL INFORMATION:
;  APPLICANT: Dransfield, Daniel T.
;  APPLICANT:  Rookey, Kristin
;  APPLICANT:  Ladner, Robert C.
;  TITLE OF INVENTION: Metalloproteinase-Binding Proteins
;  FILE REFERENCE: 10280-088001
;  CURRENT APPLICATION NUMBER: US/10/993,543
;  CURRENT FILING DATE:  2004-11-19
;  PRIOR APPLICATION NUMBER: US 60/523,745
;  PRIOR FILING DATE: 2003-11-19
;  NUMBER OF SEQ ID NOS: 299
;  SOFTWARE: PatentIn version 3.3
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; SEQ ID NO 283
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-993-543-283

  Query Match             100.0%;  Score 86;  DB 6;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 22
US-11-054-669-54
; Sequence 54, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
;  FILE REFERENCE: 30219/US/3
;  CURRENT APPLICATION NUMBER: US/11/054,669
;  CURRENT FILING DATE:  2005-02-08
;  PRIOR APPLICATION NUMBER: US 10/194,975
;  PRIOR FILING DATE: 2002-07-12
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 54
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-669-54

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 23
US-11-054-669-55
; Sequence 55, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
;  FILE REFERENCE: 30219/US/3
;  CURRENT APPLICATION NUMBER: US/11/054,669
;  CURRENT FILING DATE:  2005-02-08
;  PRIOR APPLICATION NUMBER: US 10/194,975
;  PRIOR FILING DATE: 2002-07-12
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-669-55

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 24
US-11-054-669-56
; Sequence 56, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
;  FILE REFERENCE: 30219/US/3
;  CURRENT APPLICATION NUMBER: US/11/054,669
;  CURRENT FILING DATE:  2005-02-08
;  PRIOR APPLICATION NUMBER: US 10/194,975
;  PRIOR FILING DATE: 2002-07-12
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 56
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-669-56

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 25
US-11-054-669-57
; Sequence 57, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
;  FILE REFERENCE: 30219/US/3
;  CURRENT APPLICATION NUMBER: US/11/054,669
;  CURRENT FILING DATE:  2005-02-08
;  PRIOR APPLICATION NUMBER: US 10/194,975
;  PRIOR FILING DATE: 2002-07-12
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 57
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-669-57

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 26
US-11-054-669-63
; Sequence 63, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
```

```
;  FILE REFERENCE: 30219/US/3
;  CURRENT APPLICATION NUMBER: US/11/054,669
;  CURRENT FILING DATE:  2005-02-08
;  PRIOR APPLICATION NUMBER: US 10/194,975
;  PRIOR FILING DATE: 2002-07-12
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 63
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-669-63

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 27
US-11-054-669-64
; Sequence 64, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
;  FILE REFERENCE: 30219/US/3
;  CURRENT APPLICATION NUMBER: US/11/054,669
;  CURRENT FILING DATE:  2005-02-08
;  PRIOR APPLICATION NUMBER: US 10/194,975
;  PRIOR FILING DATE: 2002-07-12
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 64
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-669-64

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 28
US-11-054-669-65
; Sequence 65, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
;  FILE REFERENCE: 30219/US/3
;  CURRENT APPLICATION NUMBER: US/11/054,669
;  CURRENT FILING DATE:  2005-02-08
;  PRIOR APPLICATION NUMBER: US 10/194,975
;  PRIOR FILING DATE: 2002-07-12
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 65
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-669-65

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 29
US-11-054-669-66
; Sequence 66, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
;  FILE REFERENCE: 30219/US/3
;  CURRENT APPLICATION NUMBER: US/11/054,669
;  CURRENT FILING DATE:  2005-02-08
;  PRIOR APPLICATION NUMBER: US 10/194,975
;  PRIOR FILING DATE: 2002-07-12
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-669-66

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 30
US-11-054-669-67
; Sequence 67, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
;  FILE REFERENCE: 30219/US/3
;  CURRENT APPLICATION NUMBER: US/11/054,669
;  CURRENT FILING DATE:  2005-02-08
;  PRIOR APPLICATION NUMBER: US 10/194,975
;  PRIOR FILING DATE: 2002-07-12
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 67
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-669-67

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49
```

```
RESULT 31
US-11-054-669-69
; Sequence 69, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
;  FILE REFERENCE: 30219/US/3
;  CURRENT APPLICATION NUMBER: US/11/054,669
;  CURRENT FILING DATE:  2005-02-08
;  PRIOR APPLICATION NUMBER: US 10/194,975
;  PRIOR FILING DATE: 2002-07-12
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 69
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-669-69

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 32
US-11-054-669-71
; Sequence 71, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
;  FILE REFERENCE: 30219/US/3
;  CURRENT APPLICATION NUMBER: US/11/054,669
;  CURRENT FILING DATE:  2005-02-08
;  PRIOR APPLICATION NUMBER: US 10/194,975
;  PRIOR FILING DATE: 2002-07-12
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 71
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-669-71

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 33
US-11-054-669-72
; Sequence 72, Application US/11054669
; Publication No. US20050261480A1
; GENERAL INFORMATION:
;  APPLICANT: Foote, Jefferson
;  TITLE OF INVENTION: SUPER HUMANIZED ANTIBODIES
;  FILE REFERENCE: 30219/US/3
;  CURRENT APPLICATION NUMBER: US/11/054,669
;  CURRENT FILING DATE:  2005-02-08
;  PRIOR APPLICATION NUMBER: US 10/194,975
;  PRIOR FILING DATE: 2002-07-12
;  PRIOR APPLICATION NUMBER: US 60/305,111
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 124
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 72
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-054-669-72

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 34
US-11-084-554-123
; Sequence 123, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 123
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-123

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 35
US-11-084-554-124
; Sequence 124, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
```

```
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 124
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-124

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 36
US-11-084-554-128
; Sequence 128, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 128
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-128

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 37
US-11-084-554-129
; Sequence 129, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 129
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-129

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 38
US-11-084-554-136
; Sequence 136, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 136
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-136

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 39
US-11-084-554-137
; Sequence 137, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 137
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-137

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
```

```
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 40
US-11-084-554-139
; Sequence 139, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 139
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-139

  Query Match            100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 41
US-11-084-554-140
; Sequence 140, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 140
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-140

  Query Match            100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 42
US-11-084-554-143
; Sequence 143, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 143
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-143

  Query Match            100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 43
US-11-084-554-145
; Sequence 145, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 145
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-145

  Query Match            100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              ||||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 44
US-11-084-554-146
; Sequence 146, Application US/11084554
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; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 146
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-146

  Query Match            100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 45
US-11-084-554-148
; Sequence 148, Application US/11084554
; Publication No. US20050260679A1
; GENERAL INFORMATION:
;  APPLICANT: Kellermann, Sirid-Ai
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Korver, Wouter
;  TITLE OF INVENTION: REDUCING THE RISK OF HUMAN ANTI-HUMAN
;  TITLE OF INVENTION:  ANTIBODIES THROUGH V GENE MANIPULATION
;  FILE REFERENCE: ABGENIX.100A
;  CURRENT APPLICATION NUMBER: US/11/084,554
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: 60/554,372
;  PRIOR FILING DATE: 2004-03-19
;  PRIOR APPLICATION NUMBER: 60/574,661
;  PRIOR FILING DATE: 2004-05-24
;  NUMBER OF SEQ ID NOS: 266
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 148
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-084-554-148

  Query Match            100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 46
US-11-061-848-33
; Sequence 33, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
;  APPLICANT: Wilson, David S.
;  APPLICANT:  Nock, Steffen
;  APPLICANT:  Larrick, James W.
;  TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
;  FILE REFERENCE: 186280/US
;  CURRENT APPLICATION NUMBER: US/11/061,848
;  CURRENT FILING DATE:  2005-02-17
;  PRIOR APPLICATION NUMBER: US 60/545,011
;  PRIOR FILING DATE: 2004-02-17
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 33
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-061-848-33

  Query Match            100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 47
US-11-061-848-36
; Sequence 36, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
;  APPLICANT: Wilson, David S.
;  APPLICANT:  Nock, Steffen
;  APPLICANT:  Larrick, James W.
;  TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
;  FILE REFERENCE: 186280/US
;  CURRENT APPLICATION NUMBER: US/11/061,848
;  CURRENT FILING DATE:  2005-02-17
;  PRIOR APPLICATION NUMBER: US 60/545,011
;  PRIOR FILING DATE: 2004-02-17
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 36
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-061-848-36

  Query Match            100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity  100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 48
US-11-061-848-37
; Sequence 37, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
;  APPLICANT: Wilson, David S.
;  APPLICANT:  Nock, Steffen
;  APPLICANT:  Larrick, James W.
;  TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
;  FILE REFERENCE: 186280/US
;  CURRENT APPLICATION NUMBER: US/11/061,848
;  CURRENT FILING DATE:  2005-02-17
;  PRIOR APPLICATION NUMBER: US 60/545,011
;  PRIOR FILING DATE: 2004-02-17
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 37
;   LENGTH: 95
;   TYPE: PRT
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;   ORGANISM: Homo sapiens
US-11-061-848-37

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 49
US-11-061-848-40
; Sequence 40, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
;  APPLICANT: Wilson, David S.
;  APPLICANT:  Nock, Steffen
;  APPLICANT:  Larrick, James W.
;  TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
;  FILE REFERENCE: 186280/US
;  CURRENT APPLICATION NUMBER: US/11/061,848
;  CURRENT FILING DATE:  2005-02-17
;  PRIOR APPLICATION NUMBER: US 60/545,011
;  PRIOR FILING DATE: 2004-02-17
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 40
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-061-848-40

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49


RESULT 50
US-11-061-848-41
; Sequence 41, Application US/11061848
; Publication No. US20050288491A1
; GENERAL INFORMATION:
;  APPLICANT: Wilson, David S.
;  APPLICANT:  Nock, Steffen
;  APPLICANT:  Larrick, James W.
;  TITLE OF INVENTION: SUPER-HUMANIZED ANTIBODIES AGAINST RESPIRATORY SYNCYTIAL VIRUS
;  FILE REFERENCE: 186280/US
;  CURRENT APPLICATION NUMBER: US/11/061,848
;  CURRENT FILING DATE:  2005-02-17
;  PRIOR APPLICATION NUMBER: US 60/545,011
;  PRIOR FILING DATE: 2004-02-17
;  NUMBER OF SEQ ID NOS: 78
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41
;   LENGTH: 95
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-061-848-41

  Query Match             100.0%;  Score 86;  DB 7;  Length 95;
  Best Local Similarity   100.0%;  Pred. No. 3.1e-06;
  Matches   15;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 WYQQKPGKAPKLLIY 15
              |||||||||||||||
Db         35 WYQQKPGKAPKLLIY 49
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